(12) STANDARD PATENT (11) Application No. **AU 2017267665 C1**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Modulatory polynucleotides

(51) International Patent Classification(s)
C12N 15/113 (2010.01) ***C12N 15/85*** (2006.01)

(21) Application No: **2017267665** (22) Date of Filing: **2017.05.18**

(87) WIPO No: **WO17/201248**

(30) Priority Data

(31) Number	(32) Date	(33) Country
62/338,137	**2016.05.18**	**US**
62/485,050	**2017.04.13**	**US**

(43) Publication Date: **2017.11.23**
(44) Accepted Journal Date: **2023.03.16**
(44) Amended Journal Date: **2023.10.05**

(71) Applicant(s)
Voyager Therapeutics, Inc.

(72) Inventor(s)
Sah, Dinah Wen-Yee;Hou, Jinzhao;Nonnenmacher, Mathieu

(74) Agent / Attorney
Griffith Hack, Level 10 161 Collins St, MELBOURNE, VIC, 3000, AU

(56) Related Art
WO 2013/126605 A1

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) **World Intellectual Property Organization**
International Bureau

(43) **International Publication Date**
23 November 2017 (23.11.2017)

(10) **International Publication Number**
WO 2017/201248 A1

(51) **International Patent Classification:**
C12N 15/113 (2010.01) *C12N 15/85* (2006.01)

(21) **International Application Number:**
PCT/US2017/033268

(22) **International Filing Date:**
18 May 2017 (18.05.2017)

(25) **Filing Language:** English

(26) **Publication Language:** English

(30) **Priority Data:**
62/338,137 18 May 2016 (18.05.2016) US
62/485,050 13 April 2017 (13.04.2017) US

(71) **Applicant: VOYAGER THERAPEUTICS, INC.** [US/US]; 75 SIDNEY STREET, CAMBRIDGE, Massachusetts 02139 (US).

(72) **Inventors: SAH, Dinah Wen-Yee**; 75 Sidney Street, Cambridge, Massachusetts 02139 (US). **HOU, Jinzhao**; 75 Sidney Street, Cambridge, Massachusetts 02139 (US). **NONNENMACHER, Mathieu**; 75 Sidney Street, Cambridge, Massachusetts 02139 (US).

(74) **Agent: WARD, Donna T.** et al.; DT WARD, PC, 142A Main Street, Groton, Massachusetts 01450 (US).

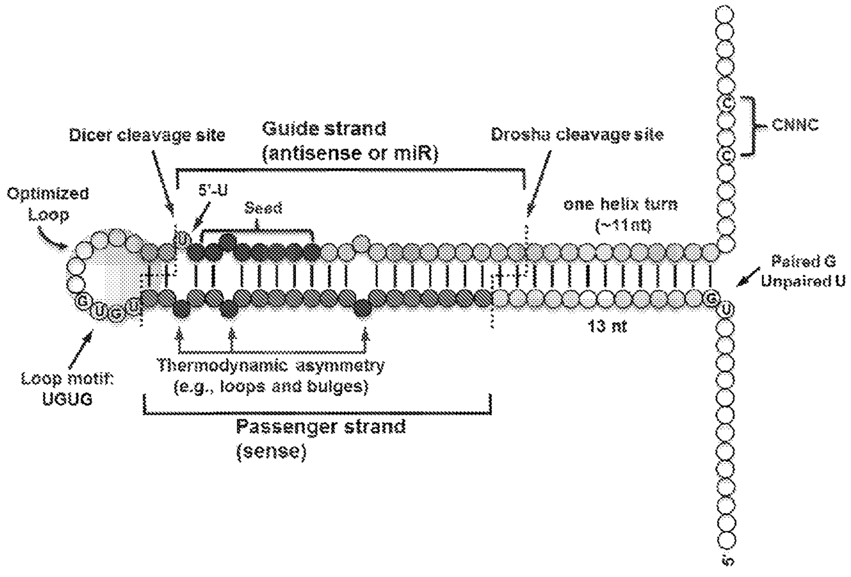
(81) **Designated States** *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report (Art. 21(3))*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
— *with sequence listing part of description (Rule 5.2(a))*

(54) **Title:** MODULATORY POLYNUCLEOTIDES

FIG. 1



(57) **Abstract:** The invention relates to compositions and methods for the preparation, manufacture and therapeutic use of modulatory polynucleotides.

WO 2017/201248 A1

MODULATORY POLYNUCLEOTIDES

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to US Provisional Patent Application No. 62/338,137, filed on May 18, 2016, entitled Modulatory Polynucleotides, and US Provisional Patent Application No. 62/485,050, filed on April 13, 2017, entitled Modulatory Polynucleotides, the contents each of which are herein incorporated by reference in their entireties.

REFERENCE TO THE SEQUENCE LISTING

[0002] The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled 20571039PCT.txt, created on May 18, 2017, which is 4,301,289 bytes in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

[0003] The invention relates to compositions, methods, processes, kits and devices for the design, preparation, manufacture and/or formulation of modulatory polynucleotides. In some embodiments such modulatory polynucleotides may be encoded by or within recombinant adeno-associated viruses (AAV) and may comprise artificial microRNAs, artificial pre-microRNAs and/or artificial pri-microRNAs.

BACKGROUND OF THE INVENTION

[0004] MicroRNAs (or miRNAs or miRs) are small, non-coding, single stranded ribonucleic acid molecules (RNAs), which are usually 19-25 nucleotides in length. More than a thousand microRNAs have been identified in mammalian genomes. The mature microRNAs primarily bind to the 3’ untranslated region (3’-UTR) of target messenger RNAs (mRNAs) through partially or fully pairing with the complementary sequences of target mRNAs, promoting the degradation of target mRNAs at a post-transcriptional level, and in some cases, inhibiting the initiation of translation. MicroRNAs play a critical role in many key biological processes, such as the regulation of cell cycle and growth, apoptosis, cell proliferation and tissue development.

[0005] miRNA genes are generally transcribed as long primary transcripts of miRNAs (i.e. pri-miRNAs). The pri-miRNA is cleaved into a precursor of a miRNA (i.e. pre-miRNA) which is further processed to generate the mature and functional miRNA.

[0006] While many target expression strategies employ nucleic acid based modalities, there remains a need for improved nucleic acid modalities which have higher specificity and with fewer off target effects.

[0007] The present invention provides such improved modalities in the form of artificial pri-, pre- and mature microRNA constructs and methods of their design. These novel constructs may be synthetic stand-alone molecules or be encoded in a plasmid or expression vector for delivery to cells. Such vectors include, but are not limited to adeno-associated viral vectors such as vector genomes of any of the AAV serotypes or other viral delivery vehicles such as lentivirus, etc.

SUMMARY OF THE INVENTION

[0008] Described herein are compositions, methods, processes, kits and devices for the design, preparation, manufacture and/or formulation of modulatory polynucleotides.

[0009] In some embodiments such modulatory polynucleotides may be encoded by or contained within plasmids or vectors or recombinant adeno-associated viruses (AAV) and may comprise artificial microRNAs, artificial pre-microRNAs and/or artificial pri-microRNAs.

The present invention as claimed herein is described in the following items 1 to 26:

1. A modulatory polynucleotide comprising:

(a) a 5' flanking region comprising the nucleotide sequence of SEQ ID NO: 7;

(b) a loop region comprising the nucleotide sequence of SEQ ID NO: 16; and

(c) a 3' flanking region comprising the nucleotide sequence of SEQ ID NO: 26.

2. The modulatory polynucleotide of item 1, further comprising a passenger strand and a guide strand.

3. The modulatory polynucleotide of item 2, wherein the passenger strand is located between the 5' flanking region and the loop region and the guide strand is located between the loop region and the 3' flanking region.

4. The modulatory polynucleotide of item 2, wherein the guide strand is located between the 5' flanking region and the loop region and the passenger strand is located between the loop region and the 3' flanking region.

5. The modulatory polynucleotide of any one of items 2-5, wherein the guide strand, the passenger strand, or both the guide strand and the passenger strand are between 15-30 or 21-25 nucleotides in length.

6. The modulatory polynucleotide of any one of items 2-5, wherein the guide strand and the passenger strand are each 21 nucleotides in length.

7. The modulatory polynucleotide of any one of items 2-6, wherein:

(i) the passenger strand is at least 70% complementary to the guide strand; and/or

(ii) the guide strand is at least 60% complementary to a target RNA, wherein said target RNA is expressed in a neurologic cell, tissue or organ.

8. The modulatory polynucleotide of any one of items 1-7, wherein the modulatory polynucleotide targets the expression of a SOD1 gene.

9. The modulatory polynucleotide of any one of items 1-8, wherein the modulatory polynucleotide targets the expression of an HTT gene.

10. A viral genome which comprises a nucleic acid sequence positioned between two inverted terminal repeats (ITRs), wherein the nucleic acid sequence encodes the modulatory polynucleotide of any one of items 1-9.

11. The viral genome of item 10, which further comprises one, two, three, or all of:

(i) a promoter operably linked to the nucleotide sequence encoding the modulatory polynucleotide;

(ii) an enhancer;

(iii) an intron region; and

(iv) a poly A signal region.

12. The viral genome of item 11, wherein:

(i) the promoter is a CBA promoter, an H1 promoter, a PGK promoter, a synapsin promoter, a GFAP promoter, or an EF-1α promoter;

(ii) the enhancer is a CMV enhancer; or

(iii) the intron is an SV40 intron.

13. The viral genome of any one of items 10-12, wherein the viral genome is single stranded or self-complementary.

14. A recombinant adeno-associated virus (rAAV) comprising the viral genome of any one of items 10-13, and an AAV capsid protein.

15. The rAAV of item 14, comprising an AAV1 capsid protein or variant thereof, an AAV5 capsid protein or variant thereof, an AAVrh10 capsid protein or a variant thereof, or AAV9 capsid protein or a variant thereof.

16. A vector encoding the modulatory polynucleotide of any of items 1-9 or comprising the viral genome of any one of items 10-13.

17. A cell comprising the modulatory polynucleotide of any one of items 1-9, the viral genome of any one of items 10-13, the rAAV of item 14 or 25, or the vector of item 16.

18. The cell of item 17, which is a mammalian cell, an HEK293 cell, an insect cell, an Sf9 cell, a cell of the central nervous system, a neuron, medium spiny neuron, a motor neuron, or an astrocyte.

19. A pharmaceutical composition comprising the modulatory polynucleotide of any one of items 1-9, the viral genome of any one of items 10-13, or the rAAV of item 14 or 15, and a pharmaceutically acceptable excipient.

20. A composition comprising the modulatory polynucleotide of any one of items 1-9, the viral genome of any one of items 10-13, the rAAV of item 14 or 15, or the pharmaceutical composition of item 19, for use in treating a disease of the central nervous system.

21. A method of treating a disease of the central nervous system in a subject, the method comprising administering an effective amount of a composition comprising the modulatory polynucleotide of any one of items 1-9, the viral genome of any one of items 10-13, the rAAV of item 14 or 15, or the pharmaceutical composition of item 19 to the subject, thereby treating the disease of the central nervous system in the subject.

22. The composition for use of item 20, or the method of item 21, wherein the disease of the central nervous system is ALS.

23. The composition for use of any one of items 20-22, or the method of any one of items 21-22, where the composition is administered via intravenous administration or via intracisternal administration.

24. A method of producing a recombinant AAV, comprising providing a cell with a polynucleotide comprising the viral genome of any one of items 10-13, at least one polynucleotide encoding AAV rep genes, and at least one polynucleotide encoding AAV cap genes; and harvesting the recombinant AAV from the cell.

25. Use of the modulatory polynucleotide of any one of items 1-9, the viral genome of any one of items 10-13, the rAAV of item 14 or 15, or the pharmaceutical composition of item 19, in the manufacture of a medicament for treating a disease of the central nervous system in a subject.

[0010] The details of various embodiments of the invention are set forth in the description below. Other features, objects, and advantages of the invention will be apparent from the description and the drawings, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0010] The foregoing and other objects, features and advantages will be apparent from the following description of particular embodiments of the invention, as illustrated in the accompanying drawings in which like reference characters refer to the same parts throughout the different views. The drawings are not necessarily to scale, emphasis instead being placed upon illustrating the principles of various embodiments of the invention.

[0011] FIG. 1 is a schematic of an artificial pri-microRNA that is part of a viral genome packaged in an AAV vector according to the present invention. FIG. 1 discloses SEQ ID NO: 943.

[0012] FIG. 2 is a diagram showing the location of the modulatory polynucleotide (MP) in relation to the ITRs, the intron (I) and the polyA (P).

DETAILED DESCRIPTION

I. COMPOSITIONS OF THE INVENTION

Modulatory Polynucleotides

[0013] According to the present invention, modulatory polynucleotides are provided which function as artificial microRNAs. As used herein a “modulatory polynucleotide” is any nucleic acid polymer which functions to modulate (either increase or decrease) the level or amount of a target gene. Modulatory polynucleotides include precursor molecules which are processed inside the cell prior to modulation. Modulatory polynucleotides or the processed forms thereof may be encoded in a plasmid, vector, genome or other nucleic acid expression vector for delivery to a cell.

[0014] In one embodiment, the modulatory polynucleotides may comprise at least one nucleic acid sequence encoding at least one siRNA molecule. The nucleic acids may, independently if there is more than one, encode 1, 2, 3, 4, 5, 6, 7, 8, 9, or more than 9 siRNA molecules.

[0015] In some embodiments modulatory polynucleotides are designed as primary microRNA (pri-miRs) or precursor microRNAs (pre-miRs) which are processed within the cell to produce highly specific artificial microRNAs.

[0016] The modulatory polynucleotides, especially the artificial microRNAs of the invention, may be designed based on the sequence or structure scaffold of a canonical or known microRNA, pri-microRNA or pre-microRNA. Such sequences may correspond to any known microRNA or its precursor such as those taught in US Publication US2005/0261218 and US Publication US2005/0059005, the contents of which are incorporated herein by reference in their entirety.

[0017] microRNAs (or miRNA or miRs) are 19-25 nucleotide long noncoding RNAs that bind to the 3′UTR of nucleic acid molecules and down-regulate gene expression either by reducing nucleic acid molecule stability or by inhibiting translation. The modulatory polynucleotides of the invention may comprise one or more microRNA sequences, microRNA seeds or artificial microRNAs, e.g., sequences which function as a microRNA.

[0018] A microRNA sequence comprises a "seed" region, i.e., a sequence in the region of positions 2-9 of the mature microRNA, which sequence has perfect Watson-Crick complementarity to the miRNA target sequence. A microRNA seed may comprise positions 2-8 or 2-7 or 2-9 of the mature microRNA. In some embodiments, a microRNA seed may comprise 7 nucleotides (e.g., nucleotides 2-8 of the mature microRNA), wherein the seed-complementary site in the corresponding miRNA target is flanked by an adenine (A) opposed to microRNA position 1. In some embodiments, a microRNA seed may comprise 6 nucleotides (e.g., nucleotides 2-7 of the mature microRNA), wherein the seed-complementary site in the corresponding miRNA target is flanked by an adenine (A) opposed to microRNA position 1. See for example, Grimson A, Farh KK, Johnston WK, Garrett-Engele P, Lim LP, Bartel DP; Mol Cell. 2007 Jul 6;27(1):91-105; each of which is herein incorporated by reference in their entirety. In naturally occurring microRNA, the bases of the microRNA seed have complete complementarity with the target sequence.

[0019] As taught herein, design parameters, or rules, have been identified and applied to design modulatory polynucleotides (e.g., artificial microRNAs) which have superior target gene modulatory properties with limited off target effects.

[0020] In one embodiment, the molecular scaffold of the modulatory polynucleotide described herein may be designed and optimized to create a modulatory polynucleotide that has the desired target gene modulatory properties. As a non-limiting example, the modulatory polynucleotide can have superior target gene modulatory properties with limited off target effects.

[0021] In one embodiment, the modulatory polynucleotides of the invention, such as artificial miRs, are comprised of modular elements or sequence motifs assembled according to a set of rules that result in highly specific target recognition and low guide/passenger ratio. Such modules or sequence motifs include, but are not limited to, double stranded regions, flanking regions, loops, optimized loops, UGUG loops, GU domains, spacers (to control proximal and distal motif or module spacing or to introduce structural elements such as turns, loops or bulges), CNNC motifs, and thermodynamic asymmetry regions which may embrace loops, bulges, mismatches, wobbles, and/or combinations thereof. Non limiting examples of rules which may be applied alone or in combination when constructing artificial miRs include those taught in Seitz et al. *Silence* 2011, 2:4; Gu, et al., *Cell* 151, 900–911, November 9, 2012; Schwartz, et al., *Cell*, Vol. 115, 199–208, October 17, 2003; Park, et al., *Nature*, Vol. 475, 101, 14 July 2011; Ketley et al., 2013, *PLoS ONE* 8(6); Liu, et al., *Nucleic Acids Research*, 2008, Vol. 36, No. 9 2811–2824; Dow, et al., 2013, Nat Protoc. ; 7(2): 374–393. doi:10.1038/nprot.2011.446; Auyeung, et al., *Cell* 152, 844–858, February 14, 2013; Gu et al., *Cell* 2012 Nov 9, 151(4):900-11; Fellmann et al. Molecular Cell 41, 733-746, 2011; Han et al. Cell 125, 887-907, 2006; Betancur et al. Frontiers in Genetics, Vol. 3, Art. 127, 1-6 July 2012; Schwarz et al. Cell Vol 115, 199-208, 2003; the contents of each of which are herein incorporated by reference in their entirety.

[0022] In one embodiment, any of the known RNAi constructs or RNAi agents may serve as the starting construct for the design of the passenger and/or guide strand of a modulatory polynucleotides or artificial microRNAs of the invention. These include canonical siRNAs, small interfering RNAs (siRNA), double stranded RNAs (dsRNAs), inverted repeats, short hairpin RNAs (shRNAs), small temporally regulated RNAs (stRNA), clustered inhibitory RNAs (cRNAs), including radial clustered inhibitory RNA, asymmetric clustered inhibitory RNA, linear clustered inhibitory RNA, and complex or compound clustered inhibitory RNA, dicer substrates, DNA-directed RNAi (ddRNAi), single-stranded RNAi (ssRNAi), microRNA (miRNA) antagonists, microRNA mimics, microRNA agonists, blockmirs (a.k.a. Xmirs), microRNA mimetics, microRNA addbacks, supermiRs, the oligomeric constructs disclosed in PCT Publication WO/2005/013901 the contents of which are incorporated herein in their entirety, tripartite RNAi constructs such as those disclosed in US Publication 20090131360, the contents of which are incorporated herein in their entirety, the solo-rxRNA constructs disclosed in PCT Publication WO/2010/011346, the contents of which are incorporated herein by reference in their entirety; the sd-rxRNA constructs disclosed in PCT Publication WO/2010/033247 the contents of which are incorporated herein by reference in their entirety, dual acting RNAi constructs which reduce RNA levels and also modulate the immune response as disclosed in PCT Publications WO/2010/002851 and WO/2009/141146 the contents of which are incorporated herein by reference in their entirety and antigene RNAs (agRNA) or small activating RNAs (saRNAs) which increase expression of the target to which they are designed disclosed in PCT Publications WO/2006/130201, WO/2007/086990, WO/2009/046397, WO/2009/149182, WO/2009/086428 the contents of which are incorporated herein by reference in their entirety.

[0023] Likewise, any pri- or pre-microRNA precursor of the above listed microRNA may also serve as the molecular scaffold of the modulatory polynucleotides of the invention.

[0024] In one embodiment, the starting construct may be derived from any relevant species such as, not limited to, mouse, rat, dog, monkey or human.

[0025] In one embodiment, the modulatory polynucleotide may be located in an expression vector downstream of a promoter such as, but not limited to, CMV, U6, H1, CBA or a CBA promoter with a SV40 or a human betaGlobin intron. Further, the modulatory polynucleotide may also be located upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the modulatory polynucleotide may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the modulatory polynucleotide may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the modulatory polynucleotide may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the modulatory polynucleotide may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector.

[0026] In one embodiment, the modulatory polynucleotide may be located upstream of the polyadenylation sequence in an expression vector. Further, the modulatory polynucleotide may be located downstream of a promoter such as, but not limited to, CMV, U6, H1, CBA or a CBA promoter with a SV40 or a human betaGlobin intron in an expression vector. As a non-limiting example, the modulatory polynucleotide may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the modulatory polynucleotide may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the modulatory polynucleotide may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the modulatory polynucleotide may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector.

[0027] In one embodiment, the modulatory polynucleotide may be located in a scAAV.

[0028] In one embodiment, the modulatory polynucleotide may be located in an ssAAV.

[0029] In one embodiment, the modulatory polynucleotide may be located near the 5' end of the flip ITR in an expression vector. In another embodiment, the modulatory polynucleotide may be located near the 3'end of the flip ITR in an expression vector. In yet another embodiment, the modulatory polynucleotide may be located near the 5' end of the flop ITR in an expression vector. In yet another embodiment, the modulatory polynucleotide may be located near the 3' end of the flop ITR in an expression vector. In one embodiment, the modulatory polynucleotide may be located between the 5' end of the flip ITR and the 3' end of the flop ITR in an expression vector. In one embodiment, the modulatory polynucleotide may be located between (e.g., half-way between the 5' end of the flip ITR and 3' end of the flop ITR or the 3' end of the flop ITR and the 5' end of the flip ITR), the 3' end of the flip ITR and the 5' end of the flip ITR in an expression vector. As a non-limiting example, the modulatory polynucleotide may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As a non-limiting example, the modulatory polynucleotide may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the modulatory polynucleotide may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the modulatory polynucleotide may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As a non-limiting example, the modulatory polynucleotide may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the modulatory polynucleotide may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector.

[0030] In addition to the modules or sequence motifs, modulatory polynucleotides comprise at least one of or both a passenger and guide strand. The passenger and guide strand may be positioned or located on the 5' arm or 3' arm of a stem loop structure of the modulatory polynucleotide.

[0031] In one embodiment, the 3' stem arm of the modulatory polynucleotides may have 11 nucleotides downstream of the 3' end of the guide strand which have complementarity to the 11 of the 13 nucleotides upstream of the 5' end of the passenger strand in the 5' stem arm.

[0032] In one embodiment, the modulatory polynucleotides may have a cysteine which is 6 nucleotides downstream of the 3' end of the 3' stem arm of the modulatory polynucleotide.

[0033] In one embodiment, the modulatory polynucleotides comprise a miRNA seed match for the guide strand. In another embodiment, the modulatory polynucleotides comprise a miRNA seed match for the passenger strand. In yet another embodiment, the modulatory polynucleotides do no comprise a seed match for the guide or passenger strand.

[0034] In one embodiment, the modulatory polynucleotides may have almost no significant full-length off targets for the guide strand. In another embodiment, the modulatory polynucleotides may have almost no significant full-length off targets for the passenger strand. In yet another embodiment, the modulatory polynucleotides may have almost no significant full-length off targets for the guide strand or the passenger strand.

[0035] In one embodiment, the modulatory polynucleotides may have high activity *in vitro*. In another embodiment, the modulatory polynucleotides may have low activity *in vitro*. In yet another embodiment, the modulatory polynucleotides may have high guide strand activity and low passenger strand activity *in vitro*.

[0036] In one embodiment, the modulatory polynucleotides have a high guide strand activity and low passenger strand activity *in vitro*. The target knock-down (KD) by the guide strand may be at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 99.5% or 100%. The target knock-down by the guide strand may be 60-65%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 60-99%, 60-99.5%, 60-100%, 65-70%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 65-99%, 65-99.5%, 65-100%, 70-75%, 70-80%, 70-85%, 70-90%, 70-95%, 70-99%, 70-99.5%, 70-100%, 75-80%, 75-85%, 75-90%, 75-95%, 75-99%, 75-99.5%, 75-100%, 80-85%, 80-90%, 80-95%, 80-99%, 80-99.5%, 80-100%, 85-90%, 85-95%, 85-99%, 85-99.5%, 85-100%, 90-95%, 90-99%, 90-99.5%, 90-100%, 95-99%, 95-99.5%, 95-100%, 99-99.5%, 99-100% or 99.5-100%. As a non-limiting example, the target knock-down (KD) by the guide strand is greater than 70%.

[0037] In one embodiment, the IC50 of the passenger strand for the nearest off target is greater than 100 multiplied by the IC50 of the guide strand for the target. As a non-limiting example, if the IC50 of the passenger strand for the nearest off target is greater than 100 multiplied by the IC50 of the guide strand for the target then the modulatory polynucleotide is said to have high guide strand activity and a low passenger strand activity *in vitro*.

[0038] In one embodiment, the 5' processing of the guide strand has a correct start (n) at the 5' end at least 75%, 80%, 85%, 90%, 95%, 99% or 100% of the time *in vitro* or *in vivo*. As a non-limiting example, the 5' processing of the guide strand is precise and has a correct start (n) at the 5' end at least 99% of the time *in vitro*. As a non-limiting example, the 5' processing of the guide strand is precise and has a correct start (n) at the 5' end at least 99% of the time *in vivo*.

[0039] In one embodiment, the guide-to-passenger (G:P) strand ratio is 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1;1, 2:10, 2:9, 2:8, 2:7, 2:6, 2:5, 2:4, 2:3, 2:2, 2:1, 3:10, 3:9, 3:8, 3:7, 3:6, 3:5, 3:4, 3:3, 3:2, 3:1, 4:10, 4:9, 4:8, 4:7, 4:6, 4:5, 4:4, 4:3, 4:2, 4:1, 5:10, 5:9, 5:8, 5:7, 5:6, 5:5, 5:4, 5:3, 5:2, 5:1, 6:10, 6:9, 6:8, 6:7, 6:6, 6:5, 6:4, 6:3, 6:2, 6:1, 7:10, 7:9, 7:8, 7:7, 7:6, 7:5, 7:4, 7:3, 7:2, 7:1, 8:10, 8:9, 8:8, 8:7, 8:6, 8:5, 8:4, 8:3, 8:2, 8:1, 9:10, 9:9, 9:8, 9:7, 9:6, 9:5, 9:4, 9:3, 9:2, 9:1, 10:10, 10:9, 10:8, 10:7, 10:6, 10:5, 10:4, 10:3, 10:2, 10:1, 1:99, 5:95, 10:90, 15:85, 20:80, 25:75, 30:70, 35:65, 40:60, 45:55, 50:50, 55:45, 60:40, 65:35, 70:30, 75:25, 80:20, 85:15, 90:10, 95:5, or 99:1 *in vitro* or *in vivo.*

[0040] The guide to passenger ratio refers to the ratio of the guide strands to the passenger strands after the excision of the guide strand. For example, a 80:20 guide to passenger ratio would have 8 guide strands to every 2 passenger strands clipped out of the precursor. As a non-limiting example, the guide-to-passenger strand ratio is 8:2 *in vitro.* As a non-limiting example, the guide-to-passenger strand ratio is 8:2 *in vivo.* As a non-limiting example, the guide-to-passenger strand ratio is 9:1 *in vitro.* As a non-limiting example, the guide-to-passenger strand ratio is 9:1 *in vivo.*

[0041] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is greater than 1.

[0042] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is greater than 2.

[0043] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is greater than 5.

[0044] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is greater than 10.

[0045] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is greater than 20.

[0046] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is greater than 50.

[0047] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is at least 3:1.

[0048] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is at least 5:1.

[0049] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is at least 10:1.

[0050] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is at least 20:1.

[0051] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is at least 50:1.

[0052] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1;1, 2:10, 2:9, 2:8, 2:7, 2:6, 2:5, 2:4, 2:3, 2:2, 2:1, 3:10, 3:9, 3:8, 3:7, 3:6, 3:5, 3:4, 3:3, 3:2, 3:1, 4:10, 4:9, 4:8, 4:7, 4:6, 4:5, 4:4, 4:3, 4:2, 4:1, 5:10, 5:9, 5:8, 5:7, 5:6, 5:5, 5:4, 5:3, 5:2, 5:1, 6:10, 6:9, 6:8, 6:7, 6:6, 6:5, 6:4, 6:3, 6:2, 6:1, 7:10, 7:9, 7:8, 7:7, 7:6, 7:5, 7:4, 7:3, 7:2, 7:1, 8:10, 8:9, 8:8, 8:7, 8:6, 8:5, 8:4, 8:3, 8:2, 8:1, 9:10, 9:9, 9:8, 9:7, 9:6, 9:5, 9:4, 9:3, 9:2, 9:1, 10:10, 10:9, 10:8, 10:7, 10:6, 10:5, 10:4, 10:3, 10:2, 10:1, 1:99, 5:95, 10:90, 15:85, 20:80, 25:75, 30:70, 35:65, 40:60, 45:55, 50:50, 55:45, 60:40, 65:35, 70:30, 75:25, 80:20, 85:15, 90:10, 95:5, or 99:1 *in vitro* or *in vivo.* The passenger to guide ratio refers to the ratio of the passenger strands to the guide strands after the excision of the guide strand. For example, a 80:20 passenger to guide ratio would have 8 passenger strands to every 2 guide strands clipped out of the precursor. As a non-limiting example, the passenger-to-guide strand ratio is 80:20 *in vitro.* As a non-limiting example, the passenger-to-guide strand ratio is 80:20 *in vivo.* As a non-limiting example, the passenger-to-guide strand ratio is 8:2 *in vitro.* As a non-limiting example, the passenger-to-guide strand ratio is 8:2 *in vivo.* As a non-limiting example, the passenger-to-guide strand ratio is 9:1 *in vitro.* As a non-limiting example, the passenger-to-guide strand ratio is 9:1 *in vivo.*

[0053] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is greater than 1.

[0054] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is greater than 2.

[0055] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is greater than 5.

[0056] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is greater than 10.

[0057] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is greater than 20.

[0058] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is greater than 50.

[0059] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is at least 3:1.

[0060] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is at least 5:1.

[0061] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is at least 10:1.

[0062] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is at least 20:1.

[0063] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is at least 50:1.

[0064] In one embodiment, a passenger-guide strand duplex is considered effective when the pri- or pre-microRNAs demonstrate, but methods known in the art and described herein, greater than 2-fold guide to passenger strand ratio when processing is measured. As a non-limiting examples, the pri- or pre-microRNAs demonstrate great than 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 11-fold, 12-fold, 13-fold, 14-fold, 15-fold, or 2 to 5-fold, 2 to 10-fold, 2 to 15-fold, 3 to 5-fold, 3 to 10-fold, 3 to 15-fold, 4 to 5-fold, 4 to 10-fold, 4 to 15-fold, 5 to 10-fold, 5 to 15-fold, 6 to 10-fold, 6 to 15-fold, 7 to 10-fold, 7 to 15-fold, 8 to 10-fold, 8 to 15-fold, 9 to 10-fold, 9 to 15-fold, 10 to 15-fold, 11 to 15-fold, 12 to 15-fold, 13 to 15-fold, or 14 to 15-fold guide to passenger strand ratio when processing is measured.

[0065] In one embodiment, the integrity of the vector genome is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99% of the full length of the construct.

Target nucleic acids

[0066] The modulatory polynucleotides of the invention may be targeted to any gene or nucleic acid construct including coding and non-coding genes. Genes (DNA or mRNA) that encode human or primate proteins may be targeted. Further, non-coding genes may also be targeted, e.g., long noncoding RNAs (lncRNA).

[0067] Examples of such lncRNA molecules and RNAi constructs designed to target such lncRNA any of which may be targeted by or encoded in the modulatory polynucleotides, respectively are taught in International Publication, WO2012/018881 A2, the contents of which are incorporated herein by reference in their entirety.

[0068] In one embodiment, the modulatory polynucleotides of the invention may target any gene known in the art. As a non-limiting example, the gene may be SOD1.

[0069] In one embodiment, the modulatory polynucleotides of the invention may target any gene known in the art. As a non-limiting example, the gene may be Htt.

[0070] In one embodiment, the modulatory polynucleotide may be designed to target any gene or mRNA in the human genome, e.g., genes associated with CNS disorders such as, but not limited to, Huntington's Disease, ALS and the like.

Molecular Scaffolds

[0071] In some embodiments the starting molecular scaffold of the modulatory polynucleotide is a known or wild type pri- or pre-microRNA. In other embodiments the molecular scaffold of the modulatory polynucleotides is designed *ab initio.* (See Cullen, *Gene Therapy* (2006) 13, 503–

508 work with miR30; Chung, et al., *Nucleic Acids Research*, 2006, Vol. 34, No. 7 working with miR-155; the contents of which are herein incorporated by reference in their entirety).

[0072] As used herein a “molecular scaffold” is a framework or starting molecule that forms the sequence or structural basis against which to design or make a subsequent molecule.

[0073] The modulatory polynucleotides of the present invention may be designed as a pri-miR as shown in FIG. 1. In the figure, a pri-miR molecular scaffold is shown. The modulatory polynucleotide which comprises the payload (e.g., siRNA, miRNA or other RNAi agent described herein) comprises a leading 5’ flanking sequence which may be of any length and may be derived in whole or in part from wild type microRNA sequence or be completely artificial.

[0074] In one embodiment, the molecular scaffold comprises at least one 5’ flanking region. As a non-limiting example, the 5’ flanking region may comprise a 5’ flanking sequence which may be of any length and may be derived in whole or in part from wild type microRNA sequence or be a completely artificial sequence.

[0075] In one embodiment, the molecular scaffold comprises at least one 3’ flanking region. As a non-limiting example, the 3’ flanking region may comprise a 3’ flanking sequence which may be of any length and may be derived in whole or in part from wild type microRNA sequence or be a completely artificial sequence.

[0076] In one embodiment, the molecular scaffold comprises at least one loop motif region. As a non-limiting example, the loop motif region may comprise a sequence which may be of any length.

[0077] In one embodiment, the molecular scaffold comprises a 5’ flanking region, a loop motif region and/or a 3’ flanking region.

[0078] In one embodiment, at least one payload (e.g., siRNA, miRNA or other RNAi agent described herein) may be encoded by a modulatory polynucleotide which may also comprise at least one molecular scaffold. The molecular scaffold may comprise a 5’ flanking sequence and/or a 3’ flanking sequence which may be of any length and may be derived in whole or in part from wild type microRNA sequence or be completely artificial. The 3’ flanking sequence may mirror the 5’ flanking sequence in size and origin. Either flanking sequence may be absent. The 3’ flanking sequence may optionally contain one or more CNNC motifs, where “N” represents any nucleotide.

[0079] Forming the stem of the stem loop structure shown is a minimum of the modulatory polynucleotide encoding at least one payload sequence. In some embodiments the payload sequence comprises at least one nucleic acid sequence which is in part complementary or will hybridize to a target sequence. In some embodiments the payload is a wild type microRNA. In some embodiments the payload is an siRNA molecule or fragment of an siRNA molecule. In some embodiments the payload is a substantially double stranded construct which may comprise one or more microRNAs, artificial microRNAs or siRNAs.

[0080] In some embodiments, the 5' arm of the stem loop of the modulatory polynucleotide comprises a nucleic acid sequence encoding a passenger strand. This strand is also known as the sense strand in that it reflects an identity to a target. The passenger strand may be between 15-30 nucleotides in length. It may be 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 nucleotides in length.

[0081] In some embodiments, the 3' arm of the stem loop of the modulatory polynucleotide comprises a nucleic acid sequence encoding a guide strand. This strand is also known as the antisense strand in that it reflects homology to a target. The guide strand may be between 15-30 nucleotides in length, 21-25 nucleotides or 22 nucleotides in length. It may be 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 nucleotides in length. The guide strand, in some instances, comprises a "G" nucleotide at the 5' most end.

[0082] In some embodiments, where the guide strand comprises a microRNA, or artificial microRNAs, the guide strand may comprise one or more microRNA seed sequences. The seed sequence may be located at positions 2-7, 2-8 or 2-9 of the guide strand relative to the first 5' nucleotide of the guide strand or relative to a dicer cleavage site.

[0083] In other embodiments, the passenger strand may reside on the 3' arm while the guide strand resides on the 5' arm of the stem of the stem loop structure of the modulatory polynucleotide.

[0084] The passenger and guide strands may be completely complementary across a substantial portion of their length. In other embodiments the passenger strand and guide strand may be at least 70, 80, 90, 95 or 99% complementary across independently at least 50, 60, 70, 80, 85, 90, 95, or 99 % of the length of the strands.

[0085] Neither the identity of the passenger strand nor the homology of the guide strand need be 100% complementary to the target sequence.

[0086] In one embodiment, separating the passenger and guide strand of the stem loop structure of the modulatory polynucleotide is a loop sequence (also known as a loop motif, linker or linker motif). The loop sequence may be of any length, between 4-30 nucleotides, between 4-20 nucleotides, between 4-15 nucleotides, between 5-15 nucleotides, between 6-12 nucleotides, 6 nucleotides, 7, nucleotides, 8 nucleotides, 9 nucleotides, 10 nucleotides, 11 nucleotides, 12 nucleotides, 13 nucleotides, 14 nucleotides, and/or 15 nucleotides.

[0087] In some embodiments the loop sequence comprises a nucleic acid sequence encoding at least one UGUG motif. In some embodiments, the nucleic acid sequence encoding the UGUG motif is located at the 5' terminus of the loop sequence.

[0088] In one embodiment, spacer regions may be present in the modulatory polynucleotide to separate one or more modules (e.g., 5' flanking region, loop motif region, 3' flanking region, sense sequences, antisense sequence) from one another. There may be one or more such spacer regions present.

[0089] In one embodiment a spacer region of between 8-20, i.e., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides may be present between the passenger strand and a flanking region sequence.

[0090] In one embodiment, the length of the spacer region is 13 nucleotides and is located between the 5' terminus of the passenger strand and the 3' terminus of the flanking sequence. In one embodiment a spacer is of sufficient length to form approximately one helical turn of the sequence.

[0091] In one embodiment a spacer region of between 8-20, i.e., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides may be present between the guide strand and a flanking sequence.

[0092] In one embodiment, the spacer sequence is between 10-13, i.e., 10, 11, 12 or 13 nucleotides and is located between the 3' terminus of the guide strand and the 5' terminus of a flanking sequence. In one embodiment a spacer is of sufficient length to form approximately one helical turn of the sequence.

[0093] In one embodiment the modulatory polynucleotide comprises at least one UG motif at the base of the stem whereby the G nucleotide is paired and the U nucleotide is unpaired. In some embodiments the unpaired U nucleotide is located in a flanking sequence.

[0094] In one embodiment, the modulatory polynucleotide comprises in the 5' to 3' direction, a 5' flanking sequence, a 5' arm, a loop motif, a 3' arm and a 3' flanking sequence. As a non-limiting example, the 5' arm may comprise a passenger strand and the 3' arm comprises the guide strand. In another non-limiting example, the 5' arm comprises the guide strand and the 3' arm comprises the passenger strand.

[0095] In one embodiment, the 5' arm, payload (e.g., passenger and/or guide strand), loop motif and/or 3' arm sequence may be altered (e.g., substituting 1 or more nucleotides, adding nucleotides and/or deleting nucleotides). The alteration may cause a beneficial change in the function of the construct (e.g., increase knock-down of the target sequence, reduce degradation of the construct, reduce off target effect, increase efficiency of the payload, and reduce degradation of the payload).

[0096] In one embodiment, the passenger strand sequence may be altered (e.g., substituting 1 or more nucleotides, adding nucleotides and/or deleting nucleotides). As a non-limiting example, the passenger strand sequence may comprise 1 or 2 substitutions within the last 4 nucleotides of the sequence (e.g., C substituted for a G). As another non-limiting example, the passenger strand sequence may comprise 1 or 2 substitutions within the 7-15 nucleotides from the 5'end of the sequence (e.g., U substituted for an A or C substituted for a G).

[0097] In one embodiment, the 3' arm strand sequence may be altered (e.g., substituting 1 or more nucleotides, adding nucleotides and/or deleting nucleotides). As a non-limiting example, the sequence of the 3' arm may comprise 1 or 2 substitutions within the first 4 nucleotides of the sequence (e.g., A substituted for a U).

[0098] In one embodiment, the molecular scaffold of the payload construct may comprise a 5' flanking region, a loop motif and a 3' flanking region. Between the 5' flanking region and the loop motif may be a first payload region and between the loop motif and the 3' flanking region may be a second payload region. The first and second payload regions may comprise siRNA, miRNA or other RNAi agents, fragments or variants described herein. The first and second payload regions may also comprise a sequence which is the same, different or complementary to each other. As a non-limiting example, the first payload region sequence may be a passenger strand of a siRNA construct and the second payload region sequence may be a guide strand of an siRNA construct. The passenger and guide sequences may be substantially complementary to each other. As another non-limiting example, the first payload region sequence may be a guide strand of a siRNA construct and the second payload region sequence may be a passenger strand of an siRNA construct. The passenger and guide sequences may be substantially complementary to each other.

[0099] In one embodiment, the molecular scaffold of the modulatory polynucleotides described herein may comprise a 5' flanking region, a loop motif region and a 3' flanking region. Non-limiting examples of the sequences for the 5' flanking region, loop motif region and the 3' flanking region which may be encoded by the modulatory polynucleotide described herein are shown in Tables 1-3.

Table 1. 5' Flanking Regions for Molecular Scaffold

5' Flanking Region Name	5' Flanking Region Sequence	5' Flanking Region SEQ ID NO
5F1	UUUAUGCCUCAUCCUCUGAGUGCUGAAGGCUUGCUGUAGGCUGUAUGCUG	1
5F2	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGCGCUCUUCGGAA	2
5F3	GAAGCAAAGAAGGGGCAGAGGGAGCCCGUGAGCUGAGUGGGCCAGGGACUGGGAGAAGGA	3

	GUGAGGAGGCAGGGCCGGCAUGCCUCUGCUGCUGGCCAGA	
5F4	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGCGCUCUUCGGGA	4
5F5	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGCGCUCCACGGAA	5
5F6	GGGCCCUCCCGCAGAACACCAUGCGCUCCACGGAA	6
5F7	CUCCCGCAGAACACCAUGCGCUCCACGGAA	7
5F8	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGCGCUCCACGGAAG	8
5F9	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGCGCUCCUCGGAA	9

Table 2. Loop Motif Regions for Molecular Scaffold

Loop Motif Region Name	Loop Motif Region Sequence	Loop Motif Region SEQ ID NO
L1	UGUGACCUGG	10
L2	UGUGAUUUGG	11
L3	UAUAAUUUGG	12
L4	CCUGACCCAGU	13
L5	GUCUGCACCUGUCACUAG	14
L6	GUGACCCAAG	15
L7	GUGGCCACUGAGAAG	16
L8	GUGACCCAAU	17
L9	GUGACCCAAC	18
L10	GUGGCCACUGAGAAA	19

Table 3. 3'Flanking Regions for Molecular Scaffold

3' Flanking Region Name	3' Flanking Region Sequence	3' Flanking Region SEQ ID NO
3F1	AGUGUAUGAUGCCUGUUACUAGCAUUCACAUGGAACAAAUUGCUGCCGUG	20
3F2	CUGAGGAGCGCCUUGACAGCAGCCAUGGGAGGGCCGCCCCCUACCUCAGUGA	21
3F3	CUGUGGAGCGCCUUGACAGCAGCCAUGGGAGGGCCGCCCCCUACCUCAGUGA	22
3F4	UGGCCGUGUAGUGCUACCCAGCGCUGGCUGCCUCCUCAGCAUUGCAAUUCCUCUCCCAUCUGGGCACCAGUCAGCUACCCUGGUGGGAAUCUGGGUAGCC	23
3F5	GGCCGUGUAGUGCUACCCAGCGCUGGCUGCCUCCUCAGCAUUGCAAUUCCUCUCCCAUCUGGGCACCAGUCAGCUACCCUGGUGGGAAUCUGGGUAGCC	24
3F6	UCCUGAGGAGCGCCUUGACAGCAGCCAUGGGAGGGCCGCCCCCUACCUCAGUGA	25
3F7	CUGAGGAGCGCCUUGACAGCAGCCAUGGGAGGGCC	26
3F8	CUGCGGAGCGCCUUGACAGCAGCCAUGGGAGGGCCGCCCCCUACCUCAGUGA	27

[00100] Any of the regions described in Tables 1-3, where U is T, may be used as modules in the molecular scaffolds described herein.

[00101] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5' flanking region listed in Table 1. As a non-limiting example, the 5' flanking region may be 5F1, 5F2, 5F3, 5F4, 5F5, 5F6, 5F7, 5F8 or 5F9.

[00102] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region.

[00103] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region.

[00104] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region.

[00105] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region.

[00106] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region.

[00107] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region.

[00108] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region.

[00109] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region.

[00110] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region.

[00111] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one one loop motif region listed in Table 2. As a non-limiting example, the loop motif region may be L1, L2, L3, L4, L5, L6, L7, L8, L9, or L10.

[00112] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00113] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00114] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00115] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00116] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00117] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00118] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00119] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00120] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00121] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00122] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3' flanking region listed in Table 3. As a non-limiting example, the molecular scaffold may comprise the 3' flanking region 3F1, 3F2, 3F3, 3F4, 3F5, 3F6, 3F7 or 3F8.

[00123] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3F1 flanking region.

[00124] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3F2 flanking region.

[00125] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3F3 flanking region.

[00126] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3F4 flanking region.

[00127] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3F5 flanking region.

[00128] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3F6 flanking region.

[00129] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3F7 flanking region.

[00130] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 3F8 flanking region.

[00131] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5' flanking region and at least one loop motif region as described in Tables 1 and 2. As a non-limiting example, the 5' flanking region and the loop motif region may be 5F1 and L1, 5F1 and L2, 5F1 and L3, 5F1 and L4, 5F1 and L5, 5F1 and L6, 5F1 and L7, 5F1 and L8, 5F1 and L9, 5F1 and L10, 5F1 and L11, 5F2 and L1, 5F2 and L2, 5F2 and L3, 5F2 and L4, 5F2 and L5, 5F2 and L6, 5F2 and L7, 5F2 and L8, 5F2 and L9, 5F2 and L10, 5F2 and L11, 5F3 and L1, 5F3 and L2, 5F3 and L3, 5F3 and L4, 5F3 and L5, 5F3 and L6, 5F3 and L7, 5F3 and L8, 5F3 and L9, 5F3 and L10, 5F3 and L11, 5F4 and L1, 5F4 and L2, 5F4 and L3, 5F4 and L4, 5F4 and L5, 5F4 and L6, 5F4 and L7, 5F4 and L8, 5F4 and L9, 5F4 and L10, 5F4 and L11, 5F5 and L1, 5F5 and L2, 5F5 and L3, 5F5 and L4, 5F5 and L5, 5F5 and L6, 5F5 and L7, 5F5 and L8, 5F5 and L9, 5F5 and L10, 5F5 and L11, 5F6 and L1, 5F6 and L2, 5F6 and L3, 5F6 and L4, 5F6 and L5, 5F6 and L6, 5F6 and L7, 5F6 and L8, 5F6 and L9, 5F6 and L10, 5F6 and L11, 5F7 and L1, 5F7 and L2, 5F7 and L3, 5F7 and L4, 5F7 and L5, 5F7 and L6, 5F7 and L7, 5F7 and L8, 5F7 and L9, 5F7 and L10, 5F7 and L11, 5F8 and L1, 5F8 and L2, 5F8 and L3, 5F8 and L4, 5F8 and L5, 5F8 and L6, 5F8 and L7, 5F8 and L8, 5F8 and L9, 5F8 and L10, 5F8 and L11, 5F9 and L1, 5F9 and L2, 5F9 and L3, 5F9 and L4, 5F9 and L5, 5F9 and L6, 5F9 and L7, 5F9 and L8, 5F9 and L9, 5F9 and L10, or 5F9 and L11.

[00132] In one embodiment, the molecular scaffold may comprise at least one 3' flanking region and at least one loop motif region as described in Tables 2 and 3. As a non-limiting example, the molecular scaffold may comprise 3F1 and L1, 3F1 and L2, 3F1 and L3, 3F1 and L4, 3F1 and L5, 3F1 and L6, 3F1 and L7, 3F1 and L8, 3F1 and L9, 3F1 and L10, 3F1 and L11, 3F2 and L1, 3F2 and L2, 3F2 and L3, 3F2 and L4, 3F2 and L5, 3F2 and L6, 3F2 and L7, 3F2 and L8, 3F2 and L9, 3F2 and L10, 3F2 and L11, 3F3 and L1, 3F3 and L2, 3F3 and L3, 3F3 and L4, 3F3 and L5, 3F3 and L6, 3F3 and L7, 3F3 and L8, 3F3 and L9, 3F3 and L10, 3F3 and L11, 3F4 and L1, 3F4 and L2, 3F4 and L3, 3F4 and L4, 3F4 and L5, 3F4 and L6, 3F4 and L7, 3F4 and L8, 3F4 and L9, 3F4 and L10, 3F4 and L11, 3F5 and L1, 3F5 and L2, 3F5 and L3, 3F5 and L4, 3F5 and L5, 3F5 and L6, 3F5 and L7, 3F5 and L8, 3F5 and L9, 3F5 and L10, 3F5 and L11, 3F6 and L1, 3F6 and L2, 3F6 and L3, 3F6 and L4, 3F6 and L5, 3F6 and L6, 3F6 and L7, 3F6 and L8, 3F6 and L9, 3F6 and L10, 3F6 and L11, 3F7 and L1, 3F7 and L2, 3F7 and L3, 3F7 and L4, 3F7 and L5, 3F7 and L6, 3F7 and L7, 3F7 and L8, 3F7 and L9, 3F7 and L10, 3F7 and L11, 3F8 and L1, 3F8 and L2, 3F8 and L3, 3F8 and L4, 3F8 and L5, 3F8 and L6, 3F8 and L7, 3F8 and L8, 3F8 and L9, 3F8 and L10, or 3F8 and L11.

[00133] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00134] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00135] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00136] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00137] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00138] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00139] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00140] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00141] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00142] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00143] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00144] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00145] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00146] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00147] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00148] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00149] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00150] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00151] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00152] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00153] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00154] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00155] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00156] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00157] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00158] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00159] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00160] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00161] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00162] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00163] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00164] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00165] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00166] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00167] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00168] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00169] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00170] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00171] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00172] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00173] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00174] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00175] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00176] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00177] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00178] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00179] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00180] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00181] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00182] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00183] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00184] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00185] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00186] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00187] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00188] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00189] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00190] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00191] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00192] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00193] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00194] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00195] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00196] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00197] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00198] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00199] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00200] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00201] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00202] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00203] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00204] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00205] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00206] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00207] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00208] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00209] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00210] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00211] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00212] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00213] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00214] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00215] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00216] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00217] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00218] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00219] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00220] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00221] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L1 loop motif region.

[00222] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L2 loop motif region.

[00223] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L3 loop motif region.

[00224] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L4 loop motif region.

[00225] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L5 loop motif region.

[00226] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L6 loop motif region.

[00227] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L7 loop motif region.

[00228] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L8 loop motif region.

[00229] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L9 loop motif region.

[00230] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L10 loop motif region.

[00231] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 flanking region and at least one nucleic acid sequence encoding at least one L11 loop motif region.

[00232] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5’ flanking region and at least one nucleic acid sequence encoding at least 3’ flanking region as described in Tables 1 and 3. As a non-limiting example, the molecular scaffold may comprise 5F1 and 3F1, 5F1 and 3F2, 5F1 and 3F3, 5F1 and 3F4, 5F1 and 3F5, 5F1 and 3F6, 5F1 and 3F7, 5F1 and 3F8, 5F2 and 3F1, 5F2 and 3F2, 5F2 and 3F3, 5F2 and 3F4, 5F2 and 3F5, 5F2 and 3F6, 5F2 and 3F7, 5F2 and 3F8, 5F3 and 3F1, 5F3 and 3F2, 5F3 and 3F3, 5F3 and 3F4, 5F3 and 3F5, 5F3 and 3F6, 5F3 and 3F7, 5F3 and 3F8, 5F4 and 3F1, 5F4 and 3F2, 5F4 and 3F3, 5F4 and 3F4, 5F4 and 3F5, 5F4 and 3F6, 5F4 and 3F7, 5F4 and 3F8, 5F5 and 3F1, 5F5 and 3F2, 5F5 and 3F3, 5F5 and 3F4, 5F5 and 3F5, 5F5 and 3F6, 5F5 and 3F7, 5F5 and 3F8, 5F6 and 3F1, 5F6 and 3F2, 5F6 and 3F3, 5F6 and 3F4, 5F6 and 3F5, 5F6 and 3F6, 5F6 and 3F7, 5F6 and 3F8, 5F7 and 3F1, 5F7 and 3F2, 5F7 and 3F3, 5F7 and 3F4, 5F7 and 3F5, 5F7 and 3F6, 5F7 and 3F7, 5F7 and 3F8, 5F8 and 3F1, 5F8 and 3F2, 5F8 and 3F3, 5F8 and 3F4, 5F8 and 3F5, 5F8 and 3F6, 5F8 and 3F7, 5F8 and 3F8, 5F9 and 3F1, 5F9 and 3F2, 5F9 and 3F3, 5F9 and 3F4, 5F9 and 3F5, 5F9 and 3F6, 5F9 and 3F7, or 5F9 and 3F8.

[00233] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00234] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00235] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00236] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00237] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00238] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00239] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00240] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00241] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00242] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00243] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00244] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00245] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00246] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00247] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00248] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00249] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00250] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00251] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00252] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00253] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00254] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00255] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00256] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00257] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00258] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00259] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00260] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00261] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00262] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00263] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00264] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00265] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00266] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00267] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00268] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00269] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00270] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00271] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00272] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00273] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00274] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00275] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00276] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00277] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00278] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00279] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00280] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00281] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00282] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00283] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00284] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00285] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00286] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00287] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00288] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00289] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00290] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00291] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00292] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00293] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00294] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00295] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00296] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00297] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00298] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00299] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00300] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00301] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00302] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00303] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00304] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00305] In one embodiment, the molecular scaffold may comprise at least one 5' flanking region, at least one loop motif region and at least one 3' flanking region. As a non-limiting example, the molecular scaffold may comprise 5F1, L1 and 3F1; 5F1, L1 and 3F2; 5F1, L1 and 3F3; 5F1, L1 and 3F4; 5F1, L1 and 3F5; 5F1, L1 and 3F6; 5F1, L1 and 3F7; 5F1, L1 and 3F8; 5F2, L1 and 3F1; 5F2, L1 and 3F2; 5F2, L1 and 3F3; 5F2, L1 and 3F4; 5F2, L1 and 3F5; 5F2, L1 and 3F6; 5F2, L1 and 3F7; 5F2, L1 and 3F8; 5F3, L1 and 3F1; 5F3, L1 and 3F2; 5F3, L1 and 3F3; 5F3, L1 and 3F4; 5F3, L1 and 3F5; 5F3, L1 and 3F6; 5F3, L1 and 3F7; 5F3, L1 and 3F8;

5F4, L1 and 3F1; 5F4, L1 and 3F2; 5F4, L1 and 3F3; 5F4, L1 and 3F4; 5F4, L1 and 3F5; 5F4, L1 and 3F6; 5F4, L1 and 3F7; 5F4, L1 and 3F8; 5F5, L1 and 3F1; 5F5, L1 and 3F2; 5F5, L1 and 3F3; 5F5, L1 and 3F4; 5F5, L1 and 3F5; 5F5, L1 and 3F6; 5F5, L1 and 3F7; 5F5, L1 and 3F8; 5F6, L1 and 3F1; 5F6, L1 and 3F2; 5F6, L1 and 3F3; 5F6, L1 and 3F4; 5F6, L1 and 3F5; 5F6, L1 and 3F6; 5F6, L1 and 3F7; 5F6, L1 and 3F8; 5F7, L1 and 3F1; 5F7, L1 and 3F2; 5F7, L1 and 3F3; 5F7, L1 and 3F4; 5F7, L1 and 3F5; 5F7, L1 and 3F6; 5F7, L1 and 3F7; 5F7, L1 and 3F8; 5F8, L1 and 3F1; 5F8, L1 and 3F2; 5F8, L1 and 3F3; 5F8, L1 and 3F4; 5F8, L1 and 3F5; 5F8, L1 and 3F6; 5F8, L1 and 3F7; 5F8, L1 and 3F8; 5F9, L1 and 3F1; 5F9, L1 and 3F2; 5F9, L1 and 3F3; 5F9, L1 and 3F4; 5F9, L1 and 3F5; 5F9, L1 and 3F6; 5F9, L1 and 3F7; 5F9, L1 and 3F8; 5F1, L2 and 3F1; 5F1, L2 and 3F2; 5F1, L2 and 3F3; 5F1, L2 and 3F4; 5F1, L2 and 3F5; 5F1, L2 and 3F6; 5F1, L2 and 3F7; 5F1, L2 and 3F8; 5F2, L2 and 3F1; 5F2, L2 and 3F2; 5F2, L2 and 3F3; 5F2, L2 and 3F4; 5F2, L2 and 3F5; 5F2, L2 and 3F6; 5F2, L2 and 3F7; 5F2, L2 and 3F8; 5F3, L2 and 3F1; 5F3, L2 and 3F2; 5F3, L2 and 3F3; 5F3, L2 and 3F4; 5F3, L2 and 3F5; 5F3, L2 and 3F6; 5F3, L2 and 3F7; 5F3, L2 and 3F8; 5F4, L2 and 3F1; 5F4, L2 and 3F2; 5F4, L2 and 3F3; 5F4, L2 and 3F4; 5F4, L2 and 3F5; 5F4, L2 and 3F6; 5F4, L2 and 3F7; 5F4, L2 and 3F8; 5F5, L2 and 3F1; 5F5, L2 and 3F2; 5F5, L2 and 3F3; 5F5, L2 and 3F4; 5F5, L2 and 3F5; 5F5, L2 and 3F6; 5F5, L2 and 3F7; 5F5, L2 and 3F8; 5F6, L2 and 3F1; 5F6, L2 and 3F2; 5F6, L2 and 3F3; 5F6, L2 and 3F4; 5F6, L2 and 3F5; 5F6, L2 and 3F6; 5F6, L2 and 3F7; 5F6, L2 and 3F8; 5F7, L2 and 3F1; 5F7, L2 and 3F2; 5F7, L2 and 3F3; 5F7, L2 and 3F4; 5F7, L2 and 3F5; 5F7, L2 and 3F6; 5F7, L2 and 3F7; 5F7, L2 and 3F8; 5F8, L2 and 3F1; 5F8, L2 and 3F2; 5F8, L2 and 3F3; 5F8, L2 and 3F4; 5F8, L2 and 3F5; 5F8, L2 and 3F6; 5F8, L2 and 3F7; 5F8, L2 and 3F8; 5F9, L2 and 3F1; 5F9, L2 and 3F2; 5F9, L2 and 3F3; 5F9, L2 and 3F4; 5F9, L2 and 3F5; 5F9, L2 and 3F6; 5F9, L2 and 3F7; 5F9, L2 and 3F8; 5F1, L3 and 3F1; 5F1, L3 and 3F2; 5F1, L3 and 3F3; 5F1, L3 and 3F4; 5F1, L3 and 3F5; 5F1, L3 and 3F6; 5F1, L3 and 3F7; 5F1, L3 and 3F8; 5F2, L3 and 3F1; 5F2, L3 and 3F2; 5F2, L3 and 3F3; 5F2, L3 and 3F4; 5F2, L3 and 3F5; 5F2, L3 and 3F6; 5F2, L3 and 3F7; 5F2, L3 and 3F8; 5F3, L3 and 3F1; 5F3, L3 and 3F2; 5F3, L3 and 3F3; 5F3, L3 and 3F4; 5F3, L3 and 3F5; 5F3, L3 and 3F6; 5F3, L3 and 3F7; 5F3, L3 and 3F8; 5F4, L3 and 3F1; 5F4, L3 and 3F2; 5F4, L3 and 3F3; 5F4, L3 and 3F4; 5F4, L3 and 3F5; 5F4, L3 and 3F6; 5F4, L3 and 3F7; 5F4, L3 and 3F8; 5F5, L3 and 3F1; 5F5, L3 and 3F2; 5F5, L3 and 3F3; 5F5, L3 and 3F4; 5F5, L3 and 3F5; 5F5, L3 and 3F6; 5F5, L3 and 3F7; 5F5, L3 and 3F8; 5F6, L3 and 3F1; 5F6, L3 and 3F2; 5F6, L3 and 3F3; 5F6, L3 and 3F4; 5F6, L3 and 3F5; 5F6, L3 and 3F6; 5F6, L3 and 3F7; 5F6, L3 and 3F8; 5F7, L3 and 3F1; 5F7, L3 and 3F2; 5F7, L3 and 3F3; 5F7, L3 and 3F4; 5F7, L3 and 3F5; 5F7, L3 and 3F6; 5F7, L3 and 3F7; 5F7, L3 and 3F8; 5F8, L3 and 3F1; 5F8, L3 and 3F2; 5F8, L3 and 3F3; 5F8, L3 and 3F4; 5F8, L3 and 3F5; 5F8, L3 and 3F6; 5F8, L3 and 3F7; 5F8, L3 and 3F8; 5F9, L3 and 3F1; 5F9, L3 and 3F2; 5F9, L3 and 3F3; 5F9, L3 and 3F4; 5F9, L3 and 3F5; 5F9, L3 and 3F6; 5F9, L3 and 3F7; 5F9, L3 and 3F8; 5F1, L4 and 3F1; 5F1, L4 and 3F2; 5F1, L4 and 3F3; 5F1, L4 and 3F4; 5F1, L4 and 3F5; 5F1, L4 and 3F6; 5F1, L4 and 3F7; 5F1, L4 and 3F8; 5F2, L4 and 3F1; 5F2, L4 and 3F2; 5F2, L4 and 3F3; 5F2, L4 and 3F4; 5F2, L4 and 3F5; 5F2, L4 and 3F6; 5F2, L4 and 3F7; 5F2, L4 and 3F8; 5F3, L4 and 3F1; 5F3, L4 and 3F2; 5F3, L4 and 3F3; 5F3, L4 and 3F4; 5F3, L4 and 3F5; 5F3, L4 and 3F6; 5F3, L4 and 3F7; 5F3, L4 and 3F8; 5F4, L4 and 3F1; 5F4, L4 and 3F2; 5F4, L4 and 3F3; 5F4, L4 and 3F4; 5F4, L4 and 3F5; 5F4, L4 and 3F6; 5F4, L4 and 3F7; 5F4, L4 and 3F8; 5F5, L4 and 3F1; 5F5, L4 and 3F2; 5F5, L4 and 3F3; 5F5, L4 and 3F4; 5F5, L4 and 3F5; 5F5, L4 and 3F6; 5F5, L4 and 3F7; 5F5, L4 and 3F8; 5F6, L4 and 3F1; 5F6, L4 and 3F2; 5F6, L4 and 3F3; 5F6, L4 and 3F4; 5F6, L4 and 3F5; 5F6, L4 and 3F6; 5F6, L4 and 3F7; 5F6, L4 and 3F8; 5F7, L4 and 3F1; 5F7, L4 and 3F2; 5F7, L4 and 3F3; 5F7, L4 and 3F4; 5F7, L4 and 3F5; 5F7, L4 and 3F6; 5F7, L4 and 3F7; 5F7, L4 and 3F8; 5F8, L4 and 3F1; 5F8, L4 and 3F2; 5F8, L4 and 3F3; 5F8, L4 and 3F4; 5F8, L4 and 3F5; 5F8, L4 and 3F6; 5F8, L4 and 3F7; 5F8, L4 and 3F8; 5F9, L4 and 3F1; 5F9, L4 and 3F2; 5F9, L4 and 3F3; 5F9, L4 and 3F4; 5F9, L4 and 3F5; 5F9, L4 and 3F6; 5F9, L4 and 3F7; 5F9, L4 and 3F8; 5F1, L5 and 3F1; 5F1, L5 and 3F2; 5F1, L5 and 3F3; 5F1, L5 and 3F4; 5F1, L5 and 3F5; 5F1, L5 and 3F6; 5F1, L5 and 3F7; 5F1, L5 and 3F8; 5F2, L5 and 3F1; 5F2, L5 and 3F2; 5F2, L5 and 3F3; 5F2, L5 and 3F4; 5F2, L5 and 3F5; 5F2, L5 and 3F6; 5F2, L5 and 3F7; 5F2, L5 and 3F8; 5F3, L5 and 3F1; 5F3, L5 and 3F2; 5F3, L5 and 3F3; 5F3, L5 and 3F4; 5F3, L5 and 3F5; 5F3, L5 and 3F6; 5F3, L5 and 3F7; 5F3, L5 and 3F8; 5F4, L5 and 3F1; 5F4, L5 and 3F2; 5F4, L5 and 3F3; 5F4, L5 and 3F4; 5F4, L5 and 3F5; 5F4, L5 and 3F6; 5F4, L5 and 3F7; 5F4, L5 and 3F8; 5F5, L5 and 3F1; 5F5, L5 and 3F2; 5F5, L5 and 3F3; 5F5, L5 and 3F4; 5F5, L5 and 3F5; 5F5, L5 and 3F6; 5F5, L5 and 3F7; 5F5, L5 and 3F8; 5F6, L5 and 3F1; 5F6, L5 and 3F2; 5F6, L5 and 3F3; 5F6, L5 and 3F4; 5F6, L5 and 3F5; 5F6, L5 and 3F6; 5F6, L5 and 3F7; 5F6, L5 and 3F8; 5F7, L5 and 3F1; 5F7, L5 and 3F2; 5F7, L5 and 3F3; 5F7, L5 and 3F4; 5F7, L5 and 3F5; 5F7, L5 and 3F6; 5F7, L5 and 3F7; 5F7, L5 and 3F8; 5F8, L5 and 3F1; 5F8, L5 and 3F2; 5F8, L5 and 3F3; 5F8, L5 and 3F4; 5F8, L5 and 3F5; 5F8, L5 and 3F6; 5F8, L5 and 3F7; 5F8, L5 and 3F8; 5F9, L5 and 3F1; 5F9, L5 and 3F2; 5F9, L5 and 3F3; 5F9, L5 and 3F4; 5F9, L5 and 3F5; 5F9, L5 and 3F6; 5F9, L5 and 3F7; or 5F9, L5 and 3F8.

[00306] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00307] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00308] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00309] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00310] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00311] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00312] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00313] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00314] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00315] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence

encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00316] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00317] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00318] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00319] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00320] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00321] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00322] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00323] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00324] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00325] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00326] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00327] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00328] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00329] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00330] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00331] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00332] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence

encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00333] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00334] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00335] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00336] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00337] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00338] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00339] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00340] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00341] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00342] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00343] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00344] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00345] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00346] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00347] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00348] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00349] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence

encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00350] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00351] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00352] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00353] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00354] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00355] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00356] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00357] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00358] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00359] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00360] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00361] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00362] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00363] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00364] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00365] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00366] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence

encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00367] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00368] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00369] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00370] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00371] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00372] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00373] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00374] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00375] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00376] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00377] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L1 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00378] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00379] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00380] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00381] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00382] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00383] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence

encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00384] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00385] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00386] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00387] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00388] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00389] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00390] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00391] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00392] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00393] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00394] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00395] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00396] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00397] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00398] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00399] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00400] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence

encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00401] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00402] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00403] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00404] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00405] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00406] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00407] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00408] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00409] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00410] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00411] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00412] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00413] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00414] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00415] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00416] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00417] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence

encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00418] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00419] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00420] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00421] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00422] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00423] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00424] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00425] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00426] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00427] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00428] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00429] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00430] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00431] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00432] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00433] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00434] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence

encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00435] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00436] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00437] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00438] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00439] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00440] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00441] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00442] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00443] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00444] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00445] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00446] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00447] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00448] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00449] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L2 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00450] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00451] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence

encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00452] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00453] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00454] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00455] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00456] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00457] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00458] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00459] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00460] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00461] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00462] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00463] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00464] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00465] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00466] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00467] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00468] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence

encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00469] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00470] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00471] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00472] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00473] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00474] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00475] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00476] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00477] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00478] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00479] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00480] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00481] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00482] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00483] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00484] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00485] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence

encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00486] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00487] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00488] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00489] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00490] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00491] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00492] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00493] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5’ flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00494] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00495] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00496] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00497] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00498] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00499] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00500] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00501] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00502] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence

encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00503] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00504] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00505] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00506] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00507] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00508] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00509] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00510] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00511] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00512] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00513] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00514] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00515] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00516] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00517] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00518] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00519] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence

encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00520] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00521] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L3 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00522] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00523] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00524] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00525] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00526] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00527] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00528] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00529] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00530] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00531] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00532] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00533] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00534] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00535] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00536] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5’ flanking region, at least one nucleic acid sequence

encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00537] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00538] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00539] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00540] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00541] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00542] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00543] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00544] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00545] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00546] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00547] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00548] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00549] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00550] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00551] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00552] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00553] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5’ flanking region, at least one nucleic acid sequence

encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00554] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00555] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00556] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00557] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00558] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00559] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00560] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00561] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00562] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00563] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00564] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00565] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00566] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00567] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00568] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00569] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00570] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence

encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00571] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00572] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00573] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00574] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00575] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00576] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00577] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00578] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00579] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00580] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00581] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00582] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00583] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00584] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00585] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00586] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00587] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence

encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00588] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00589] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00590] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00591] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00592] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00593] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L4 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00594] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00595] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00596] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00597] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00598] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00599] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00600] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00601] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F1 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00602] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00603] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00604] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence

encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00605] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00606] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00607] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00608] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00609] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F2 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00610] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00611] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00612] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00613] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00614] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00615] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00616] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00617] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F3 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00618] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00619] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00620] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00621] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence

encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00622] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00623] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00624] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00625] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F4 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00626] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00627] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00628] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00629] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00630] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00631] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00632] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00633] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F5 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00634] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00635] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00636] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00637] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00638] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence

encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00639] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00640] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00641] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F6 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00642] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00643] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00644] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00645] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00646] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00647] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3' flanking region.

[00648] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00649] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F7 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00650] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3' flanking region.

[00651] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3' flanking region.

[00652] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3' flanking region.

[00653] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3' flanking region.

[00654] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3' flanking region.

[00655] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5' flanking region, at least one nucleic acid sequence

encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00656] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3’ flanking region.

[00657] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F8 5’ flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3’ flanking region.

[00658] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F1 3’ flanking region.

[00659] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F2 3’ flanking region.

[00660] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F3 3’ flanking region.

[00661] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F4 3’ flanking region.

[00662] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F5 3’ flanking region.

[00663] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5’ flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F6 3’ flanking region.

[00664] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F7 3' flanking region.

[00665] In one embodiment, the molecular scaffold may comprise at least one nucleic acid sequence encoding at least one 5F9 5' flanking region, at least one nucleic acid sequence encoding at least one L5 loop motif region, and at least one nucleic acid sequence encoding at least one 3F8 3' flanking region.

[00666] In one embodiment, the molecular scaffold may comprise one or more linkers known in the art. The linkers may separate regions or one molecular scaffold from another. As a non-limiting example, the molecular scaffold may be polycistronic.

[00667] In one embodiment, the modulatory polynucleotide is designed using at least one of the following properties: loop variant, seed mismatch/bulge/wobble variant, stem mismatch, loop variant and vassal stem mismatch variant, seed mismatch and basal stem mismatch variant, stem mismatch and basal stem mismatch variant, seed wobble and basal stem wobble variant, or a stem sequence variant.

[00668] In one embodiment, the molecular scaffold may be located between the two ITRs of an expression vector. As a non-limiting example, the molecular scaffold may be inserted into an expression vector at at least one of six different locations as shown in FIG. 2. In FIG. 2, "ITR" is the inverted terminal repeat, "I" represents intron, "P" is the polyA and "MP" is the modulatory polynucleotide.

[00669] In one embodiment, the molecular scaffold may be located downstream of a promoter such as, but not limited to, CMV, U6, H1, CBA or a CBA promoter with a SV40 or a human betaGlobin intron. Further, the molecular scaffold may also be located upstream of the polyadenylation sequence. As a non-limiting example, the molecular scaffold may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence. As another non-limiting example, the molecular scaffold may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence. As a non-limiting example, the molecular scaffold may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence. As another non-limiting example, the molecular scaffold may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the promoter and/or upstream of the polyadenylation sequence.

[00670] In one embodiment, the molecular scaffold may be located upstream of the polyadenylation sequence. Further, the molecular scaffold may be located downstream of a promoter such as, but not limited to, CMV, U6, H1, CBA or a CBA promoter with a SV40 or a human betaGlobin intron. As a non-limiting example, the molecular scaffold may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence. As another non-limiting example, the molecular scaffold may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence. As a non-limiting example, the molecular scaffold may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence. As another non-limiting example, the molecular scaffold may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the promoter and/or upstream of the polyadenylation sequence.

[00671] In one embodiment, the molecular scaffold may be located in a scAAV.

[00672] In one embodiment, the molecular scaffold may be located in an ssAAV.

[00673] In one embodiment, the molecular scaffold may be located near the 5' end of the flip ITR. In another embodiment, the molecular scaffold may be located near the 3'end of the flip ITR. In yet another embodiment, the molecular scaffold may be located near the 5' end of the flop ITR. In yet another embodiment, the molecular scaffold may be located near the 3' end of the flop ITR. In one embodiment, the molecular scaffold may be located between the 5' end of the flip ITR and the 3' end of the flop ITR. In one embodiment, the molecular scaffold may be located between (e.g., half-way between the 5' end of the flip ITR and 3' end of the flop ITR or the 3' end of the flop ITR and the 5' end of the flip ITR), the 3' end of the flip ITR and the 5' end of the flip ITR. As a non-limiting example, the molecular scaffold may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR). As a non-limiting example, the molecular scaffold may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than

30 nucleotides upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR). As another non-limiting example, the molecular scaffold may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR). As another non-limiting example, the molecular scaffold may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR). As a non-limiting example, the molecular scaffold may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR). As another non-limiting example, the molecular scaffold may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR).

Vectors

[00674] In some embodiments, the siRNA molecules described herein can be encoded by vectors such as plasmids or viral vectors. In one embodiment, the siRNA molecules are encoded by viral vectors. Viral vectors may be, but are not limited to, Herpesvirus (HSV) vectors, retroviral vectors, adenoviral vectors, adeno-associated viral vectors, lentiviral vectors, and the like. In some specific embodiments, the viral vectors are AAV vectors.

Retroviral vectors

[00675] In some embodiments, the siRNA duplex targeting SOD1 or HTT may be encoded by a retroviral vector (See, e.g., U.S. Pat. Nos. 5,399,346; 5,124,263; 4,650,764 and 4,980,289; the content of each of which are incorporated herein by reference in their entirety).

Adenoviral vectors

[00676] Adenoviruses are eukaryotic DNA viruses that can be modified to efficiently deliver a nucleic acid to a variety of cell types in vivo, and have been used extensively in gene therapy protocols, including for targeting genes to neural cells. Various replication defective adenovirus and minimum adenovirus vectors have been described for nucleic acid therapeutics (See, e.g., PCT Patent Publication Nos. WO199426914, WO 199502697, WO199428152, WO199412649, WO199502697 and WO199622378; the content of each of which is incorporated by reference in their entirety). Such adenoviral vectors may also be used to deliver siRNA molecules of the present invention to cells.

Adeno-associated viral (AAV) vectors

[00677] An adeno-associated virus (AAV) is a dependent parvovirus (like other parvoviruses) which is a single stranded non-enveloped DNA virus having a genome of about 5000 nucleotides in length and which contains two open reading frames encoding the proteins responsible for replication (Rep) and the structural protein of the capsid (Cap). The open reading frames are flanked by two Inverted Terminal Repeat (ITR) sequences, which serve as the origin of replication of the viral genome. Furthermore, the AAV genome contains a packaging sequence, allowing packaging of the viral genome into an AAV capsid. The AAV vector requires a co-helper (e.g., adenovirus) to undergo productive infection in infected cells. In the absence of such helper functions, the AAV virions essentially enter host cells but do not integrate into the cells' genome.

[00678] AAV vectors have been investigated for siRNA delivery because of several unique features. Non-limiting examples of the features include (i) the ability to infect both dividing and non-dividing cells; (ii) a broad host range for infectivity, including human cells; (iii) wild-type AAV has not been associated with any disease and has not been shown to replicate in infected cells; (iv) the lack of cell-mediated immune response against the vector and (v) the non-integrative nature in a host chromosome thereby reducing potential for long-term genetic alterations. Moreover, infection with AAV vectors has minimal influence on changing the pattern of cellular gene expression (Stilwell and Samulski et al., Biotechniques, 2003, 34, 148).

[00679] Typically, AAV vectors for siRNA delivery may be recombinant viral vectors which are replication defective as they lack sequences encoding functional Rep and Cap proteins within the viral genome. In some cases, the defective AAV vectors may lack most or all coding sequences and essentially only contains one or two AAV ITR sequences and a packaging sequence.

[00680] In one embodiment, the AAV vectors comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be introduced into mammalian cells.

[00681] AAV vectors may be modified to enhance the efficiency of delivery. Such modified AAV vectors comprising the nucleic acid sequence encoding the siRNA molecules of the present invention can be packaged efficiently and can be used to successfully infect the target cells at high frequency and with minimal toxicity.

[00682] In some embodiments, the AAV vector comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be a human serotype AAV vector. Such human AAV vector may be derived from any known serotype, e.g., from any one of serotypes AAV1-AAV11. As non-limiting examples, AAV vectors may be vectors comprising an AAV1-derived genome in an AAV1-derived capsid; vectors comprising an AAV2-derived genome in an

AAV2-derived capsid; vectors comprising an AAV4-derived genome in an AAV4 derived capsid; vectors comprising an AAV6-derived genome in an AAV6 derived capsid or vectors comprising an AAV9-derived genome in an AAV9 derived capsid.

[00683] In other embodiments, the AAV vector comprising a nucleic acid sequence for encoding siRNA molecules of the present invention may be a pseudotyped hybrid or chimeric AAV vector which contains sequences and/or components originating from at least two different AAV serotypes. Pseudotyped AAV vectors may be vectors comprising an AAV genome derived from one AAV serotype and a capsid protein derived at least in part from a different AAV serotype. As non-limiting examples, such pseudotyped AAV vectors may be vectors comprising an AAV2-derived genome in an AAV1-derived capsid; or vectors comprising an AAV2-derived genome in an AAV6-derived capsid; or vectors comprising an AAV2-derived genome in an AAV4-derived capsid; or an AAV2-derived genome in an AAV9-derived capsid. In like fashion, the present invention contemplates any hybrid or chimeric AAV vector.

[00684] In other embodiments, AAV vectors comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to deliver siRNA molecules to the central nervous system (e.g., U.S. Pat. No. 6,180,613; the contents of which is herein incorporated by reference in its entirety).

[00685] In some aspects, the AAV vectors comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may further comprise a modified capsid including peptides from non-viral origin. In other aspects, the AAV vector may contain a CNS specific chimeric capsid to facilitate the delivery of encoded siRNA duplexes into the brain and the spinal cord. For example, an alignment of cap nucleotide sequences from AAV variants exhibiting CNS tropism may be constructed to identify variable region (VR) sequence and structure.

[00686] In one embodiment, the AAV vector comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may encode siRNA molecules which are polycistronic molecules. The siRNA molecules may additionally comprise one or more linkers between regions of the siRNA molecules.

Self-Complemtary and Single Strand Vectors

[00687] In one embodiment, the AAV vector used in the present invention is a single strand vector (ssAAV).

[00688] In another embodiment, the AAV vectors may be self-complementary AAV vectors (scAAVs). scAAV vectors contain both DNA strands which anneal together to form double stranded DNA. By skipping second strand synthesis, scAAVs allow for rapid expression in the cell.

[00689] In one embodiment, the AAV vector used in the present invention is a scAAV.

[00690] Methods for producing and/or modifying AAV vectors are disclosed in the art such as pseudotyped AAV vectors (International Patent Publication Nos. WO200028004; WO200123001; WO2004112727; WO 2005005610 and WO 2005072364, the content of each of which are incorporated herein by reference in their entirety).

AAV Serotypes

[00691] AAV particles of the present invention may comprise or be derived from any natural or recombinant AAV serotype. According to the present invention, the AAV particles may utilize or be based on a serotype selected from any of the following AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T , AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101 , AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2 , AAV Shuffle 100-1 , AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8 , AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV

CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, AAVF9/HSC9, AAV-PHP.B (PHP.B), AAV-PHP.A (PHP.A), G2B-26, G2B-13, TH1.1-32 and/or TH1.1-35, and variants thereof. As a non-limiting example, the capsid of the recombinant AAV virus is AAV2. As a non-limiting example, the capsid of the recombinant AAV virus is AAVrh10. As a non-limiting example, the capsid of the recombinant AAV virus is AAV9(hu14). As a non-limiting example, the capsid of the recombinant AAV virus is AAV-DJ. As a non-limiting example, the capsid of the recombinant AAV virus is AAV9.47. As a non-limiting example, the capsid of the recombinant AAV virus is AAV-DJ8. As a non-limiting example, the capsid of the recombinant AAV virus is AAV-PHP.B. As a non-limiting example, the capsid of the recombinant AAV virus is AAV-PHP.A.

[00692] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Publication No. US20030138772, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV1 (SEQ ID NO: 6 and 64 of US20030138772), AAV2 (SEQ ID NO: 7 and 70 of US20030138772), AAV3 (SEQ ID NO: 8 and 71 of US20030138772), AAV4 (SEQ ID NO: 63 of US20030138772), AAV5 (SEQ ID NO: 114 of US20030138772), AAV6 (SEQ ID NO: 65 of US20030138772), AAV7 (SEQ ID NO: 1-3 of US20030138772), AAV8 (SEQ ID NO: 4 and 95 of US20030138772), AAV9 (SEQ ID NO: 5 and 100 of US20030138772), AAV10 (SEQ ID NO: 117 of US20030138772), AAV11 (SEQ

ID NO: 118 of US20030138772), AAV12 (SEQ ID NO: 119 of US20030138772), AAVrh10 (amino acids 1 to 738 of SEQ ID NO: 81 of US20030138772), AAV16.3 (US20030138772 SEQ ID NO: 10), AAV29.3/bb.1 (US20030138772 SEQ ID NO: 11), AAV29.4 (US20030138772 SEQ ID NO: 12), AAV29.5/bb.2 (US20030138772 SEQ ID NO: 13), AAV1.3 (US20030138772 SEQ ID NO: 14), AAV13.3 (US20030138772 SEQ ID NO: 15), AAV24.1 (US20030138772 SEQ ID NO: 16), AAV27.3 (US20030138772 SEQ ID NO: 17), AAV7.2 (US20030138772 SEQ ID NO: 18), AAVC1 (US20030138772 SEQ ID NO: 19), AAVC3 (US20030138772 SEQ ID NO: 20), AAVC5 (US20030138772 SEQ ID NO: 21), AAVF1 (US20030138772 SEQ ID NO: 22), AAVF3 (US20030138772 SEQ ID NO: 23), AAVF5 (US20030138772 SEQ ID NO: 24), AAVH6 (US20030138772 SEQ ID NO: 25), AAVH2 (US20030138772 SEQ ID NO: 26), AAV42-8 (US20030138772 SEQ ID NO: 27), AAV42-15 (US20030138772 SEQ ID NO: 28), AAV42-5b (US20030138772 SEQ ID NO: 29), AAV42-1b (US20030138772 SEQ ID NO: 30), AAV42-13 (US20030138772 SEQ ID NO: 31), AAV42-3a (US20030138772 SEQ ID NO: 32), AAV42-4 (US20030138772 SEQ ID NO: 33), AAV42-5a (US20030138772 SEQ ID NO: 34), AAV42-10 (US20030138772 SEQ ID NO: 35), AAV42-3b (US20030138772 SEQ ID NO: 36), AAV42-11 (US20030138772 SEQ ID NO: 37), AAV42-6b (US20030138772 SEQ ID NO: 38), AAV43-1 (US20030138772 SEQ ID NO: 39), AAV43-5 (US20030138772 SEQ ID NO: 40), AAV43-12 (US20030138772 SEQ ID NO: 41), AAV43-20 (US20030138772 SEQ ID NO: 42), AAV43-21 (US20030138772 SEQ ID NO: 43), AAV43-23 (US20030138772 SEQ ID NO: 44), AAV43-25 (US20030138772 SEQ ID NO: 45), AAV44.1 (US20030138772 SEQ ID NO: 46), AAV44.5 (US20030138772 SEQ ID NO: 47), AAV223.1 (US20030138772 SEQ ID NO: 48), AAV223.2 (US20030138772 SEQ ID NO: 49), AAV223.4 (US20030138772 SEQ ID NO: 50), AAV223.5 (US20030138772 SEQ ID NO: 51), AAV223.6 (US20030138772 SEQ ID NO: 52), AAV223.7 (US20030138772 SEQ ID NO: 53), AAVA3.4 (US20030138772 SEQ ID NO: 54), AAVA3.5 (US20030138772 SEQ ID NO: 55), AAVA3.7 (US20030138772 SEQ ID NO: 56), AAVA3.3 (US20030138772 SEQ ID NO: 57), AAV42.12 (US20030138772 SEQ ID NO: 58), AAV44.2 (US20030138772 SEQ ID NO: 59), AAV42-2 (US20030138772 SEQ ID NO: 9), or variants thereof.

[00693] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Publication No. US20150159173, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV2 (SEQ ID NO: 7 and 23 of US20150159173), rh20 (SEQ ID NO: 1 of US20150159173), rh32/33 (SEQ ID NO: 2 of US20150159173), rh39 (SEQ ID NO: 3, 20 and 36 of US20150159173), rh46 (SEQ ID NO: 4 and 22 of US20150159173), rh73 (SEQ ID NO: 5 of US20150159173), rh74 (SEQ ID NO: 6 of

US20150159173), AAV6.1 (SEQ ID NO: 29 of US20150159173), rh.8 (SEQ ID NO: 41 of US20150159173), rh.48.1 (SEQ ID NO: 44 of US20150159173), hu.44 (SEQ ID NO: 45 of US20150159173), hu.29 (SEQ ID NO: 42 of US20150159173), hu.48 (SEQ ID NO: 38 of US20150159173), rh54 (SEQ ID NO: 49 of US20150159173), AAV2 (SEQ ID NO: 7 of US20150159173), cy.5 (SEQ ID NO: 8 and 24 of US20150159173), rh.10 (SEQ ID NO: 9 and 25 of US20150159173), rh.13 (SEQ ID NO: 10 and 26 of US20150159173), AAV1 (SEQ ID NO: 11 and 27 of US20150159173), AAV3 (SEQ ID NO: 12 and 28 of US20150159173), AAV6 (SEQ ID NO: 13 and 29 of US20150159173), AAV7 (SEQ ID NO: 14 and 30 of US20150159173), AAV8 (SEQ ID NO: 15 and 31 of US20150159173), hu.13 (SEQ ID NO: 16 and 32 of US20150159173), hu.26 (SEQ ID NO: 17 and 33 of US20150159173), hu.37 (SEQ ID NO: 18 and 34 of US20150159173), hu.53 (SEQ ID NO: 19 and 35 of US20150159173), rh.43 (SEQ ID NO: 21 and 37 of US20150159173), rh2 (SEQ ID NO: 39 of US20150159173), rh.37 (SEQ ID NO: 40 of US20150159173), rh.64 (SEQ ID NO: 43 of US20150159173), rh.48 (SEQ ID NO: 44 of US20150159173), ch.5 (SEQ ID NO 46 of US20150159173), rh.67 (SEQ ID NO: 47 of US20150159173), rh.58 (SEQ ID NO: 48 of US20150159173), or variants thereof including, but not limited to Cy5R1, Cy5R2, Cy5R3, Cy5R4, rh.13R, rh.37R2, rh.2R, rh.8R, rh.48.1, rh.48.2, rh.48.1.2, hu.44R1, hu.44R2, hu.44R3, hu.29R, ch.5R1, rh64R1, rh64R2, AAV6.2, AAV6.1, AAV6.12, hu.48R1, hu.48R2, and hu.48R3.

[00694] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US 7198951, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV9 (SEQ ID NO: 1-3 of US 7198951), AAV2 (SEQ ID NO: 4 of US 7198951), AAV1 (SEQ ID NO: 5 of US 7198951), AAV3 (SEQ ID NO: 6 of US 7198951), and AAV8 (SEQ ID NO: 7 of US7198951).

[00695] In some embodiments, the AAV serotype may be, or have, a mutation in the AAV9 sequence as described by N Pulicherla et al. (Molecular Therapy 19(6):1070-1078 (2011), herein incorporated by reference in its entirety), such as but not limited to, AAV9.9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84.

[00696] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US 6156303, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV3B (SEQ ID NO: 1 and 10 of US 6156303), AAV6 (SEQ ID NO: 2, 7 and 11 of US 6156303), AAV2 (SEQ ID NO: 3 and 8 of US 6156303), AAV3A (SEQ ID NO: 4 and 9, of US 6156303), or derivatives thereof.

[00697] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Publication No. US20140359799, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV8 (SEQ ID NO: 1 of US20140359799), AAVDJ (SEQ ID NO: 2 and 3 of US20140359799), or variants thereof.

[00698] In some embodiments, the serotype may be AAVDJ or a variant thereof, such as AAVDJ8 (or AAV-DJ8), as described by Grimm et al. (Journal of Virology 82(12): 5887-5911 (2008), herein incorporated by reference in its entirety). The amino acid sequence of AAVDJ8 may comprise two or more mutations in order to remove the heparin binding domain (HBD). As a non-limiting example, the AAV-DJ sequence described as SEQ ID NO: 1 in US Patent No. 7,588,772, the contents of which are herein incorporated by reference in their entirety, may comprise two mutations: (1) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (2) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr). As another non-limiting example, may comprise three mutations: (1) K406R where lysine (K; Lys) at amino acid 406 is changed to arginine (R; Arg), (2) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (3) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr).

[00699] In some embodiments, the AAV serotype may be, or have, a sequence of AAV4 as described in International Publication No. WO1998011244, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV4 (SEQ ID NO: 1-20 of WO1998011244).

[00700] In some embodiments, the AAV serotype may be, or have, a mutation in the AAV2 sequence to generate AAV2G9 as described in International Publication No. WO2014144229 and herein incorporated by reference in its entirety.

[00701] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2005033321, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV3-3 (SEQ ID NO: 217 of WO2005033321), AAV1 (SEQ ID NO: 219 and 202 of WO2005033321), AAV106.1/hu.37 (SEQ ID No: 10 of WO2005033321), AAV114.3/hu.40 (SEQ ID No: 11 of WO2005033321), AAV127.2/hu.41 (SEQ ID NO:6 and 8 of WO2005033321), AAV128.3/hu.44 (SEQ ID No: 81 of WO2005033321), AAV130.4/hu.48 (SEQ ID NO: 78 of WO2005033321), AAV145.1/hu.53 (SEQ ID No: 176 and 177 of WO2005033321), AAV145.6/hu.56 (SEQ ID NO: 168 and 192 of WO2005033321), AAV16.12/hu.11 (SEQ ID NO: 153 and 57 of WO2005033321), AAV16.8/hu.10 (SEQ ID NO: 156 and 56 of WO2005033321), AAV161.10/hu.60 (SEQ ID No: 170 of WO2005033321), AAV161.6/hu.61 (SEQ ID No: 174 of WO2005033321), AAV1-7/rh.48 (SEQ ID NO: 32 of WO2005033321), AAV1-8/rh.49 (SEQ ID NOs: 103 and 25 of WO2005033321), AAV2 (SEQ ID NO: 211 and 221 of WO2005033321), AAV2-15/rh.62 (SEQ

ID No: 33 and 114 of WO2005033321), AAV2-3/rh.61 (SEQ ID NO: 21 of WO2005033321), AAV2-4/rh.50 (SEQ ID No: 23 and 108 of WO2005033321), AAV2-5/rh.51 (SEQ ID NO: 104 and 22 of WO2005033321), AAV3.1/hu.6 (SEQ ID NO: 5 and 84 of WO2005033321), AAV3.1/hu.9 (SEQ ID NO: 155 and 58 of WO2005033321), AAV3-11/rh.53 (SEQ ID NO: 186 and 176 of WO2005033321), AAV3-3 (SEQ ID NO: 200 of WO2005033321), AAV33.12/hu.17 (SEQ ID NO:4 of WO2005033321), AAV33.4/hu.15 (SEQ ID No: 50 of WO2005033321), AAV33.8/hu.16 (SEQ ID No: 51 of WO2005033321), AAV3-9/rh.52 (SEQ ID NO: 96 and 18 of WO2005033321), AAV4-19/rh.55 (SEQ ID NO: 117 of WO2005033321), AAV4-4 (SEQ ID NO: 201 and 218 of WO2005033321), AAV4-9/rh.54 (SEQ ID NO: 116 of WO2005033321), AAV5 (SEQ ID NO: 199 and 216 of WO2005033321), AAV52.1/hu.20 (SEQ ID NO: 63 of WO2005033321), AAV52/hu.19 (SEQ ID NO: 133 of WO2005033321), AAV5-22/rh.58 (SEQ ID No: 27 of WO2005033321), AAV5-3/rh.57 (SEQ ID NO: 105 of WO2005033321), AAV5-3/rh.57 (SEQ ID No: 26 of WO2005033321), AAV58.2/hu.25 (SEQ ID No: 49 of WO2005033321), AAV6 (SEQ ID NO: 203 and 220 of WO2005033321), AAV7 (SEQ ID NO: 222 and 213 of WO2005033321), AAV7.3/hu.7 (SEQ ID No: 55 of WO2005033321), AAV8 (SEQ ID NO: 223 and 214 of WO2005033321), AAVH-1/hu.1 (SEQ ID No: 46 of WO2005033321), AAVH-5/hu.3 (SEQ ID No: 44 of WO2005033321), AAVhu.1 (SEQ ID NO: 144 of WO2005033321), AAVhu.10 (SEQ ID NO: 156 of WO2005033321), AAVhu.11 (SEQ ID NO: 153 of WO2005033321), AAVhu.12 (WO2005033321 SEQ ID NO: 59), AAVhu.13 (SEQ ID NO: 129 of WO2005033321), AAVhu.14/AAV9 (SEQ ID NO: 123 and 3 of WO2005033321), AAVhu.15 (SEQ ID NO: 147 of WO2005033321), AAVhu.16 (SEQ ID NO: 148 of WO2005033321), AAVhu.17 (SEQ ID NO: 83 of WO2005033321), AAVhu.18 (SEQ ID NO: 149 of WO2005033321), AAVhu.19 (SEQ ID NO: 133 of WO2005033321), AAVhu.2 (SEQ ID NO: 143 of WO2005033321), AAVhu.20 (SEQ ID NO: 134 of WO2005033321), AAVhu.21 (SEQ ID NO: 135 of WO2005033321), AAVhu.22 (SEQ ID NO: 138 of WO2005033321), AAVhu.23.2 (SEQ ID NO: 137 of WO2005033321), AAVhu.24 (SEQ ID NO: 136 of WO2005033321), AAVhu.25 (SEQ ID NO: 146 of WO2005033321), AAVhu.27 (SEQ ID NO: 140 of WO2005033321), AAVhu.29 (SEQ ID NO: 132 of WO2005033321), AAVhu.3 (SEQ ID NO: 145 of WO2005033321), AAVhu.31 (SEQ ID NO: 121 of WO2005033321), AAVhu.32 (SEQ ID NO: 122 of WO2005033321), AAVhu.34 (SEQ ID NO: 125 of WO2005033321), AAVhu.35 (SEQ ID NO: 164 of WO2005033321), AAVhu.37 (SEQ ID NO: 88 of WO2005033321), AAVhu.39 (SEQ ID NO: 102 of WO2005033321), AAVhu.4 (SEQ ID NO: 141 of WO2005033321), AAVhu.40 (SEQ ID NO: 87 of WO2005033321), AAVhu.41 (SEQ ID NO: 91 of WO2005033321), AAVhu.42 (SEQ ID NO: 85 of

WO2005033321), AAVhu.43 (SEQ ID NO: 160 of WO2005033321), AAVhu.44 (SEQ ID NO: 144 of WO2005033321), AAVhu.45 (SEQ ID NO: 127 of WO2005033321), AAVhu.46 (SEQ ID NO: 159 of WO2005033321), AAVhu.47 (SEQ ID NO: 128 of WO2005033321), AAVhu.48 (SEQ ID NO: 157 of WO2005033321), AAVhu.49 (SEQ ID NO: 189 of WO2005033321), AAVhu.51 (SEQ ID NO: 190 of WO2005033321), AAVhu.52 (SEQ ID NO: 191 of WO2005033321), AAVhu.53 (SEQ ID NO: 186 of WO2005033321), AAVhu.54 (SEQ ID NO: 188 of WO2005033321), AAVhu.55 (SEQ ID NO: 187 of WO2005033321), AAVhu.56 (SEQ ID NO: 192 of WO2005033321), AAVhu.57 (SEQ ID NO: 193 of WO2005033321), AAVhu.58 (SEQ ID NO: 194 of WO2005033321), AAVhu.6 (SEQ ID NO: 84 of WO2005033321), AAVhu.60 (SEQ ID NO: 184 of WO2005033321), AAVhu.61 (SEQ ID NO: 185 of WO2005033321), AAVhu.63 (SEQ ID NO: 195 of WO2005033321), AAVhu.64 (SEQ ID NO: 196 of WO2005033321), AAVhu.66 (SEQ ID NO: 197 of WO2005033321), AAVhu.67 (SEQ ID NO: 198 of WO2005033321), AAVhu.7 (SEQ ID NO: 150 of WO2005033321), AAVhu.8 (WO2005033321 SEQ ID NO: 12), AAVhu.9 (SEQ ID NO: 155 of WO2005033321), AAVLG-10/rh.40 (SEQ ID No: 14 of WO2005033321), AAVLG-4/rh.38 (SEQ ID NO: 86 of WO2005033321), AAVLG-4/rh.38 (SEQ ID No: 7 of WO2005033321), AAVN721-8/rh.43 (SEQ ID NO: 163 of WO2005033321), AAVN721-8/rh.43 (SEQ ID No: 43 of WO2005033321), AAVpi.1 (WO2005033321 SEQ ID NO: 28), AAVpi.2 (WO2005033321 SEQ ID NO: 30), AAVpi.3 (WO2005033321 SEQ ID NO: 29), AAVrh.38 (SEQ ID NO: 86 of WO2005033321), AAVrh.40 (SEQ ID NO: 92 of WO2005033321), AAVrh.43 (SEQ ID NO: 163 of WO2005033321), AAVrh.44 (WO2005033321 SEQ ID NO: 34), AAVrh.45 (WO2005033321 SEQ ID NO: 41), AAVrh.47 (WO2005033321 SEQ ID NO: 38), AAVrh.48 (SEQ ID NO: 115 of WO2005033321), AAVrh.49 (SEQ ID NO: 103 of WO2005033321), AAVrh.50 (SEQ ID NO: 108 of WO2005033321), AAVrh.51 (SEQ ID NO: 104 of WO2005033321), AAVrh.52 (SEQ ID NO: 96 of WO2005033321), AAVrh.53 (SEQ ID NO: 97 of WO2005033321), AAVrh.55 (WO2005033321 SEQ ID NO: 37), AAVrh.56 (SEQ ID NO: 152 of WO2005033321), AAVrh.57 (SEQ ID NO: 105 of WO2005033321), AAVrh.58 (SEQ ID NO: 106 of WO2005033321), AAVrh.59 (WO2005033321 SEQ ID NO: 42), AAVrh.60 (WO2005033321 SEQ ID NO: 31), AAVrh.61 (SEQ ID NO: 107 of WO2005033321), AAVrh.62 (SEQ ID NO: 114 of WO2005033321), AAVrh.64 (SEQ ID NO: 99 of WO2005033321), AAVrh.65 (WO2005033321 SEQ ID NO: 35), AAVrh.68 (WO2005033321 SEQ ID NO: 16), AAVrh.69 (WO2005033321 SEQ ID NO: 39), AAVrh.70 (WO2005033321 SEQ ID NO: 20), AAVrh.72 (WO2005033321 SEQ ID NO: 9), or variants thereof including, but not limited to, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVcy.6, AAVrh.12, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.25/42 15, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh14. Non limiting examples of variants include SEQ ID NO: 13, 15, 17, 19, 24, 36, 40, 45, 47, 48, 51-54, 60-62, 64-77, 79, 80, 82, 89, 90, 93-95, 98, 100, 101, , 109-113, 118-120, 124, 126, 131, 139, 142, 151,154, 158, 161, 162, 165-183, 202, 204-212, 215, 219, 224-236, of WO2005033321, the contents of which are herein incorporated by reference in their entirety.

[00702] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2015168666, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAVrh8R (SEQ ID NO: 9 of WO2015168666), AAVrh8R A586R mutant (SEQ ID NO: 10 of WO2015168666), AAVrh8R R533A mutant (SEQ ID NO: 11 of WO2015168666), or variants thereof.

[00703] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US9233131, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAVhE1.1 (SEQ ID NO:44 of US9233131), AAVhEr1.5 (SEQ ID NO:45 of US9233131), AAVhER1.14 (SEQ ID NO:46 of US9233131), AAVhEr1.8 (SEQ ID NO:47 of US9233131), AAVhEr1.16 (SEQ ID NO:48 of US9233131), AAVhEr1.18 (SEQ ID NO:49 of US9233131), AAVhEr1.35 (SEQ ID NO:50 of US9233131), AAVhEr1.7 (SEQ ID NO:51 of US9233131), AAVhEr1.36 (SEQ ID NO:52 of US9233131), AAVhEr2.29 (SEQ ID NO:53 of US9233131), AAVhEr2.4 (SEQ ID NO:54 of US9233131), AAVhEr2.16 (SEQ ID NO:55 of US9233131), AAVhEr2.30 (SEQ ID NO:56 of US9233131), AAVhEr2.31 (SEQ ID NO:58 of US9233131), AAVhEr2.36 (SEQ ID NO:57 of US9233131), AAVhER1.23 (SEQ ID NO:53 of US9233131), AAVhEr3.1 (SEQ ID NO:59 of US9233131), AAV2.5T (SEQ ID NO:42 of US9233131), or variants thereof.

[00704] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20150376607, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-PAEC (SEQ ID NO:1 of US20150376607), AAV-LK01 (SEQ ID NO:2 of US20150376607), AAV-LK02 (SEQ ID NO:3 of US20150376607), AAV-LK03 (SEQ ID NO:4 of US20150376607), AAV-LK04 (SEQ ID NO:5 of US20150376607), AAV-LK05 (SEQ ID NO:6 of US20150376607), AAV-LK06 (SEQ ID NO:7 of US20150376607), AAV-LK07 (SEQ ID NO:8 of US20150376607), AAV-LK08 (SEQ ID NO:9 of US20150376607), AAV-LK09 (SEQ ID NO:10 of US20150376607), AAV-LK10 (SEQ ID NO:11 of US20150376607), AAV-LK11 (SEQ ID NO:12 of US20150376607), AAV-LK12 (SEQ ID NO:13 of US20150376607), AAV-LK13 (SEQ ID NO:14 of US20150376607), AAV-LK14 (SEQ ID NO:15 of US20150376607), AAV-

LK15 (SEQ ID NO:16 of US20150376607), AAV-LK16 (SEQ ID NO:17 of US20150376607), AAV-LK17 (SEQ ID NO:18 of US20150376607), AAV-LK18 (SEQ ID NO:19 of US20150376607), AAV-LK19 (SEQ ID NO:20 of US20150376607), AAV-PAEC2 (SEQ ID NO:21 of US20150376607), AAV-PAEC4 (SEQ ID NO:22 of US20150376607), AAV-PAEC6 (SEQ ID NO:23 of US20150376607), AAV-PAEC7 (SEQ ID NO:24 of US20150376607), AAV-PAEC8 (SEQ ID NO:25 of US20150376607), AAV-PAEC11 (SEQ ID NO:26 of US20150376607), AAV-PAEC12 (SEQ ID NO:27, of US20150376607), or variants thereof.

[00705] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US9163261, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-2-pre-miRNA-101 (SEQ ID NO: 1 US9163261), or variants thereof.

[00706] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20150376240, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-8h (SEQ ID NO: 6 of US20150376240), AAV-8b (SEQ ID NO: 5 of US20150376240), AAV-h (SEQ ID NO: 2 of US20150376240), AAV-b (SEQ ID NO: 1 of US20150376240), or variants thereof.

[00707] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20160017295, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV SM 10-2 (SEQ ID NO: 22 of US20160017295), AAV Shuffle 100-1 (SEQ ID NO: 23 of US20160017295), AAV Shuffle 100-3 (SEQ ID NO: 24 of US20160017295), AAV Shuffle 100-7 (SEQ ID NO: 25 of US20160017295), AAV Shuffle 10-2 (SEQ ID NO: 34 of US20160017295), AAV Shuffle 10-6 (SEQ ID NO: 35 of US20160017295), AAV Shuffle 10-8 (SEQ ID NO: 36 of US20160017295), AAV Shuffle 100-2 (SEQ ID NO: 37 of US20160017295), AAV SM 10-1 (SEQ ID NO: 38 of US20160017295), AAV SM 10-8 (SEQ ID NO: 39 of US20160017295), AAV SM 100-3 (SEQ ID NO: 40 of US20160017295), AAV SM 100-10 (SEQ ID NO: 41 of US20160017295), or variants thereof.

[00708] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20150238550, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BNP61 AAV (SEQ ID NO: 1 of US20150238550), BNP62 AAV (SEQ ID NO: 3 of US20150238550), BNP63 AAV (SEQ ID NO: 4 of US20150238550), or variants thereof.

[00709] In some embodiments, the AAV serotype may be or may have a sequence as described in United States Patent Publication No. US20150315612, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAVrh.50 (SEQ ID NO: 108 of US20150315612), AAVrh.43 (SEQ ID NO: 163 of US20150315612), AAVrh.62 (SEQ ID NO: 114 of US20150315612), AAVrh.48 (SEQ ID NO: 115 of US20150315612), AAVhu.19 (SEQ ID NO: 133 of US20150315612), AAVhu.11 (SEQ ID NO: 153 of US20150315612), AAVhu.53 (SEQ ID NO: 186 of US20150315612), AAV4-8/rh.64 (SEQ ID No: 15 of US20150315612), AAVLG-9/hu.39 (SEQ ID No: 24 of US20150315612), AAV54.5/hu.23 (SEQ ID No: 60 of US20150315612), AAV54.2/hu.22 (SEQ ID No: 67 of US20150315612), AAV54.7/hu.24 (SEQ ID No: 66 of US20150315612), AAV54.1/hu.21 (SEQ ID No: 65 of US20150315612), AAV54.4R/hu.27 (SEQ ID No: 64 of US20150315612), AAV46.2/hu.28 (SEQ ID No: 68 of US20150315612), AAV46.6/hu.29 (SEQ ID No: 69 of US20150315612), AAV128.1/hu.43 (SEQ ID No: 80 of US20150315612), or variants thereof.

[00710] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2015121501, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, true type AAV (ttAAV) (SEQ ID NO: 2 of WO2015121501), "UPenn AAV10" (SEQ ID NO: 8 of WO2015121501), "Japanese AAV10" (SEQ ID NO: 9 of WO2015121501), or variants thereof.

[00711] According to the present invention, AAV capsid serotype selection or use may be from a variety of species. In one embodiment, the AAV may be an avian AAV (AAAV). The AAAV serotype may be, or have, a sequence as described in United States Patent No. US 9238800, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAAV (SEQ ID NO: 1, 2, 4, 6, 8, 10, 12, and 14 of US 9,238,800), or variants thereof.

[00712] In one embodiment, the AAV may be a bovine AAV (BAAV). The BAAV serotype may be, or have, a sequence as described in United States Patent No. US 9,193,769, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BAAV (SEQ ID NO: 1 and 6 of US 9193769), or variants thereof. The BAAV serotype may be or have a sequence as described in United States Patent No. US7427396, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BAAV (SEQ ID NO: 5 and 6 of US7427396), or variants thereof.

[00713] In one embodiment, the AAV may be a caprine AAV. The caprine AAV serotype may be, or have, a sequence as described in United States Patent No. US7427396, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, caprine AAV (SEQ ID NO: 3 of US7427396), or variants thereof.

[00714] In other embodiments the AAV may be engineered as a hybrid AAV from two or more parental serotypes. In one embodiment, the AAV may be AAV2G9 which comprises sequences from AAV2 and AAV9. The AAV2G9 AAV serotype may be, or have, a sequence as described in United States Patent Publication No. US20160017005, the contents of which are herein incorporated by reference in its entirety.

[00715] In one embodiment, the AAV may be a serotype generated by the AAV9 capsid library with mutations in amino acids 390-627 (VP1 numbering) as described by Pulicherla et al. (Molecular Therapy 19(6):1070-1078 (2011), the contents of which are herein incorporated by reference in their entirety. The serotype and corresponding nucleotide and amino acid substitutions may be, but is not limited to, AAV9.1 (G1594C; D532H), AAV6.2 (T1418A and T1436X; V473D and I479K), AAV9.3 (T1238A; F413Y), AAV9.4 (T1250C and A1617T; F417S), AAV9.5 (A1235G, A1314T, A1642G, C1760T; Q412R, T548A, A587V), AAV9.6 (T1231A; F411I), AAV9.9 (G1203A, G1785T; W595C), AAV9.10 (A1500G, T1676C; M559T), AAV9.11 (A1425T, A1702C, A1769T; T568P, Q590L), AAV9.13 (A1369C, A1720T; N457H, T574S), AAV9.14 (T1340A, T1362C, T1560C, G1713A; L447H), AAV9.16 (A1775T; Q592L), AAV9.24 (T1507C, T1521G; W503R), AAV9.26 (A1337G, A1769C; Y446C, Q590P), AAV9.33 (A1667C; D556A), AAV9.34 (A1534G, C1794T; N512D), AAV9.35 (A1289T, T1450A, C1494T, A1515T, C1794A, G1816A; Q430L, Y484N, N98K, V606I), AAV9.40 (A1694T, E565V), AAV9.41 (A1348T, T1362C; T450S), AAV9.44 (A1684C, A1701T, A1737G; N562H, K567N), AAV9.45 (A1492T, C1804T; N498Y, L602F), AAV9.46 (G1441C, T1525C, T1549G; G481R, W509R, L517V), 9.47 (G1241A, G1358A, A1669G, C1745T; S414N, G453D, K557E, T582I), AAV9.48 (C1445T, A1736T; P482L, Q579L), AAV9.50 (A1638T, C1683T, T1805A; Q546H, L602H), AAV9.53 (G1301A, A1405C, C1664T, G1811T; R134Q, S469R, A555V, G604V), AAV9.54 (C1531A, T1609A; L511I, L537M), AAV9.55 (T1605A; F535L), AAV9.58 (C1475T, C1579A; T492I, H527N), AAV.59 (T1336C; Y446H), AAV9.61 (A1493T; N498I), AAV9.64 (C1531A, A1617T; L511I), AAV9.65 (C1335T, T1530C, C1568A; A523D), AAV9.68 (C1510A; P504T), AAV9.80 (G1441A,;G481R), AAV9.83 (C1402A, A1500T; P468T, E500D), AAV9.87 (T1464C, T1468C; S490P), AAV9.90 (A1196T; Y399F), AAV9.91 (T1316G, A1583T, C1782G, T1806C; L439R, K528I), AAV9.93 (A1273G, A1421G, A1638C, C1712T, G1732A, A1744T, A1832T; S425G, Q474R, Q546H, P571L, G578R, T582S, D611V), AAV9.94 (A1675T; M559L) and AAV9.95 (T1605A; F535L).

[00716] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2016049230, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAVF1/HSC1 (SEQ ID NO: 2 and 20 of WO2016049230), AAVF2/HSC2 (SEQ ID NO: 3 and 21 of WO2016049230), AAVF3/HSC3 (SEQ ID NO: 5 and 22 of WO2016049230), AAVF4/HSC4 (SEQ ID NO: 6 and 23 of

WO2016049230), AAVF5/HSC5 (SEQ ID NO: 11 and 25 of WO2016049230), AAVF6/HSC6 (SEQ ID NO: 7 and 24 of WO2016049230), AAVF7/HSC7 (SEQ ID NO: 8 and 27 of WO2016049230), AAVF8/HSC8 (SEQ ID NO: 9 and 28 of WO2016049230), AAVF9/HSC9 (SEQ ID NO: 10 and 29 of WO2016049230), AAVF11/HSC11 (SEQ ID NO: 4 and 26 of WO2016049230), AAVF12/HSC12 (SEQ ID NO: 12 and 30 of WO2016049230), AAVF13/HSC13 (SEQ ID NO: 14 and 31 of WO2016049230), AAVF14/HSC14 (SEQ ID NO: 15 and 32 of WO2016049230), AAVF15/HSC15 (SEQ ID NO: 16 and 33 of WO2016049230), AAVF16/HSC16 (SEQ ID NO: 17 and 34 of WO2016049230), AAVF17/HSC17 (SEQ ID NO: 13 and 35 of WO2016049230), or variants or derivatives thereof.

[00717] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US 8734809, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV CBr-E1 (SEQ ID NO: 13 and 87 of US8734809), AAV CBr-E2 (SEQ ID NO: 14 and 88 of US8734809), AAV CBr-E3 (SEQ ID NO: 15 and 89 of US8734809), AAV CBr-E4 (SEQ ID NO: 16 and 90 of US8734809), AAV CBr-E5 (SEQ ID NO: 17 and 91 of US8734809), AAV CBr-e5 (SEQ ID NO: 18 and 92 of US8734809), AAV CBr-E6 (SEQ ID NO: 19 and 93 of US8734809), AAV CBr-E7 (SEQ ID NO: 20 and 94 of US8734809), AAV CBr-E8 (SEQ ID NO: 21 and 95 of US8734809), AAV CLv-D1 (SEQ ID NO: 22 and 96 of US8734809), AAV CLv-D2 (SEQ ID NO: 23 and 97 of US8734809), AAV CLv-D3 (SEQ ID NO: 24 and 98 of US8734809), AAV CLv-D4 (SEQ ID NO: 25 and 99 of US8734809), AAV CLv-D5 (SEQ ID NO: 26 and 100 of US8734809), AAV CLv-D6 (SEQ ID NO: 27 and 101 of US8734809), AAV CLv-D7 (SEQ ID NO: 28 and 102 of US8734809), AAV CLv-D8 (SEQ ID NO: 29 and 103 of US8734809), AAV CLv-E1 (SEQ ID NO: 13 and 87 of US8734809), AAV CLv-R1 (SEQ ID NO: 30 and 104 of US8734809), AAV CLv-R2 (SEQ ID NO: 31 and 105 of US8734809), AAV CLv-R3 (SEQ ID NO: 32 and 106 of US8734809), AAV CLv-R4 (SEQ ID NO: 33 and 107 of US8734809), AAV CLv-R5 (SEQ ID NO: 34 and 108 of US8734809), AAV CLv-R6 (SEQ ID NO: 35 and 109 of US8734809), AAV CLv-R7 (SEQ ID NO: 36 and 110 of US8734809), AAV CLv-R8 (SEQ ID NO: 37 and 111 of US8734809), AAV CLv-R9 (SEQ ID NO: 38 and 112 of US8734809), AAV CLg-F1 (SEQ ID NO: 39 and 113 of US8734809), AAV CLg-F2 (SEQ ID NO: 40 and 114 of US8734809), AAV CLg-F3 (SEQ ID NO: 41 and 115 of US8734809), AAV CLg-F4 (SEQ ID NO: 42 and 116 of US8734809), AAV CLg-F5 (SEQ ID NO: 43 and 117 of US8734809), AAV CLg-F6 (SEQ ID NO: 43 and 117 of US8734809), AAV CLg-F7 (SEQ ID NO: 44 and 118 of US8734809), AAV CLg-F8 (SEQ ID NO: 43 and 117 of US8734809), AAV CSp-1 (SEQ ID NO: 45 and 119 of US8734809), AAV CSp-10 (SEQ ID NO: 46 and 120 of US8734809), AAV CSp-11 (SEQ ID

NO: 47 and 121 of US8734809), AAV CSp-2 (SEQ ID NO: 48 and 122 of US8734809), AAV CSp-3 (SEQ ID NO: 49 and 123 of US8734809), AAV CSp-4 (SEQ ID NO: 50 and 124 of US8734809), AAV CSp-6 (SEQ ID NO: 51 and 125 of US8734809), AAV CSp-7 (SEQ ID NO: 52 and 126 of US8734809), AAV CSp-8 (SEQ ID NO: 53 and 127 of US8734809), AAV CSp-9 (SEQ ID NO: 54 and 128 of US8734809), AAV CHt-2 (SEQ ID NO: 55 and 129 of US8734809), AAV CHt-3 (SEQ ID NO: 56 and 130 of US8734809), AAV CKd-1 (SEQ ID NO: 57 and 131 of US8734809), AAV CKd-10 (SEQ ID NO: 58 and 132 of US8734809), AAV CKd-2 (SEQ ID NO: 59 and 133 of US8734809), AAV CKd-3 (SEQ ID NO: 60 and 134 of US8734809), AAV CKd-4 (SEQ ID NO: 61 and 135 of US8734809), AAV CKd-6 (SEQ ID NO: 62 and 136 of US8734809), AAV CKd-7 (SEQ ID NO: 63 and 137 of US8734809), AAV CKd-8 (SEQ ID NO: 64 and 138 of US8734809), AAV CLv-1 (SEQ ID NO: 35 and 139 of US8734809), AAV CLv-12 (SEQ ID NO: 66 and 140 of US8734809), AAV CLv-13 (SEQ ID NO: 67 and 141 of US8734809), AAV CLv-2 (SEQ ID NO: 68 and 142 of US8734809), AAV CLv-3 (SEQ ID NO: 69 and 143 of US8734809), AAV CLv-4 (SEQ ID NO: 70 and 144 of US8734809), AAV CLv-6 (SEQ ID NO: 71 and 145 of US8734809), AAV CLv-8 (SEQ ID NO: 72 and 146 of US8734809), AAV CKd-B1 (SEQ ID NO: 73 and 147 of US8734809), AAV CKd-B2 (SEQ ID NO: 74 and 148 of US8734809), AAV CKd-B3 (SEQ ID NO: 75 and 149 of US8734809), AAV CKd-B4 (SEQ ID NO: 76 and 150 of US8734809), AAV CKd-B5 (SEQ ID NO: 77 and 151 of US8734809), AAV CKd-B6 (SEQ ID NO: 78 and 152 of US8734809), AAV CKd-B7 (SEQ ID NO: 79 and 153 of US8734809), AAV CKd-B8 (SEQ ID NO: 80 and 154 of US8734809), AAV CKd-H1 (SEQ ID NO: 81 and 155 of US8734809), AAV CKd-H2 (SEQ ID NO: 82 and 156 of US8734809), AAV CKd-H3 (SEQ ID NO: 83 and 157 of US8734809), AAV CKd-H4 (SEQ ID NO: 84 and 158 of US8734809), AAV CKd-H5 (SEQ ID NO: 85 and 159 of US8734809), AAV CKd-H6 (SEQ ID NO: 77 and 151 of US8734809), AAV CHt-1 (SEQ ID NO: 86 and 160 of US8734809), AAV CLv1-1 (SEQ ID NO: 171 of US8734809), AAV CLv1-2 (SEQ ID NO: 172 of US8734809), AAV CLv1-3 (SEQ ID NO: 173 of US8734809), AAV CLv1-4 (SEQ ID NO: 174 of US8734809), AAV Clv1-7 (SEQ ID NO: 175 of US8734809), AAV Clv1-8 (SEQ ID NO: 176 of US8734809), AAV Clv1-9 (SEQ ID NO: 177 of US8734809), AAV Clv1-10 (SEQ ID NO: 178 of US8734809), AAV.VR-355 (SEQ ID NO: 181 of US8734809), AAV.hu.48R3 (SEQ ID NO: 183 of US8734809), or variants or derivatives thereof.

[00718] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2016065001, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV CHt-P2 (SEQ ID NO: 1 and 51 of

WO2016065001), AAV CHt-P5 (SEQ ID NO: 2 and 52 of WO2016065001), AAV CHt-P9 (SEQ ID NO: 3 and 53 of WO2016065001), AAV CBr-7.1 (SEQ ID NO: 4 and 54 of WO2016065001), AAV CBr-7.2 (SEQ ID NO: 5 and 55 of WO2016065001), AAV CBr-7.3 (SEQ ID NO: 6 and 56 of WO2016065001), AAV CBr-7.4 (SEQ ID NO: 7 and 57 of WO2016065001), AAV CBr-7.5 (SEQ ID NO: 8 and 58 of WO2016065001), AAV CBr-7.7 (SEQ ID NO: 9 and 59 of WO2016065001), AAV CBr-7.8 (SEQ ID NO: 10 and 60 of WO2016065001), AAV CBr-7.10 (SEQ ID NO: 11 and 61 of WO2016065001), AAV CKd-N3 (SEQ ID NO: 12 and 62 of WO2016065001), AAV CKd-N4 (SEQ ID NO: 13 and 63 of WO2016065001), AAV CKd-N9 (SEQ ID NO: 14 and 64 of WO2016065001), AAV CLv-L4 (SEQ ID NO: 15 and 65 of WO2016065001), AAV CLv-L5 (SEQ ID NO: 16 and 66 of WO2016065001), AAV CLv-L6 (SEQ ID NO: 17 and 67 of WO2016065001), AAV CLv-K1 (SEQ ID NO: 18 and 68 of WO2016065001), AAV CLv-K3 (SEQ ID NO: 19 and 69 of WO2016065001), AAV CLv-K6 (SEQ ID NO: 20 and 70 of WO2016065001), AAV CLv-M1 (SEQ ID NO: 21 and 71 of WO2016065001), AAV CLv-M11 (SEQ ID NO: 22 and 72 of WO2016065001), AAV CLv-M2 (SEQ ID NO: 23 and 73 of WO2016065001), AAV CLv-M5 (SEQ ID NO: 24 and 74 of WO2016065001), AAV CLv-M6 (SEQ ID NO: 25 and 75 of WO2016065001), AAV CLv-M7 (SEQ ID NO: 26 and 76 of WO2016065001), AAV CLv-M8 (SEQ ID NO: 27 and 77 of WO2016065001), AAV CLv-M9 (SEQ ID NO: 28 and 78 of WO2016065001), AAV CHt-P1 (SEQ ID NO: 29 and 79 of WO2016065001), AAV CHt-P6 (SEQ ID NO: 30 and 80 of WO2016065001), AAV CHt-P8 (SEQ ID NO: 31 and 81 of WO2016065001), AAV CHt-6.1 (SEQ ID NO: 32 and 82 of WO2016065001), AAV CHt-6.10 (SEQ ID NO: 33 and 83 of WO2016065001), AAV CHt-6.5 (SEQ ID NO: 34 and 84 of WO2016065001), AAV CHt-6.6 (SEQ ID NO: 35 and 85 of WO2016065001), AAV CHt-6.7 (SEQ ID NO: 36 and 86 of WO2016065001), AAV CHt-6.8 (SEQ ID NO: 37 and 87 of WO2016065001), AAV CSp-8.10 (SEQ ID NO: 38 and 88 of WO2016065001), AAV CSp-8.2 (SEQ ID NO: 39 and 89 of WO2016065001), AAV CSp-8.4 (SEQ ID NO: 40 and 90 of WO2016065001), AAV CSp-8.5 (SEQ ID NO: 41 and 91 of WO2016065001), AAV CSp-8.6 (SEQ ID NO: 42 and 92 of WO2016065001), AAV CSp-8.7 (SEQ ID NO: 43 and 93 of WO2016065001), AAV CSp-8.8 (SEQ ID NO: 44 and 94 of WO2016065001), AAV CSp-8.9 (SEQ ID NO: 45 and 95 of WO2016065001), AAV CBr-B7.3 (SEQ ID NO: 46 and 96 of WO2016065001), AAV CBr-B7.4 (SEQ ID NO: 47 and 97 of WO2016065001), AAV3B (SEQ ID NO: 48 and 98 of WO2016065001), AAV4 (SEQ ID NO: 49 and 99 of WO2016065001), AAV5 (SEQ ID NO: 50 and 100 of WO2016065001), or variants or derivatives thereof.

[00719] In one embodiment, the AAV may be a serotype comprising at least one AAV capsid CD8+ T-cell epitope. As a non-limiting example, the serotype may be AAV1, AAV2 or AAV8.

[00720] In one embodiment, the AAV may be a serotype selected from any of those found in Table 4.

[00721] In one embodiment, the AAV may comprise a sequence, fragment or variant thereof, of the sequences in Table 4.

[00722] In one embodiment, the AAV may be encoded by a sequence, fragment or variant as described in Table 4.

Table 4. AAV Serotypes

Serotype	SEQ ID NO	Reference Information
AAV1	28	US20150159173 SEQ ID NO: 11, US20150315612 SEQ ID NO: 202
AAV1	29	US20160017295 SEQ ID NO: 1US20030138772 SEQ ID NO: 64, US20150159173 SEQ ID NO: 27, US20150315612 SEQ ID NO: 219, US7198951 SEQ ID NO: 5
AAV1	30	US20030138772 SEQ ID NO: 6
AAV1.3	31	US20030138772 SEQ ID NO: 14
AAV10	32	US20030138772 SEQ ID NO: 117
AAV10	33	WO2015121501 SEQ ID NO: 9
AAV10	34	WO2015121501 SEQ ID NO: 8
AAV11	35	US20030138772 SEQ ID NO: 118
AAV12	36	US20030138772 SEQ ID NO: 119
AAV2	37	US20150159173 SEQ ID NO: 7, US20150315612 SEQ ID NO: 211
AAV2	38	US20030138772 SEQ ID NO: 70, US20150159173 SEQ ID NO: 23, US20150315612 SEQ ID NO: 221, US20160017295 SEQ ID NO: 2, US6156303 SEQ ID NO: 4, US7198951 SEQ ID NO: 4, WO2015121501 SEQ ID NO: 1
AAV2	39	US6156303 SEQ ID NO: 8
AAV2	40	US20030138772 SEQ ID NO: 7
AAV2	41	US6156303 SEQ ID NO: 3
AAV2.5T	42	US9233131 SEQ ID NO: 42
AAV223.10	43	US20030138772 SEQ ID NO: 75
AAV223.2	44	US20030138772 SEQ ID NO: 49
AAV223.2	45	US20030138772 SEQ ID NO: 76
AAV223.4	46	US20030138772 SEQ ID NO: 50
AAV223.4	47	US20030138772 SEQ ID NO: 73
AAV223.5	48	US20030138772 SEQ ID NO: 51
AAV223.5	49	US20030138772 SEQ ID NO: 74
AAV223.6	50	US20030138772 SEQ ID NO: 52
AAV223.6	51	US20030138772 SEQ ID NO: 78
AAV223.7	52	US20030138772 SEQ ID NO: 53
AAV223.7	53	US20030138772 SEQ ID NO: 77
AAV29.3	54	US20030138772 SEQ ID NO: 82
AAV29.4	55	US20030138772 SEQ ID NO: 12

AAV29.5	56	US20030138772 SEQ ID NO: 83
AAV29.5 (AAVbb.2)	57	US20030138772 SEQ ID NO: 13
AAV3	58	US20150159173 SEQ ID NO: 12
AAV3	59	US20030138772 SEQ ID NO: 71, US20150159173 SEQ ID NO: 28, US20160017295 SEQ ID NO: 3, US7198951 SEQ ID NO: 6
AAV3	60	US20030138772 SEQ ID NO: 8
AAV3.3b	61	US20030138772 SEQ ID NO: 72
AAV3-3	62	US20150315612 SEQ ID NO: 200
AAV3-3	63	US20150315612 SEQ ID NO: 217
AAV3a	64	US6156303 SEQ ID NO: 5
AAV3a	65	US6156303 SEQ ID NO: 9
AAV3b	66	US6156303 SEQ ID NO: 6
AAV3b	67	US6156303 SEQ ID NO: 10
AAV3b	68	US6156303 SEQ ID NO: 1
AAV4	69	US20140348794 SEQ ID NO: 17
AAV4	70	US20140348794 SEQ ID NO: 5
AAV4	71	US20140348794 SEQ ID NO: 3
AAV4	72	US20140348794 SEQ ID NO: 14
AAV4	73	US20140348794 SEQ ID NO: 15
AAV4	74	US20140348794 SEQ ID NO: 19
AAV4	75	US20140348794 SEQ ID NO: 12
AAV4	76	US20140348794 SEQ ID NO: 13
AAV4	77	US20140348794 SEQ ID NO: 7
AAV4	78	US20140348794 SEQ ID NO: 8
AAV4	79	US20140348794 SEQ ID NO: 9
AAV4	80	US20140348794 SEQ ID NO: 2
AAV4	81	US20140348794 SEQ ID NO: 10
AAV4	82	US20140348794 SEQ ID NO: 11
AAV4	83	US20140348794 SEQ ID NO: 18
AAV4	84	US20030138772 SEQ ID NO: 63, US20160017295 SEQ ID NO: 4, US20140348794 SEQ ID NO: 4
AAV4	85	US20140348794 SEQ ID NO: 16
AAV4	86	US20140348794 SEQ ID NO: 20
AAV4	87	US20140348794 SEQ ID NO: 6
AAV4	88	US20140348794 SEQ ID NO: 1
AAV42.2	89	US20030138772 SEQ ID NO: 9
AAV42.2	90	US20030138772 SEQ ID NO: 102
AAV42.3b	91	US20030138772 SEQ ID NO: 36
AAV42.3B	92	US20030138772 SEQ ID NO: 107
AAV42.4	93	US20030138772 SEQ ID NO: 33
AAV42.4	94	US20030138772 SEQ ID NO: 88
AAV42.8	95	US20030138772 SEQ ID NO: 27
AAV42.8	96	US20030138772 SEQ ID NO: 85
AAV43.1	97	US20030138772 SEQ ID NO: 39
AAV43.1	98	US20030138772 SEQ ID NO: 92
AAV43.12	99	US20030138772 SEQ ID NO: 41

AAV43.12	100	US20030138772 SEQ ID NO: 93
AAV43.20	101	US20030138772 SEQ ID NO: 42
AAV43.20	102	US20030138772 SEQ ID NO: 99
AAV43.21	103	US20030138772 SEQ ID NO: 43
AAV43.21	104	US20030138772 SEQ ID NO: 96
AAV43.23	105	US20030138772 SEQ ID NO: 44
AAV43.23	106	US20030138772 SEQ ID NO: 98
AAV43.25	107	US20030138772 SEQ ID NO: 45
AAV43.25	108	US20030138772 SEQ ID NO: 97
AAV43.5	109	US20030138772 SEQ ID NO: 40
AAV43.5	110	US20030138772 SEQ ID NO: 94
AAV4-4	111	US20150315612 SEQ ID NO: 201
AAV4-4	112	US20150315612 SEQ ID NO: 218
AAV44.1	113	US20030138772 SEQ ID NO: 46
AAV44.1	114	US20030138772 SEQ ID NO: 79
AAV44.5	115	US20030138772 SEQ ID NO: 47
AAV44.5	116	US20030138772 SEQ ID NO: 80
AAV4407	117	US20150315612 SEQ ID NO: 90
AAV5	118	US7427396 SEQ ID NO: 1
AAV5	119	US20030138772 SEQ ID NO: 114
AAV5	120	US20160017295 SEQ ID NO: 5, US7427396 SEQ ID NO: 2, US20150315612 SEQ ID NO: 216
AAV5	121	US20150315612 SEQ ID NO: 199
AAV6	122	US20150159173 SEQ ID NO: 13
AAV6	123	US20030138772 SEQ ID NO: 65, US20150159173 SEQ ID NO: 29, US20160017295 SEQ ID NO: 6, US6156303 SEQ ID NO: 7
AAV6	124	US6156303 SEQ ID NO: 11
AAV6	125	US6156303 SEQ ID NO: 2
AAV6	126	US20150315612 SEQ ID NO: 203
AAV6	127	US20150315612 SEQ ID NO: 220
AAV6.1	128	US20150159173
AAV6.12	129	US20150159173
AAV6.2	130	US20150159173
AAV7	131	US20150159173 SEQ ID NO: 14
AAV7	132	US20150315612 SEQ ID NO: 183
AAV7	133	US20030138772 SEQ ID NO: 2, US20150159173 SEQ ID NO: 30, US20150315612 SEQ ID NO: 181, US20160017295 SEQ ID NO: 7
AAV7	134	US20030138772 SEQ ID NO: 3
AAV7	135	US20030138772 SEQ ID NO: 1, US20150315612 SEQ ID NO: 180
AAV7	136	US20150315612 SEQ ID NO: 213
AAV7	137	US20150315612 SEQ ID NO: 222
AAV8	138	US20150159173 SEQ ID NO: 15
AAV8	139	US20150376240 SEQ ID NO: 7
AAV8	140	US20030138772 SEQ ID NO: 4, US20150315612 SEQ ID NO: 182
AAV8	141	US20030138772 SEQ ID NO: 95, US20140359799 SEQ ID NO: 1, US20150159173 SEQ ID NO: 31, US20160017295 SEQ ID NO: 8, US7198951 SEQ ID NO: 7, US20150315612 SEQ ID NO: 223

AAV8	142	US20150376240 SEQ ID NO: 8
AAV8	143	US20150315612 SEQ ID NO: 214
AAV-8b	144	US20150376240 SEQ ID NO: 5
AAV-8b	145	US20150376240 SEQ ID NO: 3
AAV-8h	146	US20150376240 SEQ ID NO: 6
AAV-8h	147	US20150376240 SEQ ID NO: 4
AAV9	148	US20030138772 SEQ ID NO: 5
AAV9	149	US7198951 SEQ ID NO: 1
AAV9	150	US20160017295 SEQ ID NO: 9
AAV9	151	US20030138772 SEQ ID NO: 100, US7198951 SEQ ID NO: 2
AAV9	152	US7198951 SEQ ID NO: 3
AAV9 (AAVhu.14)	153	US7906111 SEQ ID NO: 3; WO2015038958 SEQ ID NO: 11
AAV9 (AAVhu.14)	154	US7906111 SEQ ID NO: 123; WO2015038958 SEQ ID NO: 2
AAVA3.1	155	US20030138772 SEQ ID NO: 120
AAVA3.3	156	US20030138772 SEQ ID NO: 57
AAVA3.3	157	US20030138772 SEQ ID NO: 66
AAVA3.4	158	US20030138772 SEQ ID NO: 54
AAVA3.4	159	US20030138772 SEQ ID NO: 68
AAVA3.5	160	US20030138772 SEQ ID NO: 55
AAVA3.5	161	US20030138772 SEQ ID NO: 69
AAVA3.7	162	US20030138772 SEQ ID NO: 56
AAVA3.7	163	US20030138772 SEQ ID NO: 67
AAV29.3 (AAVbb.1)	164	US20030138772 SEQ ID NO: 11
AAVC2	165	US20030138772 SEQ ID NO: 61
AAVCh.5	166	US20150159173 SEQ ID NO: 46, US20150315612 SEQ ID NO: 234
AAVcy.2 (AAV13.3)	167	US20030138772 SEQ ID NO: 15
AAV24.1	168	US20030138772 SEQ ID NO: 101
AAVcy.3 (AAV24.1)	169	US20030138772 SEQ ID NO: 16
AAV27.3	170	US20030138772 SEQ ID NO: 104
AAVcy.4 (AAV27.3)	171	US20030138772 SEQ ID NO: 17
AAVcy.5	172	US20150315612 SEQ ID NO: 227
AAV7.2	173	US20030138772 SEQ ID NO: 103
AAVcy.5 (AAV7.2)	174	US20030138772 SEQ ID NO: 18
AAV16.3	175	US20030138772 SEQ ID NO: 105
AAVcy.6 (AAV16.3)	176	US20030138772 SEQ ID NO: 10
AAVcy.5	177	US20150159173 SEQ ID NO: 8
AAVcy.5	178	US20150159173 SEQ ID NO: 24
AAVCy.5R1	179	US20150159173
AAVCy.5R2	180	US20150159173
AAVCy.5R3	181	US20150159173
AAVCy.5R4	182	US20150159173
AAVDJ	183	US20140359799 SEQ ID NO: 3, US7588772 SEQ ID NO: 2
AAVDJ	184	US20140359799 SEQ ID NO: 2, US7588772 SEQ ID NO: 1
AAVDJ-8	185	US7588772; Grimm et al 2008
AAVDJ-8	186	US7588772; Grimm et al 2008

AAVF5	187	US20030138772 SEQ ID NO: 110
AAVH2	188	US20030138772 SEQ ID NO: 26
AAVH6	189	US20030138772 SEQ ID NO: 25
AAVhE1.1	190	US9233131 SEQ ID NO: 44
AAVhEr1.14	191	US9233131 SEQ ID NO: 46
AAVhEr1.16	192	US9233131 SEQ ID NO: 48
AAVhEr1.18	193	US9233131 SEQ ID NO: 49
AAVhEr1.23 (AAVhEr2.29)	194	US9233131 SEQ ID NO: 53
AAVhEr1.35	195	US9233131 SEQ ID NO: 50
AAVhEr1.36	196	US9233131 SEQ ID NO: 52
AAVhEr1.5	197	US9233131 SEQ ID NO: 45
AAVhEr1.7	198	US9233131 SEQ ID NO: 51
AAVhEr1.8	199	US9233131 SEQ ID NO: 47
AAVhEr2.16	200	US9233131 SEQ ID NO: 55
AAVhEr2.30	201	US9233131 SEQ ID NO: 56
AAVhEr2.31	202	US9233131 SEQ ID NO: 58
AAVhEr2.36	203	US9233131 SEQ ID NO: 57
AAVhEr2.4	204	US9233131 SEQ ID NO: 54
AAVhEr3.1	205	US9233131 SEQ ID NO: 59
AAVhu.1	206	US20150315612 SEQ ID NO: 46
AAVhu.1	207	US20150315612 SEQ ID NO: 144
AAVhu.10 (AAV16.8)	208	US20150315612 SEQ ID NO: 56
AAVhu.10 (AAV16.8)	209	US20150315612 SEQ ID NO: 156
AAVhu.11 (AAV16.12)	210	US20150315612 SEQ ID NO: 57
AAVhu.11 (AAV16.12)	211	US20150315612 SEQ ID NO: 153
AAVhu.12	212	US20150315612 SEQ ID NO: 59
AAVhu.12	213	US20150315612 SEQ ID NO: 154
AAVhu.13	214	US20150159173 SEQ ID NO: 16, US20150315612 SEQ ID NO: 71
AAVhu.13	215	US20150159173 SEQ ID NO: 32, US20150315612 SEQ ID NO: 129
AAVhu.136.1	216	US20150315612 SEQ ID NO: 165
AAVhu.140.1	217	US20150315612 SEQ ID NO: 166
AAVhu.140.2	218	US20150315612 SEQ ID NO: 167
AAVhu.145.6	219	US20150315612 SEQ ID No: 178
AAVhu.15	220	US20150315612 SEQ ID NO: 147
AAVhu.15 (AAV33.4)	221	US20150315612 SEQ ID NO: 50
AAVhu.156.1	222	US20150315612 SEQ ID No: 179
AAVhu.16	223	US20150315612 SEQ ID NO: 148
AAVhu.16 (AAV33.8)	224	US20150315612 SEQ ID NO: 51
AAVhu.17	225	US20150315612 SEQ ID NO: 83
AAVhu.17 (AAV33.12)	226	US20150315612 SEQ ID NO: 4
AAVhu.172.1	227	US20150315612 SEQ ID NO: 171
AAVhu.172.2	228	US20150315612 SEQ ID NO: 172
AAVhu.173.4	229	US20150315612 SEQ ID NO: 173
AAVhu.173.8	230	US20150315612 SEQ ID NO: 175
AAVhu.18	231	US20150315612 SEQ ID NO: 52

AAVhu.18	232	US20150315612 SEQ ID NO: 149
AAVhu.19	233	US20150315612 SEQ ID NO: 62
AAVhu.19	234	US20150315612 SEQ ID NO: 133
AAVhu.2	235	US20150315612 SEQ ID NO: 48
AAVhu.2	236	US20150315612 SEQ ID NO: 143
AAVhu.20	237	US20150315612 SEQ ID NO: 63
AAVhu.20	238	US20150315612 SEQ ID NO: 134
AAVhu.21	239	US20150315612 SEQ ID NO: 65
AAVhu.21	240	US20150315612 SEQ ID NO: 135
AAVhu.22	241	US20150315612 SEQ ID NO: 67
AAVhu.22	242	US20150315612 SEQ ID NO: 138
AAVhu.23	243	US20150315612 SEQ ID NO: 60
AAVhu.23.2	244	US20150315612 SEQ ID NO: 137
AAVhu.24	245	US20150315612 SEQ ID NO: 66
AAVhu.24	246	US20150315612 SEQ ID NO: 136
AAVhu.25	247	US20150315612 SEQ ID NO: 49
AAVhu.25	248	US20150315612 SEQ ID NO: 146
AAVhu.26	249	US20150159173 SEQ ID NO: 17, US20150315612 SEQ ID NO: 61
AAVhu.26	250	US20150159173 SEQ ID NO: 33, US20150315612 SEQ ID NO: 139
AAVhu.27	251	US20150315612 SEQ ID NO: 64
AAVhu.27	252	US20150315612 SEQ ID NO: 140
AAVhu.28	253	US20150315612 SEQ ID NO: 68
AAVhu.28	254	US20150315612 SEQ ID NO: 130
AAVhu.29	255	US20150315612 SEQ ID NO: 69
AAVhu.29	256	US20150159173 SEQ ID NO: 42, US20150315612 SEQ ID NO: 132
AAVhu.29	257	US20150315612 SEQ ID NO: 225
AAVhu.29R	258	US20150159173
AAVhu.3	259	US20150315612 SEQ ID NO: 44
AAVhu.3	260	US20150315612 SEQ ID NO: 145
AAVhu.30	261	US20150315612 SEQ ID NO: 70
AAVhu.30	262	US20150315612 SEQ ID NO: 131
AAVhu.31	263	US20150315612 SEQ ID NO: 1
AAVhu.31	264	US20150315612 SEQ ID NO: 121
AAVhu.32	265	US20150315612 SEQ ID NO: 2
AAVhu.32	266	US20150315612 SEQ ID NO: 122
AAVhu.33	267	US20150315612 SEQ ID NO: 75
AAVhu.33	268	US20150315612 SEQ ID NO: 124
AAVhu.34	269	US20150315612 SEQ ID NO: 72
AAVhu.34	270	US20150315612 SEQ ID NO: 125
AAVhu.35	271	US20150315612 SEQ ID NO: 73
AAVhu.35	272	US20150315612 SEQ ID NO: 164
AAVhu.36	273	US20150315612 SEQ ID NO: 74
AAVhu.36	274	US20150315612 SEQ ID NO: 126
AAVhu.37	275	US20150159173 SEQ ID NO: 34, US20150315612 SEQ ID NO: 88
AAVhu.37 (AAV106.1)	276	US20150315612 SEQ ID NO: 10, US20150159173 SEQ ID NO: 18

AAVhu.38	277	US20150315612 SEQ ID NO: 161
AAVhu.39	278	US20150315612 SEQ ID NO: 102
AAVhu.39 (AAVLG-9)	279	US20150315612 SEQ ID NO: 24
AAVhu.4	280	US20150315612 SEQ ID NO: 47
AAVhu.4	281	US20150315612 SEQ ID NO: 141
AAVhu.40	282	US20150315612 SEQ ID NO: 87
AAVhu.40 (AAV114.3)	283	US20150315612 SEQ ID No: 11
AAVhu.41	284	US20150315612 SEQ ID NO: 91
AAVhu.41 (AAV127.2)	285	US20150315612 SEQ ID NO: 6
AAVhu.42	286	US20150315612 SEQ ID NO: 85
AAVhu.42 (AAV127.5)	287	US20150315612 SEQ ID NO: 8
AAVhu.43	288	US20150315612 SEQ ID NO: 160
AAVhu.43	289	US20150315612 SEQ ID NO: 236
AAVhu.43 (AAV128.1)	290	US20150315612 SEQ ID NO: 80
AAVhu.44	291	US20150159173 SEQ ID NO: 45, US20150315612 SEQ ID NO: 158
AAVhu.44 (AAV128.3)	292	US20150315612 SEQ ID NO: 81
AAVhu.44R1	293	US20150159173
AAVhu.44R2	294	US20150159173
AAVhu.44R3	295	US20150159173
AAVhu.45	296	US20150315612 SEQ ID NO: 76
AAVhu.45	297	US20150315612 SEQ ID NO: 127
AAVhu.46	298	US20150315612 SEQ ID NO: 82
AAVhu.46	299	US20150315612 SEQ ID NO: 159
AAVhu.46	300	US20150315612 SEQ ID NO: 224
AAVhu.47	301	US20150315612 SEQ ID NO: 77
AAVhu.47	302	US20150315612 SEQ ID NO: 128
AAVhu.48	303	US20150159173 SEQ ID NO: 38
AAVhu.48	304	US20150315612 SEQ ID NO: 157
AAVhu.48 (AAV130.4)	305	US20150315612 SEQ ID NO: 78
AAVhu.48R1	306	US20150159173
AAVhu.48R2	307	US20150159173
AAVhu.48R3	308	US20150159173
AAVhu.49	309	US20150315612 SEQ ID NO: 209
AAVhu.49	310	US20150315612 SEQ ID NO: 189
AAVhu.5	311	US20150315612 SEQ ID NO: 45
AAVhu.5	312	US20150315612 SEQ ID NO: 142
AAVhu.51	313	US20150315612 SEQ ID NO: 208
AAVhu.51	314	US20150315612 SEQ ID NO: 190
AAVhu.52	315	US20150315612 SEQ ID NO: 210
AAVhu.52	316	US20150315612 SEQ ID NO: 191
AAVhu.53	317	US20150159173 SEQ ID NO: 19
AAVhu.53	318	US20150159173 SEQ ID NO: 35
AAVhu.53 (AAV145.1)	319	US20150315612 SEQ ID NO: 176
AAVhu.54	320	US20150315612 SEQ ID NO: 188
AAVhu.54 (AAV145.5)	321	US20150315612 SEQ ID No: 177

AAVhu.55	322	US20150315612 SEQ ID NO: 187
AAVhu.56	323	US20150315612 SEQ ID NO: 205
AAVhu.56 (AAV145.6)	324	US20150315612 SEQ ID NO: 168
AAVhu.56 (AAV145.6)	325	US20150315612 SEQ ID NO: 192
AAVhu.57	326	US20150315612 SEQ ID NO: 206
AAVhu.57	327	US20150315612 SEQ ID NO: 169
AAVhu.57	328	US20150315612 SEQ ID NO: 193
AAVhu.58	329	US20150315612 SEQ ID NO: 207
AAVhu.58	330	US20150315612 SEQ ID NO: 194
AAVhu.6 (AAV3.1)	331	US20150315612 SEQ ID NO: 5
AAVhu.6 (AAV3.1)	332	US20150315612 SEQ ID NO: 84
AAVhu.60	333	US20150315612 SEQ ID NO: 184
AAVhu.60 (AAV161.10)	334	US20150315612 SEQ ID NO: 170
AAVhu.61	335	US20150315612 SEQ ID NO: 185
AAVhu.61 (AAV161.6)	336	US20150315612 SEQ ID NO: 174
AAVhu.63	337	US20150315612 SEQ ID NO: 204
AAVhu.63	338	US20150315612 SEQ ID NO: 195
AAVhu.64	339	US20150315612 SEQ ID NO: 212
AAVhu.64	340	US20150315612 SEQ ID NO: 196
AAVhu.66	341	US20150315612 SEQ ID NO: 197
AAVhu.67	342	US20150315612 SEQ ID NO: 215
AAVhu.67	343	US20150315612 SEQ ID NO: 198
AAVhu.7	344	US20150315612 SEQ ID NO: 226
AAVhu.7	345	US20150315612 SEQ ID NO: 150
AAVhu.7 (AAV7.3)	346	US20150315612 SEQ ID NO: 55
AAVhu.71	347	US20150315612 SEQ ID NO: 79
AAVhu.8	348	US20150315612 SEQ ID NO: 53
AAVhu.8	349	US20150315612 SEQ ID NO: 12
AAVhu.8	350	US20150315612 SEQ ID NO: 151
AAVhu.9 (AAV3.1)	351	US20150315612 SEQ ID NO: 58
AAVhu.9 (AAV3.1)	352	US20150315612 SEQ ID NO: 155
AAV-LK01	353	US20150376607 SEQ ID NO: 2
AAV-LK01	354	US20150376607 SEQ ID NO: 29
AAV-LK02	355	US20150376607 SEQ ID NO: 3
AAV-LK02	356	US20150376607 SEQ ID NO: 30
AAV-LK03	357	US20150376607 SEQ ID NO: 4
AAV-LK03	358	WO2015121501 SEQ ID NO: 12, US20150376607 SEQ ID NO: 31
AAV-LK04	359	US20150376607 SEQ ID NO: 5
AAV-LK04	360	US20150376607 SEQ ID NO: 32
AAV-LK05	361	US20150376607 SEQ ID NO: 6
AAV-LK05	362	US20150376607 SEQ ID NO: 33
AAV-LK06	363	US20150376607 SEQ ID NO: 7
AAV-LK06	364	US20150376607 SEQ ID NO: 34
AAV-LK07	365	US20150376607 SEQ ID NO: 8
AAV-LK07	366	US20150376607 SEQ ID NO: 35

AAV-LK08	367	US20150376607 SEQ ID NO: 9
AAV-LK08	368	US20150376607 SEQ ID NO: 36
AAV-LK09	369	US20150376607 SEQ ID NO: 10
AAV-LK09	370	US20150376607 SEQ ID NO: 37
AAV-LK10	371	US20150376607 SEQ ID NO: 11
AAV-LK10	372	US20150376607 SEQ ID NO: 38
AAV-LK11	373	US20150376607 SEQ ID NO: 12
AAV-LK11	374	US20150376607 SEQ ID NO: 39
AAV-LK12	375	US20150376607 SEQ ID NO: 13
AAV-LK12	376	US20150376607 SEQ ID NO: 40
AAV-LK13	377	US20150376607 SEQ ID NO: 14
AAV-LK13	378	US20150376607 SEQ ID NO: 41
AAV-LK14	379	US20150376607 SEQ ID NO: 15
AAV-LK14	380	US20150376607 SEQ ID NO: 42
AAV-LK15	381	US20150376607 SEQ ID NO: 16
AAV-LK15	382	US20150376607 SEQ ID NO: 43
AAV-LK16	383	US20150376607 SEQ ID NO: 17
AAV-LK16	384	US20150376607 SEQ ID NO: 44
AAV-LK17	385	US20150376607 SEQ ID NO: 18
AAV-LK17	386	US20150376607 SEQ ID NO: 45
AAV-LK18	387	US20150376607 SEQ ID NO: 19
AAV-LK18	388	US20150376607 SEQ ID NO: 46
AAV-LK19	389	US20150376607 SEQ ID NO: 20
AAV-LK19	390	US20150376607 SEQ ID NO: 47
AAV-PAEC	391	US20150376607 SEQ ID NO: 1
AAV-PAEC	392	US20150376607 SEQ ID NO: 48
AAV-PAEC11	393	US20150376607 SEQ ID NO: 26
AAV-PAEC11	394	US20150376607 SEQ ID NO: 54
AAV-PAEC12	395	US20150376607 SEQ ID NO: 27
AAV-PAEC12	396	US20150376607 SEQ ID NO: 51
AAV-PAEC13	397	US20150376607 SEQ ID NO: 28
AAV-PAEC13	398	US20150376607 SEQ ID NO: 49
AAV-PAEC2	399	US20150376607 SEQ ID NO: 21
AAV-PAEC2	400	US20150376607 SEQ ID NO: 56
AAV-PAEC4	401	US20150376607 SEQ ID NO: 22
AAV-PAEC4	402	US20150376607 SEQ ID NO: 55
AAV-PAEC6	403	US20150376607 SEQ ID NO: 23
AAV-PAEC6	404	US20150376607 SEQ ID NO: 52
AAV-PAEC7	405	US20150376607 SEQ ID NO: 24
AAV-PAEC7	406	US20150376607 SEQ ID NO: 53
AAV-PAEC8	407	US20150376607 SEQ ID NO: 25
AAV-PAEC8	408	US20150376607 SEQ ID NO: 50
AAVpi.1	409	US20150315612 SEQ ID NO: 28
AAVpi.1	410	US20150315612 SEQ ID NO: 93
AAVpi.2	411	US20150315612 SEQ ID NO: 30

AAVpi.2	412	US20150315612 SEQ ID NO: 95
AAVpi.3	413	US20150315612 SEQ ID NO: 29
AAVpi.3	414	US20150315612 SEQ ID NO: 94
AAVrh.10	415	US20150159173 SEQ ID NO: 9
AAVrh.10	416	US20150159173 SEQ ID NO: 25
AAV44.2	417	US20030138772 SEQ ID NO: 59
AAVrh.10 (AAV44.2)	418	US20030138772 SEQ ID NO: 81
AAV42.1B	419	US20030138772 SEQ ID NO: 90
AAVrh.12 (AAV42.1b)	420	US20030138772 SEQ ID NO: 30
AAVrh.13	421	US20150159173 SEQ ID NO: 10
AAVrh.13	422	US20150159173 SEQ ID NO: 26
AAVrh.13	423	US20150315612 SEQ ID NO: 228
AAVrh.13R	424	US20150159173
AAV42.3A	425	US20030138772 SEQ ID NO: 87
AAVrh.14 (AAV42.3a)	426	US20030138772 SEQ ID NO: 32
AAV42.5A	427	US20030138772 SEQ ID NO: 89
AAVrh.17 (AAV42.5a)	428	US20030138772 SEQ ID NO: 34
AAV42.5B	429	US20030138772 SEQ ID NO: 91
AAVrh.18 (AAV42.5b)	430	US20030138772 SEQ ID NO: 29
AAV42.6B	431	US20030138772 SEQ ID NO: 112
AAVrh.19 (AAV42.6b)	432	US20030138772 SEQ ID NO: 38
AAVrh.2	433	US20150159173 SEQ ID NO: 39
AAVrh.2	434	US20150315612 SEQ ID NO: 231
AAVrh.20	435	US20150159173 SEQ ID NO: 1
AAV42.10	436	US20030138772 SEQ ID NO: 106
AAVrh.21 (AAV42.10)	437	US20030138772 SEQ ID NO: 35
AAV42.11	438	US20030138772 SEQ ID NO: 108
AAVrh.22 (AAV42.11)	439	US20030138772 SEQ ID NO: 37
AAV42.12	440	US20030138772 SEQ ID NO: 113
AAVrh.23 (AAV42.12)	441	US20030138772 SEQ ID NO: 58
AAV42.13	442	US20030138772 SEQ ID NO: 86
AAVrh.24 (AAV42.13)	443	US20030138772 SEQ ID NO: 31
AAV42.15	444	US20030138772 SEQ ID NO: 84
AAVrh.25 (AAV42.15)	445	US20030138772 SEQ ID NO: 28
AAVrh.2R	446	US20150159173
AAVrh.31 (AAV223.1)	447	US20030138772 SEQ ID NO: 48
AAVC1	448	US20030138772 SEQ ID NO: 60
AAVrh.32 (AAVC1)	449	US20030138772 SEQ ID NO: 19
AAVrh.32/33	450	US20150159173 SEQ ID NO: 2
AAVrh.33 (AAVC3)	451	US20030138772 SEQ ID NO: 20
AAVC5	452	US20030138772 SEQ ID NO: 62
AAVrh.34 (AAVC5)	453	US20030138772 SEQ ID NO: 21
AAVF1	454	US20030138772 SEQ ID NO: 109
AAVrh.35 (AAVF1)	455	US20030138772 SEQ ID NO: 22
AAVF3	456	US20030138772 SEQ ID NO: 111

AAVrh.36 (AAVF3)	457	US20030138772 SEQ ID NO: 23
AAVrh.37	458	US20030138772 SEQ ID NO: 24
AAVrh.37	459	US20150159173 SEQ ID NO: 40
AAVrh.37	460	US20150315612 SEQ ID NO: 229
AAVrh.37R2	461	US20150159173
AAVrh.38 (AAVLG-4)	462	US20150315612 SEQ ID NO: 7
AAVrh.38 (AAVLG-4)	463	US20150315612 SEQ ID NO: 86
AAVrh.39	464	US20150159173 SEQ ID NO: 20, US20150315612 SEQ ID NO: 13
AAVrh.39	465	US20150159173 SEQ ID NO: 3, US20150159173 SEQ ID NO: 36, US20150315612 SEQ ID NO: 89
AAVrh.40	466	US20150315612 SEQ ID NO: 92
AAVrh.40 (AAVLG-10)	467	US20150315612 SEQ ID No: 14
AAVrh.43 (AAVN721-8)	468	US20150315612 SEQ ID NO: 43, US20150159173 SEQ ID NO: 21
AAVrh.43 (AAVN721-8)	469	US20150315612 SEQ ID NO: 163, US20150159173 SEQ ID NO: 37
AAVrh.44	470	US20150315612 SEQ ID NO: 34
AAVrh.44	471	US20150315612 SEQ ID NO: 111
AAVrh.45	472	US20150315612 SEQ ID NO: 41
AAVrh.45	473	US20150315612 SEQ ID NO: 109
AAVrh.46	474	US20150159173 SEQ ID NO: 22, US20150315612 SEQ ID NO: 19
AAVrh.46	475	US20150159173 SEQ ID NO: 4, US20150315612 SEQ ID NO: 101
AAVrh.47	476	US20150315612 SEQ ID NO: 38
AAVrh.47	477	US20150315612 SEQ ID NO: 118
AAVrh.48	478	US20150159173 SEQ ID NO: 44, US20150315612 SEQ ID NO: 115
AAVrh.48.1	479	US20150159173
AAVrh.48.1.2	480	US20150159173
AAVrh.48.2	481	US20150159173
AAVrh.48 (AAV1-7)	482	US20150315612 SEQ ID NO: 32
AAVrh.49 (AAV1-8)	483	US20150315612 SEQ ID NO: 25
AAVrh.49 (AAV1-8)	484	US20150315612 SEQ ID NO: 103
AAVrh.50 (AAV2-4)	485	US20150315612 SEQ ID NO: 23
AAVrh.50 (AAV2-4)	486	US20150315612 SEQ ID NO: 108
AAVrh.51 (AAV2-5)	487	US20150315612 SEQ ID No: 22
AAVrh.51 (AAV2-5)	488	US20150315612 SEQ ID NO: 104
AAVrh.52 (AAV3-9)	489	US20150315612 SEQ ID NO: 18
AAVrh.52 (AAV3-9)	490	US20150315612 SEQ ID NO: 96
AAVrh.53	491	US20150315612 SEQ ID NO: 97
AAVrh.53 (AAV3-11)	492	US20150315612 SEQ ID NO: 17
AAVrh.53 (AAV3-11)	493	US20150315612 SEQ ID NO: 186
AAVrh.54	494	US20150315612 SEQ ID NO: 40
AAVrh.54	495	US20150159173 SEQ ID NO: 49, US20150315612 SEQ ID NO: 116
AAVrh.55	496	US20150315612 SEQ ID NO: 37
AAVrh.55 (AAV4-19)	497	US20150315612 SEQ ID NO: 117
AAVrh.56	498	US20150315612 SEQ ID NO: 54
AAVrh.56	499	US20150315612 SEQ ID NO: 152
AAVrh.57	500	US20150315612 SEQ ID NO: 26

AAVrh.57	501	US20150315612 SEQ ID NO: 105
AAVrh.58	502	US20150315612 SEQ ID NO: 27
AAVrh.58	503	US20150159173 SEQ ID NO: 48, US20150315612 SEQ ID NO: 106
AAVrh.58	504	US20150315612 SEQ ID NO: 232
AAVrh.59	505	US20150315612 SEQ ID NO: 42
AAVrh.59	506	US20150315612 SEQ ID NO: 110
AAVrh.60	507	US20150315612 SEQ ID NO: 31
AAVrh.60	508	US20150315612 SEQ ID NO: 120
AAVrh.61	509	US20150315612 SEQ ID NO: 107
AAVrh.61 (AAV2-3)	510	US20150315612 SEQ ID NO: 21
AAVrh.62 (AAV2-15)	511	US20150315612 SEQ ID No: 33
AAVrh.62 (AAV2-15)	512	US20150315612 SEQ ID NO: 114
AAVrh.64	513	US20150315612 SEQ ID No: 15
AAVrh.64	514	US20150159173 SEQ ID NO: 43, US20150315612 SEQ ID NO: 99
AAVrh.64	515	US20150315612 SEQ ID NO: 233
AAVRh.64R1	516	US20150159173
AAVRh.64R2	517	US20150159173
AAVrh.65	518	US20150315612 SEQ ID NO: 35
AAVrh.65	519	US20150315612 SEQ ID NO: 112
AAVrh.67	520	US20150315612 SEQ ID NO: 36
AAVrh.67	521	US20150315612 SEQ ID NO: 230
AAVrh.67	522	US20150159173 SEQ ID NO: 47, US20150315612 SEQ ID NO: 113
AAVrh.68	523	US20150315612 SEQ ID NO: 16
AAVrh.68	524	US20150315612 SEQ ID NO: 100
AAVrh.69	525	US20150315612 SEQ ID NO: 39
AAVrh.69	526	US20150315612 SEQ ID NO: 119
AAVrh.70	527	US20150315612 SEQ ID NO: 20
AAVrh.70	528	US20150315612 SEQ ID NO: 98
AAVrh.71	529	US20150315612 SEQ ID NO: 162
AAVrh.72	530	US20150315612 SEQ ID NO: 9
AAVrh.73	531	US20150159173 SEQ ID NO: 5
AAVrh.74	532	US20150159173 SEQ ID NO: 6
AAVrh.8	533	US20150159173 SEQ ID NO: 41
AAVrh.8	534	US20150315612 SEQ ID NO: 235
AAVrh.8R	535	US20150159173, WO2015168666 SEQ ID NO: 9
AAVrh.8R A586R mutant	536	WO2015168666 SEQ ID NO: 10
AAVrh.8R R533A mutant	537	WO2015168666 SEQ ID NO: 11
BAAV (bovine AAV)	538	US9193769 SEQ ID NO: 8
BAAV (bovine AAV)	539	US9193769 SEQ ID NO: 10
BAAV (bovine AAV)	540	US9193769 SEQ ID NO: 4
BAAV (bovine AAV)	541	US9193769 SEQ ID NO: 2
BAAV (bovine AAV)	542	US9193769 SEQ ID NO: 6
BAAV (bovine AAV)	543	US9193769 SEQ ID NO: 1
BAAV (bovine AAV)	544	US9193769 SEQ ID NO: 5

BAAV (bovine AAV)	545	US9193769 SEQ ID NO: 3
BAAV (bovine AAV)	546	US9193769 SEQ ID NO: 11
BAAV (bovine AAV)	547	US7427396 SEQ ID NO: 5
BAAV (bovine AAV)	548	US7427396 SEQ ID NO: 6
BAAV (bovine AAV)	549	US9193769 SEQ ID NO: 7
BAAV (bovine AAV)	550	US9193769 SEQ ID NO: 9
BNP61 AAV	551	US20150238550 SEQ ID NO: 1
BNP61 AAV	552	US20150238550 SEQ ID NO: 2
BNP62 AAV	553	US20150238550 SEQ ID NO: 3
BNP63 AAV	554	US20150238550 SEQ ID NO: 4
caprine AAV	555	US7427396 SEQ ID NO: 3
caprine AAV	556	US7427396 SEQ ID NO: 4
true type AAV (ttAAV)	557	WO2015121501 SEQ ID NO: 2
AAAV (Avian AAV)	558	US9238800 SEQ ID NO: 12
AAAV (Avian AAV)	559	US9238800 SEQ ID NO: 2
AAAV (Avian AAV)	560	US9238800 SEQ ID NO: 6
AAAV (Avian AAV)	561	US9238800 SEQ ID NO: 4
AAAV (Avian AAV)	562	US9238800 SEQ ID NO: 8
AAAV (Avian AAV)	563	US9238800 SEQ ID NO: 14
AAAV (Avian AAV)	564	US9238800 SEQ ID NO: 10
AAAV (Avian AAV)	565	US9238800 SEQ ID NO: 15
AAAV (Avian AAV)	566	US9238800 SEQ ID NO: 5
AAAV (Avian AAV)	567	US9238800 SEQ ID NO: 9
AAAV (Avian AAV)	568	US9238800 SEQ ID NO: 3
AAAV (Avian AAV)	569	US9238800 SEQ ID NO: 7
AAAV (Avian AAV)	570	US9238800 SEQ ID NO: 11
AAAV (Avian AAV)	571	US9238800 SEQ ID NO: 13
AAAV (Avian AAV)	572	US9238800 SEQ ID NO: 1
AAV Shuffle 100-1	573	US20160017295 SEQ ID NO: 23
AAV Shuffle 100-1	574	US20160017295 SEQ ID NO: 11
AAV Shuffle 100-2	575	US20160017295 SEQ ID NO: 37
AAV Shuffle 100-2	576	US20160017295 SEQ ID NO: 29
AAV Shuffle 100-3	577	US20160017295 SEQ ID NO: 24
AAV Shuffle 100-3	578	US20160017295 SEQ ID NO: 12
AAV Shuffle 100-7	579	US20160017295 SEQ ID NO: 25
AAV Shuffle 100-7	580	US20160017295 SEQ ID NO: 13
AAV Shuffle 10-2	581	US20160017295 SEQ ID NO: 34
AAV Shuffle 10-2	582	US20160017295 SEQ ID NO: 26
AAV Shuffle 10-6	583	US20160017295 SEQ ID NO: 35
AAV Shuffle 10-6	584	US20160017295 SEQ ID NO: 27
AAV Shuffle 10-8	585	US20160017295 SEQ ID NO: 36
AAV Shuffle 10-8	586	US20160017295 SEQ ID NO: 28
AAV SM 100-10	587	US20160017295 SEQ ID NO: 41
AAV SM 100-10	588	US20160017295 SEQ ID NO: 33
AAV SM 100-3	589	US20160017295 SEQ ID NO: 40
AAV SM 100-3	590	US20160017295 SEQ ID NO: 32
AAV SM 10-1	591	US20160017295 SEQ ID NO: 38

AAV SM 10-1	592	US20160017295 SEQ ID NO: 30
AAV SM 10-2	593	US20160017295 SEQ ID NO: 10
AAV SM 10-2	594	US20160017295 SEQ ID NO: 22
AAV SM 10-8	595	US20160017295 SEQ ID NO: 39
AAV SM 10-8	596	US20160017295 SEQ ID NO: 31
AAV SM 100-10	587	US20160017295 SEQ ID NO: 41
AAV SM 100-10	588	US20160017295 SEQ ID NO: 33
AAV SM 100-3	589	US20160017295 SEQ ID NO: 40
AAV SM 100-3	590	US20160017295 SEQ ID NO: 32
AAV SM 10-1	591	US20160017295 SEQ ID NO: 38
AAV SM 10-1	592	US20160017295 SEQ ID NO: 30
AAV SM 10-2	593	US20160017295 SEQ ID NO: 10
AAV SM 10-2	594	US20160017295 SEQ ID NO: 22
AAV SM 10-8	595	US20160017295 SEQ ID NO: 39
AAV SM 10-8	596	US20160017295 SEQ ID NO: 31
AAVF1/HSC1	597	WO2016049230 SEQ ID NO: 20
AAVF2/HSC2	598	WO2016049230 SEQ ID NO: 21
AAVF3/HSC3	599	WO2016049230 SEQ ID NO: 22
AAVF4/HSC4	600	WO2016049230 SEQ ID NO: 23
AAVF5/HSC5	601	WO2016049230 SEQ ID NO: 25
AAVF6/HSC6	602	WO2016049230 SEQ ID NO: 24
AAVF7/HSC7	603	WO2016049230 SEQ ID NO: 27
AAVF8/HSC8	604	WO2016049230 SEQ ID NO: 28
AAVF9/HSC9	605	WO2016049230 SEQ ID NO: 29
AAVF11/HSC11	606	WO2016049230 SEQ ID NO: 26
AAVF12/HSC12	607	WO2016049230 SEQ ID NO: 30
AAVF13/HSC13	608	WO2016049230 SEQ ID NO: 31
AAVF14/HSC14	609	WO2016049230 SEQ ID NO: 32
AAVF15/HSC15	610	WO2016049230 SEQ ID NO: 33
AAVF16/HSC16	611	WO2016049230 SEQ ID NO: 34
AAVF17/HSC17	612	WO2016049230 SEQ ID NO: 35
AAVF1/HSC1	613	WO2016049230 SEQ ID NO: 2
AAVF2/HSC2	614	WO2016049230 SEQ ID NO: 3
AAVF3/HSC3	615	WO2016049230 SEQ ID NO: 5
AAVF4/HSC4	616	WO2016049230 SEQ ID NO: 6
AAVF5/HSC5	617	WO2016049230 SEQ ID NO: 11
AAVF6/HSC6	618	WO2016049230 SEQ ID NO: 7
AAVF7/HSC7	619	WO2016049230 SEQ ID NO: 8
AAVF8/HSC8	620	WO2016049230 SEQ ID NO: 9
AAVF9/HSC9	621	WO2016049230 SEQ ID NO: 10
AAVF11/HSC11	622	WO2016049230 SEQ ID NO: 4
AAVF12/HSC12	623	WO2016049230 SEQ ID NO: 12
AAVF13/HSC13	624	WO2016049230 SEQ ID NO: 14
AAVF14/HSC14	625	WO2016049230 SEQ ID NO: 15
AAVF15/HSC15	626	WO2016049230 SEQ ID NO: 16

AAVF16/HSC16	627	WO2016049230 SEQ ID NO: 17
AAVF17/HSC17	628	WO2016049230 SEQ ID NO: 13
AAV CBr-E1	629	US8734809 SEQ ID NO: 13
AAV CBr-E2	630	US8734809 SEQ ID NO: 14
AAV CBr-E3	631	US8734809 SEQ ID NO: 15
AAV CBr-E4	632	US8734809 SEQ ID NO: 16
AAV CBr-E5	633	US8734809 SEQ ID NO: 17
AAV CBr-e5	634	US8734809 SEQ ID NO: 18
AAV CBr-E6	635	US8734809 SEQ ID NO: 19
AAV CBr-E7	636	US8734809 SEQ ID NO: 20
AAV CBr-E8	637	US8734809 SEQ ID NO: 21
AAV CLv-D1	638	US8734809 SEQ ID NO: 22
AAV CLv-D2	639	US8734809 SEQ ID NO: 23
AAV CLv-D3	640	US8734809 SEQ ID NO: 24
AAV CLv-D4	641	US8734809 SEQ ID NO: 25
AAV CLv-D5	642	US8734809 SEQ ID NO: 26
AAV CLv-D6	643	US8734809 SEQ ID NO: 27
AAV CLv-D7	644	US8734809 SEQ ID NO: 28
AAV CLv-D8	645	US8734809 SEQ ID NO: 29
AAV CLv-E1	646	US8734809 SEQ ID NO: 13
AAV CLv-R1	647	US8734809 SEQ ID NO: 30
AAV CLv-R2	648	US8734809 SEQ ID NO: 31
AAV CLv-R3	649	US8734809 SEQ ID NO: 32
AAV CLv-R4	650	US8734809 SEQ ID NO: 33
AAV CLv-R5	651	US8734809 SEQ ID NO: 34
AAV CLv-R6	652	US8734809 SEQ ID NO: 35
AAV CLv-R7	653	US8734809 SEQ ID NO: 36
AAV CLv-R8	654	US8734809 SEQ ID NO: 37
AAV CLv-R9	655	US8734809 SEQ ID NO: 38
AAV CLg-F1	656	US8734809 SEQ ID NO: 39
AAV CLg-F2	657	US8734809 SEQ ID NO: 40
AAV CLg-F3	658	US8734809 SEQ ID NO: 41
AAV CLg-F4	659	US8734809 SEQ ID NO: 42
AAV CLg-F5	660	US8734809 SEQ ID NO: 43
AAV CLg-F6	661	US8734809 SEQ ID NO: 43
AAV CLg-F7	662	US8734809 SEQ ID NO: 44
AAV CLg-F8	663	US8734809 SEQ ID NO: 43
AAV CSp-1	664	US8734809 SEQ ID NO: 45
AAV CSp-10	665	US8734809 SEQ ID NO: 46
AAV CSp-11	666	US8734809 SEQ ID NO: 47
AAV CSp-2	667	US8734809 SEQ ID NO: 48
AAV CSp-3	668	US8734809 SEQ ID NO: 49
AAV CSp-4	669	US8734809 SEQ ID NO: 50
AAV CSp-6	670	US8734809 SEQ ID NO: 51
AAV CSp-7	671	US8734809 SEQ ID NO: 52

AAV CSp-8	672	US8734809 SEQ ID NO: 53
AAV CSp-9	673	US8734809 SEQ ID NO: 54
AAV CHt-2	674	US8734809 SEQ ID NO: 55
AAV CHt-3	675	US8734809 SEQ ID NO: 56
AAV CKd-1	676	US8734809 SEQ ID NO: 57
AAV CKd-10	677	US8734809 SEQ ID NO: 58
AAV CKd-2	678	US8734809 SEQ ID NO: 59
AAV CKd-3	679	US8734809 SEQ ID NO: 60
AAV CKd-4	680	US8734809 SEQ ID NO: 61
AAV CKd-6	681	US8734809 SEQ ID NO: 62
AAV CKd-7	682	US8734809 SEQ ID NO: 63
AAV CKd-8	683	US8734809 SEQ ID NO: 64
AAV CLv-1	684	US8734809 SEQ ID NO: 65
AAV CLv-12	685	US8734809 SEQ ID NO: 66
AAV CLv-13	686	US8734809 SEQ ID NO: 67
AAV CLv-2	687	US8734809 SEQ ID NO: 68
AAV CLv-3	688	US8734809 SEQ ID NO: 69
AAV CLv-4	689	US8734809 SEQ ID NO: 70
AAV CLv-6	690	US8734809 SEQ ID NO: 71
AAV CLv-8	691	US8734809 SEQ ID NO: 72
AAV CKd-B1	692	US8734809 SEQ ID NO: 73
AAV CKd-B2	693	US8734809 SEQ ID NO: 74
AAV CKd-B3	694	US8734809 SEQ ID NO: 75
AAV CKd-B4	695	US8734809 SEQ ID NO: 76
AAV CKd-B5	696	US8734809 SEQ ID NO: 77
AAV CKd-B6	697	US8734809 SEQ ID NO: 78
AAV CKd-B7	698	US8734809 SEQ ID NO: 79
AAV CKd-B8	699	US8734809 SEQ ID NO: 80
AAV CKd-H1	700	US8734809 SEQ ID NO: 81
AAV CKd-H2	701	US8734809 SEQ ID NO: 82
AAV CKd-H3	702	US8734809 SEQ ID NO: 83
AAV CKd-H4	703	US8734809 SEQ ID NO: 84
AAV CKd-H5	704	US8734809 SEQ ID NO: 85
AAV CKd-H6	705	US8734809 SEQ ID NO: 77
AAV CHt-1	706	US8734809 SEQ ID NO: 86
AAV CLv1-1	707	US8734809 SEQ ID NO: 171
AAV CLv1-2	708	US8734809 SEQ ID NO: 172
AAV CLv1-3	709	US8734809 SEQ ID NO: 173
AAV CLv1-4	710	US8734809 SEQ ID NO: 174
AAV Clv1-7	711	US8734809 SEQ ID NO: 175
AAV Clv1-8	712	US8734809 SEQ ID NO: 176
AAV Clv1-9	713	US8734809 SEQ ID NO: 177
AAV Clv1-10	714	US8734809 SEQ ID NO: 178
AAV.VR-355	715	US8734809 SEQ ID NO: 181
AAV.hu.48R3	716	US8734809 SEQ ID NO: 183

AAV CBr-E1	717	US8734809 SEQ ID NO: 87
AAV CBr-E2	718	US8734809 SEQ ID NO: 88
AAV CBr-E3	719	US8734809 SEQ ID NO: 89
AAV CBr-E4	720	US8734809 SEQ ID NO: 90
AAV CBr-E5	721	US8734809 SEQ ID NO: 91
AAV CBr-e5	722	US8734809 SEQ ID NO: 92
AAV CBr-E6	723	US8734809 SEQ ID NO: 93
AAV CBr-E7	724	US8734809 SEQ ID NO: 94
AAV CBr-E8	725	US8734809 SEQ ID NO: 95
AAV CLv-D1	726	US8734809 SEQ ID NO: 96
AAV CLv-D2	727	US8734809 SEQ ID NO: 97
AAV CLv-D3	728	US8734809 SEQ ID NO: 98
AAV CLv-D4	729	US8734809 SEQ ID NO: 99
AAV CLv-D5	730	US8734809 SEQ ID NO: 100
AAV CLv-D6	731	US8734809 SEQ ID NO: 101
AAV CLv-D7	732	US8734809 SEQ ID NO: 102
AAV CLv-D8	733	US8734809 SEQ ID NO: 103
AAV CLv-E1	734	US8734809 SEQ ID NO: 87
AAV CLv-R1	735	US8734809 SEQ ID NO: 104
AAV CLv-R2	736	US8734809 SEQ ID NO: 105
AAV CLv-R3	737	US8734809 SEQ ID NO: 106
AAV CLv-R4	738	US8734809 SEQ ID NO: 107
AAV CLv-R5	739	US8734809 SEQ ID NO: 108
AAV CLv-R6	740	US8734809 SEQ ID NO: 109
AAV CLv-R7	741	US8734809 SEQ ID NO: 110
AAV CLv-R8	742	US8734809 SEQ ID NO: 111
AAV CLv-R9	743	US8734809 SEQ ID NO: 112
AAV CLg-F1	744	US8734809 SEQ ID NO: 113
AAV CLg-F2	745	US8734809 SEQ ID NO: 114
AAV CLg-F3	746	US8734809 SEQ ID NO: 115
AAV CLg-F4	747	US8734809 SEQ ID NO: 116
AAV CLg-F5	748	US8734809 SEQ ID NO: 117
AAV CLg-F6	749	US8734809 SEQ ID NO: 117
AAV CLg-F7	750	US8734809 SEQ ID NO: 118
AAV CLg-F8	751	US8734809 SEQ ID NO: 117
AAV CSp-1	752	US8734809 SEQ ID NO: 119
AAV CSp-10	753	US8734809 SEQ ID NO: 120
AAV CSp-11	754	US8734809 SEQ ID NO: 121
AAV CSp-2	755	US8734809 SEQ ID NO: 122
AAV CSp-3	756	US8734809 SEQ ID NO: 123
AAV CSp-4	757	US8734809 SEQ ID NO: 124
AAV CSp-6	758	US8734809 SEQ ID NO: 125
AAV CSp-7	759	US8734809 SEQ ID NO: 126
AAV CSp-8	760	US8734809 SEQ ID NO: 127
AAV CSp-9	761	US8734809 SEQ ID NO: 128

AAV CHt-2	762	US8734809 SEQ ID NO: 129
AAV CHt-3	763	US8734809 SEQ ID NO: 130
AAV CKd-1	764	US8734809 SEQ ID NO: 131
AAV CKd-10	765	US8734809 SEQ ID NO: 132
AAV CKd-2	766	US8734809 SEQ ID NO: 133
AAV CKd-3	767	US8734809 SEQ ID NO: 134
AAV CKd-4	768	US8734809 SEQ ID NO: 135
AAV CKd-6	769	US8734809 SEQ ID NO: 136
AAV CKd-7	770	US8734809 SEQ ID NO: 137
AAV CKd-8	771	US8734809 SEQ ID NO: 138
AAV CLv-1	772	US8734809 SEQ ID NO: 139
AAV CLv-12	773	US8734809 SEQ ID NO: 140
AAV CLv-13	774	US8734809 SEQ ID NO: 141
AAV CLv-2	775	US8734809 SEQ ID NO: 142
AAV CLv-3	776	US8734809 SEQ ID NO: 143
AAV CLv-4	777	US8734809 SEQ ID NO: 144
AAV CLv-6	778	US8734809 SEQ ID NO: 145
AAV CLv-8	779	US8734809 SEQ ID NO: 146
AAV CKd-B1	780	US8734809 SEQ ID NO: 147
AAV CKd-B2	781	US8734809 SEQ ID NO: 148
AAV CKd-B3	782	US8734809 SEQ ID NO: 149
AAV CKd-B4	783	US8734809 SEQ ID NO: 150
AAV CKd-B5	784	US8734809 SEQ ID NO: 151
AAV CKd-B6	785	US8734809 SEQ ID NO: 152
AAV CKd-B7	786	US8734809 SEQ ID NO: 153
AAV CKd-B8	787	US8734809 SEQ ID NO: 154
AAV CKd-H1	788	US8734809 SEQ ID NO: 155
AAV CKd-H2	789	US8734809 SEQ ID NO: 156
AAV CKd-H3	790	US8734809 SEQ ID NO: 157
AAV CKd-H4	791	US8734809 SEQ ID NO: 158
AAV CKd-H5	792	US8734809 SEQ ID NO: 159
AAV CKd-H6	793	US8734809 SEQ ID NO: 151
AAV CHt-1	794	US8734809 SEQ ID NO: 160
AAV CHt-P2	795	WO2016065001 SEQ ID NO: 1
AAV CHt-P5	796	WO2016065001 SEQ ID NO: 2
AAV CHt-P9	797	WO2016065001 SEQ ID NO: 3
AAV CBr-7.1	798	WO2016065001 SEQ ID NO: 4
AAV CBr-7.2	799	WO2016065001 SEQ ID NO: 5
AAV CBr-7.3	800	WO2016065001 SEQ ID NO: 6
AAV CBr-7.4	801	WO2016065001 SEQ ID NO: 7
AAV CBr-7.5	802	WO2016065001 SEQ ID NO: 8
AAV CBr-7.7	803	WO2016065001 SEQ ID NO: 9
AAV CBr-7.8	804	WO2016065001 SEQ ID NO: 10
AAV CBr-7.10	805	WO2016065001 SEQ ID NO: 11
AAV CKd-N3	806	WO2016065001 SEQ ID NO: 12

AAV CKd-N4	807	WO2016065001 SEQ ID NO: 13
AAV CKd-N9	808	WO2016065001 SEQ ID NO: 14
AAV CLv-L4	809	WO2016065001 SEQ ID NO: 15
AAV CLv-L5	810	WO2016065001 SEQ ID NO: 16
AAV CLv-L6	811	WO2016065001 SEQ ID NO: 17
AAV CLv-K1	812	WO2016065001 SEQ ID NO: 18
AAV CLv-K3	813	WO2016065001 SEQ ID NO: 19
AAV CLv-K6	814	WO2016065001 SEQ ID NO: 20
AAV CLv-M1	815	WO2016065001 SEQ ID NO: 21
AAV CLv-M11	816	WO2016065001 SEQ ID NO: 22
AAV CLv-M2	817	WO2016065001 SEQ ID NO: 23
AAV CLv-M5	818	WO2016065001 SEQ ID NO: 24
AAV CLv-M6	819	WO2016065001 SEQ ID NO: 25
AAV CLv-M7	820	WO2016065001 SEQ ID NO: 26
AAV CLv-M8	821	WO2016065001 SEQ ID NO: 27
AAV CLv-M9	822	WO2016065001 SEQ ID NO: 28
AAV CHt-P1	823	WO2016065001 SEQ ID NO: 29
AAV CHt-P6	824	WO2016065001 SEQ ID NO: 30
AAV CHt-P8	825	WO2016065001 SEQ ID NO: 31
AAV CHt-6.1	826	WO2016065001 SEQ ID NO: 32
AAV CHt-6.10	827	WO2016065001 SEQ ID NO: 33
AAV CHt-6.5	828	WO2016065001 SEQ ID NO: 34
AAV CHt-6.6	829	WO2016065001 SEQ ID NO: 35
AAV CHt-6.7	830	WO2016065001 SEQ ID NO: 36
AAV CHt-6.8	831	WO2016065001 SEQ ID NO: 37
AAV CSp-8.10	832	WO2016065001 SEQ ID NO: 38
AAV CSp-8.2	833	WO2016065001 SEQ ID NO: 39
AAV CSp-8.4	834	WO2016065001 SEQ ID NO: 40
AAV CSp-8.5	835	WO2016065001 SEQ ID NO: 41
AAV CSp-8.6	836	WO2016065001 SEQ ID NO: 42
AAV CSp-8.7	837	WO2016065001 SEQ ID NO: 43
AAV CSp-8.8	838	WO2016065001 SEQ ID NO: 44
AAV CSp-8.9	839	WO2016065001 SEQ ID NO: 45
AAV CBr-B7.3	840	WO2016065001 SEQ ID NO: 46
AAV CBr-B7.4	841	WO2016065001 SEQ ID NO: 47
AAV3B	842	WO2016065001 SEQ ID NO: 48
AAV4	843	WO2016065001 SEQ ID NO: 49
AAV5	844	WO2016065001 SEQ ID NO: 50
AAV CHt-P2	845	WO2016065001 SEQ ID NO: 51
AAV CHt-P5	846	WO2016065001 SEQ ID NO: 52
AAV CHt-P9	847	WO2016065001 SEQ ID NO: 53
AAV CBr-7.1	848	WO2016065001 SEQ ID NO: 54
AAV CBr-7.2	849	WO2016065001 SEQ ID NO: 55
AAV CBr-7.3	850	WO2016065001 SEQ ID NO: 56
AAV CBr-7.4	851	WO2016065001 SEQ ID NO: 57

AAV CBr-7.5	852	WO2016065001 SEQ ID NO: 58
AAV CBr-7.7	853	WO2016065001 SEQ ID NO: 59
AAV CBr-7.8	854	WO2016065001 SEQ ID NO: 60
AAV CBr-7.10	855	WO2016065001 SEQ ID NO: 61
AAV CKd-N3	856	WO2016065001 SEQ ID NO: 62
AAV CKd-N4	857	WO2016065001 SEQ ID NO: 63
AAV CKd-N9	858	WO2016065001 SEQ ID NO: 64
AAV CLv-L4	859	WO2016065001 SEQ ID NO: 65
AAV CLv-L5	860	WO2016065001 SEQ ID NO: 66
AAV CLv-L6	861	WO2016065001 SEQ ID NO: 67
AAV CLv-K1	862	WO2016065001 SEQ ID NO: 68
AAV CLv-K3	863	WO2016065001 SEQ ID NO: 69
AAV CLv-K6	864	WO2016065001 SEQ ID NO: 70
AAV CLv-M1	865	WO2016065001 SEQ ID NO: 71
AAV CLv-M11	866	WO2016065001 SEQ ID NO: 72
AAV CLv-M2	867	WO2016065001 SEQ ID NO: 73
AAV CLv-M5	868	WO2016065001 SEQ ID NO: 74
AAV CLv-M6	869	WO2016065001 SEQ ID NO: 75
AAV CLv-M7	870	WO2016065001 SEQ ID NO: 76
AAV CLv-M8	871	WO2016065001 SEQ ID NO: 77
AAV CLv-M9	872	WO2016065001 SEQ ID NO: 78
AAV CHt-P1	873	WO2016065001 SEQ ID NO: 79
AAV CHt-P6	874	WO2016065001 SEQ ID NO: 80
AAV CHt-P8	875	WO2016065001 SEQ ID NO: 81
AAV CHt-6.1	876	WO2016065001 SEQ ID NO: 82
AAV CHt-6.10	877	WO2016065001 SEQ ID NO: 83
AAV CHt-6.5	878	WO2016065001 SEQ ID NO: 84
AAV CHt-6.6	879	WO2016065001 SEQ ID NO: 85
AAV CHt-6.7	880	WO2016065001 SEQ ID NO: 86
AAV CHt-6.8	881	WO2016065001 SEQ ID NO: 87
AAV CSp-8.10	882	WO2016065001 SEQ ID NO: 88
AAV CSp-8.2	883	WO2016065001 SEQ ID NO: 89
AAV CSp-8.4	884	WO2016065001 SEQ ID NO: 90
AAV CSp-8.5	885	WO2016065001 SEQ ID NO: 91
AAV CSp-8.6	886	WO2016065001 SEQ ID NO: 92
AAV CSp-8.7	887	WO2016065001 SEQ ID NO: 93
AAV CSp-8.8	888	WO2016065001 SEQ ID NO: 94
AAV CSp-8.9	889	WO2016065001 SEQ ID NO: 95
AAV CBr-B7.3	890	WO2016065001 SEQ ID NO: 96
AAV CBr-B7.4	891	WO2016065001 SEQ ID NO: 97
AAV3B	892	WO2016065001 SEQ ID NO: 98
AAV4	893	WO2016065001 SEQ ID NO: 99
AAV5	894	WO2016065001 SEQ ID NO: 100
AAVPHP.B or G2B-26	895	WO2015038958 SEQ ID NO: 8 and 13; GenBankALU85156.1
AAVPHP.B	896	WO2015038958 SEQ ID NO: 9

AAVG2B-13	897	WO2015038958 SEQ ID NO: 12
AAVTH1.1-32	898	WO2015038958 SEQ ID NO: 14
AAVTH1.1-35	899	WO2015038958 SEQ ID NO: 15

[0010] Each of the patents, applications and/or publications listed in Table 4 are hereby incorporated by reference in their entirety.

[00723] In one embodiment, the AAV serotype may be, or may have a sequence as described in International Patent Publication WO2015038958, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV9 (SEQ ID NO: 2 and 11 of WO2015038958 or SEQ ID NO: 153 and 154 respectively herein), PHP.B (SEQ ID NO: 8 and 9 of WO2015038958, herein SEQ ID NO: 895 and 896), G2B-13 (SEQ ID NO: 12 of WO2015038958, herein SEQ ID NO: 897), G2B-26 (SEQ ID NO: 13 of WO2015038958, herein SEQ ID NO: 895 and 896), TH1.1-32 (SEQ ID NO: 14 of WO2015038958, herein SEQ ID NO: 898), TH1.1-35 (SEQ ID NO: 15 of WO2015038958, herein SEQ ID NO: 899) or variants thereof. Further, any of the targeting peptides or amino acid inserts described in WO2015038958, may be inserted into any parent AAV serotype, such as, but not limited to, AAV9 (SEQ ID NO: 153 for the DNA sequence and SEQ ID NO: 154 for the amino acid sequence). In one embodiment, the amino acid insert is inserted between amino acids 586-592 of the parent AAV (e.g., AAV9). In another embodiment, the amino acid insert is inserted between amino acids 588-589 of the parent AAV sequence. The amino acid insert may be, but is not limited to, any of the following amino acid sequences, TLAVPFK (SEQ ID NO: 1 of WO2015038958; herein SEQ ID NO: 900), KFPVALT (SEQ ID NO: 3 of WO2015038958; herein SEQ ID NO: 901), LAVPFK (SEQ ID NO: 31 of WO2015038958; herein SEQ ID NO: 902), AVPFK (SEQ ID NO: 32 of WO2015038958; herein SEQ ID NO: 903), VPFK (SEQ ID NO: 33 of WO2015038958; herein SEQ ID NO: 904), TLAVPF (SEQ ID NO: 34 of WO2015038958; herein SEQ ID NO: 905), TLAVP (SEQ ID NO: 35 of WO2015038958; herein SEQ ID NO: 906), TLAV (SEQ ID NO: 36 of WO2015038958; herein SEQ ID NO: 907), SVSKPFL (SEQ ID NO: 28 of WO2015038958; herein SEQ ID NO: 908), FTLTTPK (SEQ ID NO: 29 of WO2015038958; herein SEQ ID NO: 909), MNATKNV (SEQ ID NO: 30 of WO2015038958; herein SEQ ID NO: 910), QSSQTPR (SEQ ID NO: 54 of WO2015038958; herein SEQ ID NO: 911), ILGTGTS (SEQ ID NO: 55 of WO2015038958; herein SEQ ID NO: 912), TRTNPEA (SEQ ID NO: 56 of WO2015038958; herein SEQ ID NO: 913), NGGTSSS (SEQ ID NO: 58 of WO2015038958; herein SEQ ID NO: 914), or YTLSQGW (SEQ ID NO: 60 of WO2015038958; herein SEQ ID NO: 915). Non-limiting examples of nucleotide sequences that may encode the amino acid inserts include the following, AAGTTTCCTGTGGCGTTGACT (for SEQ ID NO: 3 of WO2015038958; herein SEQ ID NO: 916), ACTTTGGCGGTGCCTTTTAAG (SEQ ID NO: 24 and 49 of WO2015038958; herein SEQ ID NO: 917), AGTGTGAGTAAGCCTTTTTTG (SEQ ID NO: 25 of WO2015038958; herein SEQ ID NO: 918), TTTACGTTGACGACGCCTAAG (SEQ ID NO: 26 of WO2015038958; herein SEQ ID NO: 919), ATGAATGCTACGAAGAATGTG (SEQ ID NO: 27 of WO2015038958; herein SEQ ID NO: 920), CAGTCGTCGCAGACGCCTAGG (SEQ ID NO: 48 of WO2015038958; herein SEQ ID NO: 921), ATTCTGGGGACTGGTACTTCG (SEQ ID NO: 50 and 52 of WO2015038958; herein SEQ ID NO: 922), ACGCGGACTAATCCTGAGGCT (SEQ ID NO: 51 of WO2015038958; herein SEQ ID NO: 923), AATGGGGGGACTAGTAGTTCT (SEQ ID NO: 53 of WO2015038958; herein SEQ ID NO: 924), or TATACTTTGTCGCAGGGTTGG (SEQ ID NO: 59 of WO2015038958; herein SEQ ID NO: 925).

[00724] In one embodiment, the AAV serotype may be engineered to comprise at least one AAV capsid CD8+ T-cell epitope. Hui et al. (Molecular Therapy – Methods & Clinical Development (2015) 2, 15029 doi:10.1038/mtm.2015.29; the contents of which are herein incorporated by reference in its entirety) identified AAV capsid-specific CD8+ T-cell epitopes for AAV1 and AAV2 (see e.g., Table 2 in the publication). As a non-limiting example, the capsid-specific CD8+ T-cell epitope may be for an AAV2 serotype. As a non-limiting example, the capsid-specific CD8+ T-cell epitope may be for an AAV1 serotype.

[00725] In one embodiment, the AAV serotype may be engineered to comprise at least one AAV capsid CD8+ T-cell epitope for AAV2 such as, but not limited to, SADNNNSEY (SEQ ID NO: 926), LIDQYLYYL (SEQ ID NO: 927), VPQYGYLTL (SEQ ID NO: 928), TTSTRTWAL (SEQ ID NO: 929), YHLNGRDSL (SEQ ID NO: 930), SQAVGRSSF (SEQ ID NO: 931), VPANPSTTF (SEQ ID NO: 932), FPQSGVLIF (SEQ ID NO: 933), YFDFNRFHCHFSPRD (SEQ ID NO: 934), VGNSSGNWHCDSTWM (SEQ ID NO: 935), QFSQAGASDIRDQSR (SEQ ID NO: 936), GASDIRQSRNWLP (SEQ ID NO: 937) and GNRQAATADVNTQGV (SEQ ID NO: 938).

[00726] In one embodiment, the AAV serotype may be engineered to comprise at least one AAV capsid CD8+ T-cell epitope for AAV1 such as, but not limited to, LDRLMNPLI (SEQ ID NO: 939), TTSTRTWAL (SEQ ID NO: 929), and QPAKKRLNF (SEQ ID NO: 940)).

[00727] In one embodiment, peptides for inclusion in an AAV serotype may be identified using the methods described by Hui et al. (Molecular Therapy – Methods & Clinical Development (2015) 2, 15029 doi:10.1038/mtm.2015.29; the contents of which are herein incorporated by reference in its entirety). As a non-limiting example, the procedure includes isolating human splenocytes, restimulating the splenocytes in vitro using individual peptides spanning the amino acid sequence of the AAV capsid protein, IFN-gamma ELISpot with the individual peptides used for the in vitro restimulation, bioinformatics analysis to determine the HLA restriction of 15-mers identified by IFN-gamma ELISpot, idenification of candidate reactive 9-mer epitopes for a given HLA allele, synthesis candidate 9-mers, second IFN-gamma ELISpot screening of splenocytes from subjects carrying the HLA alleles to which identified AAV epitopes are predicted to bind, determine the AAV capsid-reactive CD8+ T cell epitopes and determine the frequency of subjects reacting to a given AAV epitope.

[00728] In one embodiment, the AAV may be a serotype generated by Cre-recombination-based AAV targeted evolution (CREATE) as described by Deverman et al., (Nature Biotechnology 34(2):204-209 (2016)), the contents of which are herein incorporated by reference in their entirety. In one embodiment, AAV serotypes generated in this manner have improved CNS transduction and/or neuronal and astrocytic tropism, as compared to other AAV serotypes. As non-limiting examples, the AAV serotype may be PHP.B, PHP.B2, PHP.B3, PHP.A, G2A12, G2A15. In one embodiment, these AAV serotypes may be AAV9 (SEQ ID NO: 153 and 154) derivatives with a 7-amino acid insert between amino acids 588-589. Non-limiting examples of these 7-amino acid inserts include TLAVPFK (SEQ ID NO: 900), SVSKPFL (SEQ ID NO: 908), FTLTTPK (SEQ ID NO: 909), YTLSQGW (SEQ ID NO: 915), QAVRTSL (SEQ ID NO: 941) and/or LAKERLS (SEQ ID NO: 942).

[00729] In one embodiment, the AAV serotype may be as described in Jackson et al (Frontiers in Molecular Neuroscience 9:154 (2016)), the contents of which are herein incorporated by reference in their entirety. In some embodiments, the AAV serotype is PHP.B or AAV9. In some embodiments, the AAV serotype is paired with a synapsin promoter to enhance neuronal transduction, as compared to when more ubiquitous promoters are used (i.e., CBA or CMV).

[00730] In one embodiment, peptides for inclusion in an AAV serotype may be identified by isolating human splenocytes, restimulating the splenocytes in vitro using individual peptides spanning the amino acid sequence of the AAV capsid protein, IFN-gamma ELISpot with the individual peptides used for the in vitro restimulation, bioinformatics analysis to determine the given allele restriction of 15-mers identified by IFN-gamma ELISpot, idenification of candidate reactive 9-mer epitopes for a given allele, synthesis candidate 9-mers, second IFN-gamma ELISpot screening of splenocytes from subjects carrying the specific alleles to which identified AAV epitopes are predicted to bind, determine the AAV capsid-reactive CD8+ T cell epitopes and determine the frequency of subjects reacting to a given AAV epitope.

[00731] AAV vectors comprising the nucleic acid sequence for the siRNA molecules may be prepared or derived from various serotypes of AAVs, including, but not limited to, AAV1,

AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV9.47, AAV9(hu14), AAV10, AAV11, AAV12, AAVrh8, AAVrh10, AAV-DJ8, AAV-DJ, AAV-PHP.A, and/or AAV-PHP.B. In some cases, different serotypes of AAVs may be mixed together or with other types of viruses to produce chimeric AAV vectors. As a non-limiting example, the AAV vector is derived from the AAV9 serotype.

Viral Genome Component: Inverted Terminal Repeats (ITRs)

[00732] The AAV particles of the present invention comprise a viral genome with at least one ITR region and a payload region. In one embodiment the viral genome has two ITRs. These two ITRs flank the payload region at the 5' and 3' ends. The ITRs function as origins of replication comprising recognition sites for replication. ITRs comprise sequence regions which can be complementary and symmetrically arranged. ITRs incorporated into viral genomes of the invention may be comprised of naturally occurring polynucleotide sequences or recombinantly derived polynucleotide sequences.

[00733] The ITRs may be derived from the same serotype as the capsid, selected from any of the serotypes listed in Table 6, or a derivative thereof. The ITR may be of a different serotype than the capsid. In one embodiment the AAV particle has more than one ITR. In a non-limiting example, the AAV particle has a viral genome comprising two ITRs. In one embodiment the ITRs are of the same serotype as one another. In another embodiment the ITRs are of different serotypes. Non-limiting examples include zero, one or both of the ITRs having the same serotype as the capsid. In one embodiment both ITRs of the viral genome of the AAV particle are AAV2 ITRs.

[00734] Independently, each ITR may be about 100 to about 150 nucleotides in length. An ITR may be about 100-105 nucleotides in length, 106-110 nucleotides in length, 111-115 nucleotides in length, 116-120 nucleotides in length, 121-125 nucleotides in length, 126-130 nucleotides in length, 131-135 nucleotides in length, 136-140 nucleotides in length, 141-145 nucleotides in length or 146-150 nucleotides in length. In one embodiment the ITRs are 140-142 nucleotides in length. Non limiting examples of ITR length are 102, 140, 141, 142, 145 nucleotides in length, and those having at least 95% identity thereto.

[00735] In one embodiment, the encoded siRNA molecule may be located near the 5' end of the flip ITR in an expression vector. In another embodiment, the encoded siRNA molecule may be located near the 3' end of the flip ITR in an expression vector. In yet another embodiment, the encoded siRNA molecule may be located near the 5' end of the flop ITR in an expression vector. In yet another embodiment, the encoded siRNA molecule may be located near the 3' end of the flop ITR in an expression vector. In one embodiment, the encoded siRNA molecule may be located between the 5' end of the flip ITR and the 3' end of the flop ITR in an expression vector. In one embodiment, the encoded siRNA molecule may be located between (e.g., half-way between the 5' end of the flip ITR and 3' end of the flop ITR or the 3' end of the flop ITR and the 5' end of the flip ITR), the 3' end of the flip ITR and the 5' end of the flip ITR in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector.

Viral Genome Component: Promoters

[00736] A person skilled in the art may recognize that a target cell may require a specific promoter including but not limited to a promoter that is species specific, inducible, tissue-specific, or cell cycle-specific (Parr et al., Nat. Med.3:1145-9 (1997); the contents of which are herein incorporated by reference in its entirety).

[00737] In one embodiment, the promoter is a promoter deemed to be efficient to drive the expression of the modulatory polynucleotide.

[00738] In one embodiment, the promoter is a promoter having a tropism for the cell being targeted.

[00739] In one embodiment, the promoter is a weak promoter which provides expression of a payload e.g., a modulatory polynucleotide, e.g., siRNA or dsRNA, for a period of time in targeted tissues such as, but not limited to, nervous system tissues. Expression may be for a period of 1 hour, 2, hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 2 weeks, 15 days, 16 days, 17 days, 18 days, 19 days, 20 days, 3 weeks, 22 days, 23 days, 24 days, 25 days, 26 days, 27 days, 28 days, 29 days, 30 days, 31 days, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years or more than 10 years. Expression may be for 1-5 hours, 1-12 hours, 1-2 days, 1-5 days, 1-2 weeks, 1-3 weeks, 1-4 weeks, 1-2 months, 1-4 months, 1-6 months, 2-6 months, 3-6 months, 3-9 months, 4-8 months, 6-12 months, 1-2 years, 1-5 years, 2-5 years, 3-6 years, 3-8 years, 4-8 years or 5-10 years. As a non-limiting example, the promoter is a weak promoter for sustained expression of a payload in nervous tissues.

[00740] In one embodiment, the promoter may be a promoter which is less than 1 kb. The promoter may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800. The promoter may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500, 300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-800, 600-700, 600-800 or 700-800.

[00741] In one embodiment, the promoter may be a combination of two or more components such as, but not limited to, CMV and CBA. Each component may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800. Each component may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500, 300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-

800, 600-700, 600-800 or 700-800. As a non-limiting example, the promoter is a combination of a 382 nucleotide CMV-enhancer sequence and a 260 nucleotide CBA-promoter sequence.

[00742] In one embodiment, the vector genome comprises at least one element to enhance the target specificity and expression (See e.g., Powell et al. Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy, 2015; the contents of which are herein incorporated by reference in its entirety). Non-limiting examples of elements to enhance the transgene target specificity and expression include promoters, endogenous miRNAs, post-transcriptional regulatory elements (PREs), polyadenylation (PolyA) signal sequences and upstream enhancers (USEs), CMV enhancers and introns.

[00743] In one embodiment, the vector genome comprises at least one element to enhance the target specificity and expression (See e.g., Powell et al. Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy, 2015; the contents of which are herein incorporated by reference in its entirety) such as promoters.

[00744] Promoters for which promote expression in most tissues include, but are not limited to, human elongation factor 1α-subunit (EF1α), immediate-early cytomegalovirus (CMV), chicken β-actin (CBA) and its derivative CAG, the β glucuronidase (GUSB), or ubiquitin C (UBC). Tissue-specific expression elements can be used to restrict expression to certain cell types such as, but not limited to, nervous system promoters which can be used to restrict expression to neurons, astrocytes, or oligodendrocytes. Non-limiting example of tissue-specific expression elements for neurons include neuron-specific enolase (NSE), platelet-derived growth factor (PDGF), platelet-derived growth factor B-chain (PDGF-β), the synapsin (Syn), the methyl-CpG binding protein 2 (MeCP2), CaMKII, mGluR2, NFL, NFH, nβ2, PPE, Enk and EAAT2 promoters. A non-limiting example of tissue-specific expression elements for astrocytes include the glial fibrillary acidic protein (GFAP) and EAAT2 promoters. A non-limiting example of a tissue-specific expression element for oligodendrocytes include the myelin basic protein (MBP) promoter.

[00745] In one embodiment, the vector genome comprises a ubiquitous promoter. Non-limiting examples of ubiquitous promoters include H1, U6, CMV, CBA (including derivatives CAG, CBh, etc.), EF-1α, PGK, UBC, GUSB (hGBp), and UCOE (promoter of HNRPA2B1-CBX3). Yu et al. (Molecular Pain 2011, 7:63; the contents of which are herein incorporated by reference in its entirety) evaluated the expression of eGFP under the CAG, EFIα, PGK and UBC promoters in rat DRG cells and primary DRG cells using lentiviral vectors and found that UBC showed weaker expression than the other 3 promoters and there was only 10-12% glia expression seen for all promoters. Soderblom et al. (E. Neuro 2015; the contents of which are herein incorporated by reference in its entirety) the expression of eGFP in AAV8 with CMV and UBC promoters and AAV2 with the CMV promoter after injection in the motor cortex. Intranasal administration of a plasmid containing a UBC or EFIα promoter showed a sustained airway expression greater than the expression with the CMV promoter (See e.g., Gill et al., Gene Therapy 2001, Vol. 8, 1539-1546; the contents of which are herein incorporated by reference in its entirety). Husain et al. (Gene Therapy 2009; the contents of which are herein incorporated by reference in its entirety) evaluated a HβH construct with a hGUSB promoter, a HSV-1LAT promoter and a NSE promoter and found that the HβH construct showed weaker expression than NSE in mice brain. Passini and Wolfe (J. Virol. 2001, 12382-12392, the contents of which are herein incorporated by reference in its entirety) evaluated the long term effects of the HβH vector following an intraventricular injection in neonatal mice and found that there was sustained expression for at least 1 year. Low expression in all brain regions was found by Xu et al. (Gene Therapy 2001, 8, 1323-1332; the contents of which are herein incorporated by reference in its entirety) when NF-L and NF-H promoters were used as compared to the CMV-lacZ, CMV-luc, EF, GFAP, hENK, nAChR, PPE, PPE + wpre, NSE (0.3 kb), NSE (1.8 kb) and NSE (1.8 kb + wpre). Xu et al. found that the promoter activity in descending order was NSE (1.8 kb), EF, NSE (0.3 kb), GFAP, CMV, hENK, PPE, NFL and NFH. NFL is a 650 nucleotide promoter and NFH is a 920 nucleotide promoter which are both absent in the liver but NFH is abundant in the sensory proprioceptive neurons, brain and spinal cord and NFH is present in the heart. Scn8a is a 470 nucleotide promoter which expresses throughout the DRG, spinal cord and brain with particularly high expression seen in the hippocampal neurons and cerebellar Purkinje cells, cortex, thalamus and hypothalamus (See e.g., Drews et al. 2007 and Raymond et al. 2004; the contents of each of which are herein incorporated by reference in their entireties).

[00746] In one embodiment, the vector genome comprises an UBC promoter. The UBC promoter may have a size of 300-350 nucleotides. As a non-limiting example, the UBC promoter is 332 nucleotides.

[00747] In one embodiment, the vector genome comprises a GUSB promoter. The GUSB promoter may have a size of 350-400 nucleotides. As a non-limiting example, the GUSB promoter is 378 nucleotides. As a non-limiting example, the construct may be AAV-promoter-CMV/globin intron-modulatory polynucleotide-RBG, where the AAV may be self-complementary and the AAV may be the DJ serotype.

[00748] In one embodiment, the vector genome comprises a NFL promoter. The NFL promoter may have a size of 600-700 nucleotides. As a non-limiting example, the NFL promoter is 650 nucleotides. As a non-limiting example, the construct may be AAV-promoter-CMV/globin intron-modulatory polynucleotide-RBG, where the AAV may be self-complementary and the AAV may be the DJ serotype.

[00749] In one embodiment, the vector genome comprises a NFH promoter. The NFH promoter may have a size of 900-950 nucleotides. As a non-limiting example, the NFH promoter is 920 nucleotides. As a non-limiting example, the construct may be AAV-promoter-CMV/globin intron-modulatory polynucleotide-RBG, where the AAV may be self-complementary and the AAV may be the DJ serotype.

[00750] In one embodiment, the vector genome comprises a scn8a promoter. The scn8a promoter may have a size of 450-500 nucleotides. As a non-limiting example, the scn8a promoter is 470 nucleotides. As a non-limiting example, the construct may be AAV-promoter-CMV/globin intron-modulatory polynucleotide-RBG, where the AAV may be self-complementary and the AAV may be the DJ serotype.

[00751] In one embodiment, the vector genome comprises a FXN promoter.

[00752] In one embodiment, the vector genome comprises a PGK promoter.

[00753] In one embodiment, the vector genome comprises a CBA promoter.

[00754] In one embodiment, the vector genome comprises a CMV promoter.

[00755] In one embodiment, the vector genome comprises a H1 promoter.

[00756] In one embodiment, the vector genome comprises a U6 promoter.

[00757] In one embodiment, the vector genome comprises a liver or a skeletal muscle promoter. Non-limiting examples of liver promoters include hAAT and TBG. Non-limiting examples of skeletal muscle promoters include Desmin, MCK and C5-12.

[00758] In one embodiment, the AAV vector comprises an enhancer element, a promoter and/or a 5'UTR intron. The enhancer may be, but is not limited to, a CMV enhancer, the promoter may be, but is not limited to, a CMV, CBA, UBC, GUSB, NSE, Synapsin, MeCP2, and GFAP promoter and the 5'UTR/intron may be, but is not limited to, SV40, and CBA-MVM. As a non-limiting example, the enhancer, promoter and/or intron used in combination may be: (1) CMV enhancer, CMV promoter, SV40 5'UTR intron; (2) CMV enhancer, CBA promoter, SV 40 5'UTR intron; (3) CMV enhancer, CBA promoter, CBA-MVM 5'UTR intron; (4) UBC promoter; (5) GUSB promoter; (6) NSE promoter; (7) Synapsin promoter; (8) MeCP2 promoter; (9) GFAP promoter, (10) H1 promoter; and (11) U6 promoter.

[00759] In one embodiment, the AAV vector has an engineered promoter.

Viral Genome Component: Introns

[00760] In one embodiment, the vector genome comprises at least one element to enhance the transgene target specificity and expression (See e.g., Powell et al. Viral Expression Cassette

Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy, 2015; the contents of which are herein incorporated by reference in its entirety) such as an intron. Non-limiting examples of introns include, MVM (67-97 bps), F.IX truncated intron 1 (300 bps), β-globin SD/immunoglobulin heavy chain splice acceptor (250 bps), adenovirus splice donor/immunoglobin splice acceptor (500 bps), SV40 late splice donor/splice acceptor (19S/16S) (180 bps) and hybrid adenovirus splice donor/IgG splice acceptor (230 bps).

[00761] In one embodiment, the intron may be 100-500 nucleotides in length. The intron may have a length of 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490 or 500. The promoter may have a length between 80-100, 80-120, 80-140, 80-160, 80-180, 80-200, 80-250, 80-300, 80-350, 80-400, 80-450, 80-500, 200-300, 200-400, 200-500, 300-400, 300-500, or 400-500.

[00762] In one embodiment, the AAV vector may comprise an SV40 intron or fragment or variant thereof. As a non-limiting example, the promoter may be CMV. As another non-limiting example, the promoter may be CBA. As yet another non-limiting example, the promoter may be H1.

[00763] In one embodiment, the AAV vector may comprise a beta-globin intron or a frament or variant thereof. As a non-limiting example, the promoter may be CMV. As another non-limiting example, the promoter may be CBA. As yet another non-limiting example, the promoter may be H1.

[00764] In one embodiment, the encoded siRNA molecule may be located downstream of an intron in an expression vector such as, but not limited to, SV40 intron or beta globin intron or others known in the art. Further, the encoded siRNA molecule may also be located upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the promoter with an intron and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the intron and/or upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides downstream from the intron and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% of the sequence downstream from the intron and/or upstream of the polyadenylation sequence in an expression vector.

Viral Genome Component: Polyadenylation Sequence

[00765] In one embodiment, the viral genome of the AAV particles of the present invention comprise at least one polyadenylation sequence. The viral genome of the AAV particle may comprise a polyadenylation sequence between the 3’ end of the payload coding sequence and the 5’ end of the 3’ITR.

[00766] In one embodiment, the polyadenylation sequence or “polyA sequence” may range from absent to about 500 nucleotides in length. The polyadenylation sequence may be, but is not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, and 500 nucleotides in length.

[00767] In one embodiment, the polyadenylation sequence is 50-100 nucleotides in length.

[00768] In one embodiment, the polyadenylation sequence is 50-150 nucleotides in length.

[00769] In one embodiment, the polyadenylation sequence is 50-160 nucleotides in length.

[00770] In one embodiment, the polyadenylation sequence is 50-200 nucleotides in length.

[00771] In one embodiment, the polyadenylation sequence is 60-100 nucleotides in length.

[00772] In one embodiment, the polyadenylation sequence is 60-150 nucleotides in length.

[00773] In one embodiment, the polyadenylation sequence is 60-160 nucleotides in length.

[00774] In one embodiment, the polyadenylation sequence is 60-200 nucleotides in length.

[00775] In one embodiment, the polyadenylation sequence is 70-100 nucleotides in length.

[00776] In one embodiment, the polyadenylation sequence is 70-150 nucleotides in length.

[00777] In one embodiment, the polyadenylation sequence is 70-160 nucleotides in length.

[00778] In one embodiment, the polyadenylation sequence is 70-200 nucleotides in length.

[00779] In one embodiment, the polyadenylation sequence is 80-100 nucleotides in length.

[00780] In one embodiment, the polyadenylation sequence is 80-150 nucleotides in length.

[00781] In one embodiment, the polyadenylation sequence is 80-160 nucleotides in length.

[00782] In one embodiment, the polyadenylation sequence is 80-200 nucleotides in length.

[00783] In one embodiment, the polyadenylation sequence is 90-100 nucleotides in length.

[00784] In one embodiment, the polyadenylation sequence is 90-150 nucleotides in length.

[00785] In one embodiment, the polyadenylation sequence is 90-160 nucleotides in length.

[00786] In one embodiment, the polyadenylation sequence is 90-200 nucleotides in length.

[00787] In one embodiment, the encoded siRNA molecule may be located upstream of the polyadenylation sequence in an expression vector. Further, the encoded siRNA molecule may be located downstream of a promoter such as, but not limited to, CMV, U6, H1, CBA or a CBA promoter with a SV40 or a human betaglobin intron in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector.

Expression Vector

[00788] In one embodiment, an expression vector (e.g., AAV vector) may comprise at least one of the modulatory polynucleotides encoding at least one of the siRNA sequences or duplexes described herein.

[00789] In one embodiment, an expression vector may comprise, from ITR to ITR recited 5' to 3', an ITR, a promoter, an intron, a modulatory polynucleotide, a polyA sequence and an ITR.

Genome Size

[00790] In one embodiment, the vector genome which comprises a nucleic acid sequence encoding the modulatory polynucleotides described herein may be single stranded or double stranded vector genome. The size of the vector genome may be small, medium, large or the maximum size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[00791] In one embodiment, the vector genome which comprises a nucleic acid sequence encoding the modulatory polynucleotides described herein may be a small single stranded vector genome. A small single stranded vector genome may be 2.7 to 3.5 kb in size such as about 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, and 3.5 kb in size. As a non-limiting example, the small single stranded vector genome may be 3.2 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[00792] In one embodiment, the vector genome which comprises a nucleic acid sequence encoding the modulatory polynucleotides described herein may be a small double stranded vector genome. A small double stranded vector genome may be 1.3 to 1.7 kb in size such as about 1.3, 1.4, 1.5, 1.6, and 1.7 kb in size. As a non-limiting example, the small double stranded vector genome may be 1.6 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[00793] In one embodiment, the vector genome which comprises a nucleic acid sequence encoding the modulatory polynucleotides described herein e.g., siRNA or dsRNA, may be a medium single stranded vector genome. A medium single stranded vector genome may be 3.6 to

4.3 kb in size such as about 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2 and 4.3 kb in size. As a non-limiting example, the medium single stranded vector genome may be 4.0 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[00794] In one embodiment, the vector genome which comprises a nucleic acid sequence encoding the modulatory polynucleotides described herein may be a medium double stranded vector genome. A medium double stranded vector genome may be 1.8 to 2.1 kb in size such as about 1.8, 1.9, 2.0, and 2.1 kb in size. As a non-limiting example, the medium double stranded vector genome may be 2.0 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[00795] In one embodiment, the vector genome which comprises a nucleic acid sequence encoding the modulatory polynucleotides described herein may be a large single stranded vector genome. A large single stranded vector genome may be 4.4 to 6.0 kb in size such as about 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9 and 6.0 kb in size. As a non-limiting example, the large single stranded vector genome may be 4.7 kb in size. As another non-limiting example, the large single stranded vector genome may be 4.8 kb in size. As yet another non-limiting example, the large single stranded vector genome may be 6.0 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

[00796] In one embodiment, the vector genome which comprises a nucleic acid sequence encoding the modulatory polynucleotides described herein may be a large double stranded vector genome. A large double stranded vector genome may be 2.2 to 3.0 kb in size such as about 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9 and 3.0 kb in size. As a non-limiting example, the large double stranded vector genome may be 2.4 kb in size. Additionally, the vector genome may comprise a promoter and a polyA tail.

Viral production

[00797] The present disclosure provides a method for the generation of parvoviral particles, e.g. AAV particles, by viral genome replication in a viral replication cell comprising contacting the viral replication cell with an AAV polynucleotide or AAV genome.

[00798] The present disclosure provides a method for producing an AAV particle having enhanced (increased, improved) transduction efficiency comprising the steps of: 1) co-transfecting competent bacterial cells with a bacmid vector and either a viral construct vector and/or AAV payload construct vector, 2) isolating the resultant viral construct expression vector and AAV payload construct expression vector and separately transfecting viral replication cells, 3) isolating and purifying resultant payload and viral construct particles comprising viral construct expression vector or AAV payload construct expression vector, 4) co-infecting a viral replication cell with both the AAV payload and viral construct particles comprising viral construct expression vector or AAV payload construct expression vector, 5) harvesting and purifying the viral particle comprising a parvoviral genome.

[00799] In one embodiment, the present invention provides a method for producing an AAV particle comprising the steps of 1) simultaneously co-transfecting mammalian cells, such as, but not limited to HEK293 cells, with a payload region, a construct expressing rep and cap genes and a helper construct, 2) harvesting and purifying the AAV particle comprising a viral genome.

Cells

[00800] The present disclosure provides a cell comprising an AAV polynucleotide and/or AAV genome.

[00801] Viral production disclosed herein describes processes and methods for producing AAV particles that contact a target cell to deliver a payload construct, e.g. a recombinant viral construct, which comprises a nucleotide encoding a payload molecule.

[00802] In one embodiment, the AAV particles may be produced in a viral replication cell that comprises an insect cell.

[00803] Growing conditions for insect cells in culture, and production of heterologous products in insect cells in culture are well-known in the art, see U.S. Pat. No. 6,204,059, the contents of which are herein incorporated by reference in their entirety.

[00804] Any insect cell which allows for replication of parvovirus and which can be maintained in culture can be used in accordance with the present invention. Cell lines may be used from Spodoptera frugiperda, including, but not limited to the Sf9 or Sf21 cell lines, Drosophila cell lines, or mosquito cell lines, such as Aedes albopictus derived cell lines. Use of insect cells for expression of heterologous proteins is well documented, as are methods of introducing nucleic acids, such as vectors, e.g., insect-cell compatible vectors, into such cells and methods of maintaining such cells in culture. See, for example, Methods in Molecular Biology, ed. Richard, Humana Press, NJ (1995); O'Reilly et al., Baculovirus Expression Vectors, A Laboratory Manual, Oxford Univ. Press (1994); Samulski et al., J. Vir.63:3822-8 (1989); Kajigaya et al., Proc. Nat'l. Acad. Sci. USA 88: 4646-50 (1991); Ruffing et al., J. Vir. 66:6922-30 (1992); Kimbauer et al., Vir.219:37-44 (1996); Zhao et al., Vir.272:382-93 (2000); and Samulski et al., U.S. Pat. No. 6,204,059, the contents of each of which is herein incorporated by reference in its entirety.

[00805] The viral replication cell may be selected from any biological organism, including prokaryotic (e.g., bacterial) cells, and eukaryotic cells, including, insect cells, yeast cells and mammalian cells. Viral replication cells may comprise mammalian cells such as A549, WEH1,

3T3, 10T1/2, BHK, MDCK, COS 1, COS 7, BSC 1, BSC 40, BMT 10, VERO. W138, HeLa, HEK293, Saos, C2C12, L cells, HT1080, HepG2 and primary fibroblast, hepatocyte and myoblast cells derived from mammals. Viral replication cells comprise cells derived from mammalian species including, but not limited to, human, monkey, mouse, rat, rabbit, and hamster or cell type, including but not limited to fibroblast, hepatocyte, tumor cell, cell line transformed cell, etc.

Small scale production of AAV Particles

[00806] Viral production disclosed herein describes processes and methods for producing AAV particles that contact a target cell to deliver a payload, e.g. a recombinant viral construct, which comprises a nucleotide encoding a payload.

[00807] In one embodiment, the AAV particles may be produced in a viral replication cell that comprises a mammalian cell.

[00808] Viral replication cells commonly used for production of recombinant AAV particles include, but are not limited to 293 cells, COS cells, HeLa cells, KB cells, and other mammalian cell lines as described in U.S. Pat. Nos. 6,156,303, 5,387,484, 5,741,683, 5,691,176, and 5,688,676; U.S. patent application 2002/0081721, and International Patent Applications WO 00/47757, WO 00/24916, and WO 96/17947, the contents of each of which are herein incorporated by reference in their entireties.

[00809] In one embodiment, AAV particles are produced in mammalian-cells wherein all three VP proteins are expressed at a stoichiometry approaching 1:1:10 (VP1:VP2:VP3). The regulatory mechanisms that allow this controlled level of expression include the production of two mRNAs, one for VP1, and the other for VP2 and VP3, produced by differential splicing.

[00810] In another embodiment, AAV particles are produced in mammalian cells using a triple transfection method wherein a payload construct, parvoviral Rep and parvoviral Cap and a helper construct are comprised within three different constructs. The triple transfection method of the three components of AAV particle production may be utilized to produce small lots of virus for assays including transduction efficiency, target tissue (tropism) evaluation, and stability.

Baculovirus

[00811] Particle production disclosed herein describes processes and methods for producing AAV particles that contact a target cell to deliver a payload construct which comprises a nucleotide encoding a payload.

[00812] Briefly, the viral construct vector and the AAV payload construct vector are each incorporated by a transposon donor/acceptor system into a bacmid, also known as a baculovirus plasmid, by standard molecular biology techniques known and performed by a person skilled in the art. Transfection of separate viral replication cell populations produces two baculoviruses, one that comprises the viral construct expression vector, and another that comprises the AAV payload construct expression vector. The two baculoviruses may be used to infect a single viral replication cell population for production of AAV particles.

[00813] Baculovirus expression vectors for producing viral particles in insect cells, including but not limited to Spodoptera frugiperda (Sf9) cells, provide high titers of viral particle product. Recombinant baculovirus encoding the viral construct expression vector and AAV payload construct expression vector initiates a productive infection of viral replicating cells. Infectious baculovirus particles released from the primary infection secondarily infect additional cells in the culture, exponentially infecting the entire cell culture population in a number of infection cycles that is a function of the initial multiplicity of infection, see Urabe, M. et al., J Virol. 2006 Feb; 80 (4):1874-85, the contents of which are herein incorporated by reference in their entirety.

[00814] Production of AAV particles with baculovirus in an insect cell system may address known baculovirus genetic and physical instability. In one embodiment, the production system addresses baculovirus instability over multiple passages by utilizing a titerless infected-cells preservation and scale-up system. Small scale seed cultures of viral producing cells are transfected with viral expression constructs encoding the structural, non-structural, components of the viral particle. Baculovirus-infected viral producing cells are harvested into aliquots that may be cryopreserved in liquid nitrogen; the aliquots retain viability and infectivity for infection of large scale viral producing cell culture Wasilko DJ et al., Protein Expr Purif. 2009 Jun; 65(2):122-32, the contents of which are herein incorporated by reference in their entirety.

[00815] A genetically stable baculovirus may be used to produce source of the one or more of the components for producing AAV particles in invertebrate cells. In one embodiment, defective baculovirus expression vectors may be maintained episomally in insect cells. In such an embodiment the bacmid vector is engineered with replication control elements, including but not limited to promoters, enhancers, and/or cell-cycle regulated replication elements.

[00816] In one embodiment, baculoviruses may be engineered with a (non-) selectable marker for recombination into the chitinase/cathepsin locus. The chia/v-cath locus is non-essential for propagating baculovirus in tissue culture, and the V-cath (EC 3.4.22.50) is a cysteine endoprotease that is most active on Arg-Arg dipeptide containing substrates. The Arg-Arg dipeptide is present in densovirus and parvovirus capsid structural proteins but infrequently occurs in dependovirus VP1.

[00817] In one embodiment, stable viral replication cells permissive for baculovirus infection are engineered with at least one stable integrated copy of any of the elements necessary for AAV replication and viral particle production including, but not limited to, the entire AAV genome, Rep and Cap genes, Rep genes, Cap genes, each Rep protein as a separate transcription cassette, each VP protein as a separate transcription cassette, the AAP (assembly activation protein), or at least one of the baculovirus helper genes with native or non-native promoters.

Large-scale production

[00818] In some embodiments, AAV particle production may be modified to increase the scale of production. Large scale viral production methods according to the present disclosure may include any of those taught in US Patent Nos. 5,756,283, 6,258,595, 6,261,551, 6,270,996, 6,281,010, 6,365,394, 6,475,769, 6,482,634, 6,485,966, 6,943,019, 6,953,690, 7,022,519, 7,238,526, 7,291,498 and 7,491,508 or International Publication Nos. WO1996039530, WO1998010088, WO1999014354, WO1999015685, WO1999047691, WO2000055342, WO2000075353 and WO2001023597, the contents of each of which are herein incorporated by reference in their entirety. Methods of increasing viral particle production scale typically comprise increasing the number of viral replication cells. In some embodiments, viral replication cells comprise adherent cells. To increase the scale of viral particle production by adherent viral replication cells, larger cell culture surfaces are required. In some cases, large-scale production methods comprise the use of roller bottles to increase cell culture surfaces. Other cell culture substrates with increased surface areas are known in the art. Examples of additional adherent cell culture products with increased surface areas include, but are not limited to CellSTACK®, CellCube® (Corning Corp., Corning, NY) and NuncTM Cell FactoryTM (Thermo Scientific, Waltham, MA.) In some cases, large-scale adherent cell surfaces may comprise from about 1,000 cm2 to about 100,000 cm2. In some cases, large-scale adherent cell cultures may comprise from about 107 to about 109 cells, from about 108 to about 1010 cells, from about 109 to about 1012 cells or at least 1012 cells. In some cases, large-scale adherent cultures may produce from about 109 to about 1012, from about 1010 to about 1013, from about 1011 to about 1014, from about 1012 to about 1015 or at least 1015 viral particles.

[00819] In some embodiments, large-scale viral production methods of the present disclosure may comprise the use of suspension cell cultures. Suspension cell culture allows for significantly increased numbers of cells. Typically, the number of adherent cells that can be grown on about 10-50 cm2 of surface area can be grown in about 1 cm3 volume in suspension.

[00820] Transfection of replication cells in large-scale culture formats may be carried out according to any methods known in the art. For large-scale adherent cell cultures, transfection methods may include, but are not limited to the use of inorganic compounds (e.g. calcium phosphate), organic compounds [e.g. polyethyleneimine (PEI)] or the use of non-chemical methods (e.g. electroporation.) With cells grown in suspension, transfection methods may include, but are not limited to the use of calcium phosphate and the use of PEI. In some cases, transfection of large scale suspension cultures may be carried out according to the section entitled "Transfection Procedure" described in Feng, L. et al., 2008. Biotechnol Appl. Biochem. 50:121-32, the contents of which are herein incorporated by reference in their entirety. According to such embodiments, PEI-DNA complexes may be formed for introduction of plasmids to be transfected. In some cases, cells being transfected with PEI-DNA complexes may be 'shocked' prior to transfection. This comprises lowering cell culture temperatures to 4°C for a period of about 1 hour. In some cases, cell cultures may be shocked for a period of from about 10 minutes to about 5 hours. In some cases, cell cultures may be shocked at a temperature of from about 0°C to about 20°C.

[00821] In some cases, transfections may include one or more vectors for expression of an RNA effector molecule to reduce expression of nucleic acids from one or more AAV payload construct. Such methods may enhance the production of viral particles by reducing cellular resources wasted on expressing payload constructs. In some cases, such methods may be carried according to those taught in US Publication No. US2014/0099666, the contents of which are herein incorporated by reference in their entirety.

Bioreactors

[00822] In some embodiments, cell culture bioreactors may be used for large scale viral production. In some cases, bioreactors comprise stirred tank reactors. Such reactors generally comprise a vessel, typically cylindrical in shape, with a stirrer (e.g. impeller.) In some embodiments, such bioreactor vessels may be placed within a water jacket to control vessel temperature and/or to minimize effects from ambient temperature changes. Bioreactor vessel volume may range in size from about 500 ml to about 2 L, from about 1 L to about 5 L, from about 2.5 L to about 20 L, from about 10 L to about 50 L, from about 25 L to about 100 L, from about 75 L to about 500 L, from about 250 L to about 2,000 L, from about 1,000 L to about 10,000 L, from about 5,000 L to about 50,000 L or at least 50,000 L. Vessel bottoms may be rounded or flat. In some cases, animal cell cultures may be maintained in bioreactors with rounded vessel bottoms.

[00823] In some cases, bioreactor vessels may be warmed through the use of a thermocirculator. Thermocirculators pump heated water around water jackets. In some cases, heated water may be pumped through pipes (e.g. coiled pipes) that are present within bioreactor vessels. In some cases, warm air may be circulated around bioreactors, including, but not limited to air space directly above culture medium. Additionally, pH and CO2 levels may be maintained to optimize cell viability.

[00824] In some cases, bioreactors may comprise hollow-fiber reactors. Hollow-fiber bioreactors may support the culture of both anchorage dependent and anchorage independent cells. Further bioreactors may include, but are not limited to packed-bed or fixed-bed bioreactors. Such bioreactors may comprise vessels with glass beads for adherent cell attachment. Further packed-bed reactors may comprise ceramic beads.

[00825] In some cases, viral particles are produced through the use of a disposable bioreactor. In some embodiments, such bioreactors may include WaveTM disposable bioreactors.

[00826] In some embodiments, AAV particle production in animal cell bioreactor cultures may be carried out according to the methods taught in US Patent Nos. 5,064764, 6,194,191, 6,566,118, 8,137,948 or US Patent Application No. US2011/0229971, the contents of each of which are herein incorporated by reference in their entirety.

Cell Lysis

[00827] Cells of the invention, including, but not limited to viral production cells, may be subjected to cell lysis according to any methods known in the art. Cell lysis may be carried out to obtain one or more agents (e.g. viral particles) present within any cells of the invention. In some embodiments, cell lysis may be carried out according to any of the methods listed in US Patent Nos. 7,326,555, 7,579,181, 7,048,920, 6,410,300, 6,436,394, 7,732,129, 7,510,875, 7,445,930, 6,726,907, 6,194,191, 7,125,706, 6,995,006, 6,676,935, 7,968,333, 5,756,283, 6,258,595, 6,261,551, 6,270,996, 6,281,010, 6,365,394, 6,475,769, 6,482,634, 6,485,966, 6,943,019, 6,953,690, 7,022,519, 7,238,526, 7,291,498 and 7,491,508 or International Publication Nos. WO1996039530, WO1998010088, WO1999014354, WO1999015685, WO1999047691, WO2000055342, WO2000075353 and WO2001023597, the contents of each of which are herein incorporated by reference in their entirety. Cell lysis methods may be chemical or mechanical. Chemical cell lysis typically comprises contacting one or more cells with one or more lysis agent. Mechanical lysis typically comprises subjecting one or more cells to one or more lysis condition and/or one or more lysis force.

[00828] In some embodiments, chemical lysis may be used to lyse cells. As used herein, the term “lysis agent” refers to any agent that may aid in the disruption of a cell. In some cases, lysis agents are introduced in solutions, termed lysis solutions or lysis buffers. As used herein, the term “lysis solution” refers to a solution (typically aqueous) comprising one or more lysis agent. In addition to lysis agents, lysis solutions may include one or more buffering agents, solubilizing agents, surfactants, preservatives, cryoprotectants, enzymes, enzyme inhibitors and/or chelators. Lysis buffers are lysis solutions comprising one or more buffering agent. Additional components of lysis solutions may include one or more solubilizing agent. As used herein, the term "solubilizing agent" refers to a compound that enhances the solubility of one or more components of a solution and/or the solubility of one or more entities to which solutions are applied. In some cases, solubilizing agents enhance protein solubility. In some cases, solubilizing agents are selected based on their ability to enhance protein solubility while maintaining protein conformation and/or activity.

[00829] Exemplary lysis agents may include any of those described in US Patent Nos. 8,685,734, 7,901,921, 7,732,129, 7,223,585, 7,125,706, 8,236,495, 8,110,351, 7,419,956, 7,300,797, 6,699,706 and 6,143,567, the contents of each of which are herein incorporated by reference in their entirety. In some cases, lysis agents may be selected from lysis salts, amphoteric agents, cationic agents, ionic detergents and non-ionic detergents. Lysis salts may include, but are not limited to sodium chloride (NaCl) and potassium chloride (KCl.) Further lysis salts may include any of those described in US Patent Nos. 8,614,101, 7,326,555, 7,579,181, 7,048,920, 6,410,300, 6,436,394, 7,732,129, 7,510,875, 7,445,930, 6,726,907, 6,194,191, 7,125,706, 6,995,006, 6,676,935 and 7,968,333, the contents of each of which are herein incorporated by reference in their entirety. Concentrations of salts may be increased or decreased to obtain an effective concentration for rupture of cell membranes. Amphoteric agents, as referred to herein, are compounds capable of reacting as an acid or a base. Amphoteric agents may include, but are not limited to lysophosphatidylcholine, 3-((3-Cholamidopropyl) dimethylammonium)-1-propanesulfonate (CHAPS), Zwittergent® and the like. Cationic agents may include, but are not limited to cetyltrimethylammonium bromide (C (16) TAB) and Benzalkonium chloride. Lysis agents comprising detergents may include ionic detergents or non-ionic detergents. Detergents may function to break apart or dissolve cell structures including, but not limited to cell membranes, cell walls, lipids, carbohydrates, lipoproteins and glycoproteins. Exemplary ionic detergents include any of those taught in US Patent Nos. 7,625,570 and 6,593,123 or US Publication No. US2014/0087361, the contents of each of which are herein incorporated by reference in their entirety. Some ionic detergents may include, but are not limited to sodium dodecyl sulfate (SDS), cholate and deoxycholate. In some cases, ionic detergents may be included in lysis solutions as a solubilizing agent. Non-ionic detergents may include, but are not limited to octylglucoside, digitonin, lubrol, C12E8, TWEEN®-20, TWEEN®-80, Triton X-100 and Noniodet P-40. Non-ionic detergents are typically weaker lysis agents, but may be included as solubilizing agents for solubilizing cellular and/or viral proteins.

Further lysis agents may include enzymes and urea. In some cases, one or more lysis agents may be combined in a lysis solution in order to enhance one or more of cell lysis and protein solubility. In some cases, enzyme inhibitors may be included in lysis solutions in order to prevent proteolysis that may be triggered by cell membrane disruption.

[00830] In some embodiments, mechanical cell lysis is carried out. Mechanical cell lysis methods may include the use of one or more lysis condition and/or one or more lysis force. As used herein, the term "lysis condition" refers to a state or circumstance that promotes cellular disruption. Lysis conditions may comprise certain temperatures, pressures, osmotic purity, salinity and the like. In some cases, lysis conditions comprise increased or decreased temperatures. According to some embodiments, lysis conditions comprise changes in temperature to promote cellular disruption. Cell lysis carried out according to such embodiments may include freeze-thaw lysis. As used herein, the term "freeze-thaw lysis" refers to cellular lysis in which a cell solution is subjected to one or more freeze-thaw cycle. According to freeze-thaw lysis methods, cells in solution are frozen to induce a mechanical disruption of cellular membranes caused by the formation and expansion of ice crystals. Cell solutions used according freeze-thaw lysis methods, may further comprise one or more lysis agents, solubilizing agents, buffering agents, cryoprotectants, surfactants, preservatives, enzymes, enzyme inhibitors and/or chelators. Once cell solutions subjected to freezing are thawed, such components may enhance the recovery of desired cellular products. In some cases, one or more cyroprotectants are included in cell solutions undergoing freeze-thaw lysis. As used herein, the term "cryoprotectant" refers to an agent used to protect one or more substance from damage due to freezing. Cryoprotectants may include any of those taught in US Publication No. US2013/0323302 or US Patent Nos. 6,503,888, 6,180,613, 7,888,096, 7,091,030, the contents of each of which are herein incorporated by reference in their entirety. In some cases, cryoprotectants may include, but are not limited to dimethyl sulfoxide, 1,2-propanediol, 2,3-butanediol, formamide, glycerol, ethylene glycol, 1,3-propanediol and n-dimethyl formamide, polyvinylpyrrolidone, hydroxyethyl starch, agarose, dextrans, inositol, glucose, hydroxyethylstarch, lactose, sorbitol, methyl glucose, sucrose and urea. In some embodiments, freeze-thaw lysis may be carried out according to any of the methods described in US Patent No. 7,704,721, the contents of which are herein incorporated by reference in their entirety.

[00831] As used herein, the term "lysis force" refers to a physical activity used to disrupt a cell. Lysis forces may include, but are not limited to mechanical forces, sonic forces, gravitational forces, optical forces, electrical forces and the like. Cell lysis carried out by mechanical force is referred to herein as "mechanical lysis." Mechanical forces that may be used according to mechanical lysis may include high shear fluid forces. According to such methods of mechanical lysis, a microfluidizer may be used. Microfluidizers typically comprise an inlet reservoir where cell solutions may be applied. Cell solutions may then be pumped into an interaction chamber via a pump (e.g. high-pressure pump) at high speed and/or pressure to produce shear fluid forces. Resulting lysates may then be collected in one or more output reservoir. Pump speed and/or pressure may be adjusted to modulate cell lysis and enhance recovery of products (e.g. viral particles.) Other mechanical lysis methods may include physical disruption of cells by scraping.

[00832] Cell lysis methods may be selected based on the cell culture format of cells to be lysed. For example, with adherent cell cultures, some chemical and mechanical lysis methods may be used. Such mechanical lysis methods may include freeze-thaw lysis or scraping. In another example, chemical lysis of adherent cell cultures may be carried out through incubation with lysis solutions comprising surfactant, such as Triton-X-100. In some cases, cell lysates generated from adherent cell cultures may be treated with one more nuclease to lower the viscosity of the lysates caused by liberated DNA.

[00833] In one embodiment, a method for harvesting AAV particles without lysis may be used for efficient and scalable AAV particle production. In a non-limiting example, AAV particles may be produced by culturing an AAV particle lacking a heparin binding site, thereby allowing the AAV particle to pass into the supernatant, in a cell culture, collecting supernatant from the culture; and isolating the AAV particle from the supernatant, as described in US Patent Application 20090275107, the contents of which are incorporated herein by reference in their entirety.

Clarification

[00834] Cell lysates comprising viral particles may be subjected to clarification. Clarification refers to initial steps taken in purification of viral particles from cell lysates. Clarification serves to prepare lysates for further purification by removing larger, insoluble debris. Clarification steps may include, but are not limited to centrifugation and filtration. During clarification, centrifugation may be carried out at low speeds to remove larger debris, only. Similarly, filtration may be carried out using filters with larger pore sizes so that only larger debris is removed. In some cases, tangential flow filtration may be used during clarification. Objectives of viral clarification include high throughput processing of cell lysates and to optimize ultimate viral recovery. Advantages of including a clarification step include scalability for processing of larger volumes of lysate. In some embodiments, clarification may be carried out according to any of the methods presented in US Patent Nos. 8,524,446, 5,756,283, 6,258,595, 6,261,551, 6,270,996, 6,281,010, 6,365,394, 6,475,769, 6,482,634, 6,485,966, 6,943,019, 6,953,690, 7,022,519, 7,238,526, 7,291,498, 7,491,508, US Publication Nos. US2013/0045186, US2011/0263027, US2011/0151434, US2003/0138772, and International Publication Nos. WO2002012455, WO1996039530, WO1998010088, WO1999014354, WO1999015685, WO1999047691, WO2000055342, WO2000075353 and WO2001023597, the contents of each of which are herein incorporated by reference in their entirety.

[00835] Methods of cell lysate clarification by filtration are well understood in the art and may be carried out according to a variety of available methods including, but not limited to passive filtration and flow filtration. Filters used may comprise a variety of materials and pore sizes. For example, cell lysate filters may comprise pore sizes of from about 1 µM to about 5 µM, from about 0.5 µM to about 2 µM, from about 0.1 µM to about 1 µM, from about 0.05 µM to about 0.05 µM and from about 0.001 µM to about 0.1 µM. Exemplary pore sizes for cell lysate filters may include, but are not limited to, 2.0, 1.9, 1.8, 1.7, 1.6, 1.5, 1.4, 1.3, 1.2, 1.1, 1, 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, 0.1, 0.95, 0.9, 0.85, 0.8, 0.75, 0.7, 0.65, 0.6, 0.55, 0.5, 0.45, 0.4, 0.35, 0.3, 0.25, 0.2, 0.15, 0.1, 0.05, 0.22, 0.21, 0.20, 0.19, 0.18, 0.17, 0.16, 0.15, 0.14, 0.13, 0.12, 0.11, 0.1, 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, 0.01, 0.02, 0.019, 0.018, 0.017, 0.016, 0.015, 0.014, 0.013, 0.012, 0.011, 0.01, 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002, 0.001 and 0.001 µM. In one embodiment, clarification may comprise filtration through a filter with 2.0 µM pore size to remove large debris, followed by passage through a filter with 0.45 µM pore size to remove intact cells.

[00836] Filter materials may be composed of a variety of materials. Such materials may include, but are not limited to polymeric materials and metal materials (e.g. sintered metal and pored aluminum.) Exemplary materials may include, but are not limited to nylon, cellulose materials (e.g. cellulose acetate), polyvinylidene fluoride (PVDF), polyethersulfone, polyamide, polysulfone, polypropylene, and polyethylene terephthalate. In some cases, filters useful for clarification of cell lysates may include, but are not limited to ULTIPLEAT PROFILE™ filters (Pall Corporation, Port Washington, NY), SUPOR™ membrane filters (Pall Corporation, Port Washington, NY)

[00837] In some cases, flow filtration may be carried out to increase filtration speed and/or effectiveness. In some cases, flow filtration may comprise vacuum filtration. According to such methods, a vacuum is created on the side of the filter opposite that of cell lysate to be filtered. In some cases, cell lysates may be passed through filters by centrifugal forces. In some cases, a pump is used to force cell lysate through clarification filters. Flow rate of cell lysate through one or more filters may be modulated by adjusting one of channel size and/or fluid pressure.

[00838] According to some embodiments, cell lysates may be clarified by centrifugation. Centrifugation may be used to pellet insoluble particles in the lysate. During clarification, centrifugation strength [expressed in terms of gravitational units (g), which represents multiples of standard gravitational force] may be lower than in subsequent purification steps. In some cases, centrifugation may be carried out on cell lysates at from about 200 g to about 800 g, from about 500 g to about 1500 g, from about 1000 g to about 5000 g, from about 1200 g to about 10000 g or from about 8000 g to about 15000 g. In some embodiments, cell lysate centrifugation is carried out at 8000 g for 15 minutes. In some cases, density gradient centrifugation may be carried out in order to partition particulates in the cell lysate by sedimentation rate. Gradients used according to methods of the present disclosure may include, but are not limited to cesium chloride gradients and iodixanol step gradients.

Purification: Chromatography

[00839] In some cases, AAV particles may be purified from clarified cell lysates by one or more methods of chromatography. Chromatography refers to any number of methods known in the art for separating out one or more elements from a mixture. Such methods may include, but are not limited to ion exchange chromatography (e.g. cation exchange chromatography and anion exchange chromatography), immunoaffinity chromatography and size-exclusion chromatography. In some embodiments, methods of viral chromatography may include any of those taught in US Patent Nos. 5,756,283, 6,258,595, 6,261,551, 6,270,996, 6,281,010, 6,365,394, 6,475,769, 6,482,634, 6,485,966, 6,943,019, 6,953,690, 7,022,519, 7,238,526, 7,291,498 and 7,491,508 or International Publication Nos. WO1996039530, WO1998010088, WO1999014354, WO1999015685, WO1999047691, WO2000055342, WO2000075353 and WO2001023597, the contents of each of which are herein incorporated by reference in their entirety.

[00840] In some embodiments, ion exchange chromatography may be used to isolate viral particles. Ion exchange chromatography is used to bind viral particles based on charge-charge interactions between capsid proteins and charged sites present on a stationary phase, typically a column through which viral preparations (e.g. clarified lysates) are passed. After application of viral preparations, bound viral particles may then be eluted by applying an elution solution to disrupt the charge-charge interactions. Elution solutions may be optimized by adjusting salt concentration and/or pH to enhance recovery of bound viral particles. Depending on the charge of viral capsids being isolated, cation or anion exchange chromatography methods may be selected. Methods of ion exchange chromatography may include, but are not limited to any of those taught in US Patent Nos. 7,419,817, 6,143,548, 7,094,604, 6,593,123, 7,015,026 and 8,137,948, the contents of each of which are herein incorporated by reference in their entirety.

[00841] In some embodiments, immunoaffinity chromatography may be used. Immunoaffinity chromatography is a form of chromatography that utilizes one or more immune compounds (e.g. antibodies or antibody-related structures) to retain viral particles. Immune compounds may bind specifically to one or more structures on viral particle surfaces, including, but not limited to one or more viral coat protein. In some cases, immune compounds may be specific for a particular viral variant. In some cases, immune compounds may bind to multiple viral variants. In some embodiments, immune compounds may include recombinant single-chain antibodies. Such recombinant single chain antibodies may include those described in Smith, R.H. et al., 2009. Mol. Ther. 17(11):1888-96, the contents of which are herein incorporated by reference in their entirety. Such immune compounds are capable of binding to several AAV capsid variants, including, but not limited to AAV1, AAV2, AAV6 and AAV8.

[00842] In some embodiments, size-exclusion chromatography (SEC) may be used. SEC may comprise the use of a gel to separate particles according to size. In viral particle purification, SEC filtration is sometimes referred to as “polishing.” In some cases, SEC may be carried out to generate a final product that is near-homogenous. Such final products may in some cases be used in pre-clinical studies and/or clinical studies (Kotin, R.M. 2011. Human Molecular Genetics. 20(1):R2-R6, the contents of which are herein incorporated by reference in their entirety.) In some cases, SEC may be carried out according to any of the methods taught in US Patent Nos. 6,143,548, 7,015,026, 8,476,418, 6,410,300, 8,476,418, 7,419,817, 7,094,604, 6,593,123, and 8,137,948, the contents of each of which are herein incorporated by reference in their entirety.

[00843] In one embodiment, the compositions comprising at least one AAV particle may be isolated or purified using the methods described in US Patent No. US 6146874, the contents of which are herein incorporated by reference in its entirety.

[00844] In one embodiment, the compositions comprising at least one AAV particle may be isolated or purified using the methods described in US Patent No. US 6660514, the contents of which are herein incorporated by reference in its entirety.

[00845] In one embodiment, the compositions comprising at least one AAV particle may be isolated or purified using the methods described in US Patent No. US 8283151, the contents of which are herein incorporated by reference in its entirety.

[00846] In one embodiment, the compositions comprising at least one AAV particle may be isolated or purified using the methods described in US Patent No. US 8524446, the contents of which are herein incorporated by reference in its entirety.

II. FORMULATION AND DELIVERY

Pharmaceutical Compositions and Formulation

[00847] Although the descriptions of pharmaceutical compositions, e.g., those modulatory polynucleotides (including the encoding plasmids or expression vectors, such as viruses, e.g., AAV) comprising a payload to be delivered, provided herein are principally directed to pharmaceutical compositions which are suitable for administration to humans, it will be understood by the skilled artisan that such compositions are generally suitable for administration to any other animal, *e.g.,* to non-human animals, e.g. non-human mammals. Modification of pharmaceutical compositions suitable for administration to humans in order to render the compositions suitable for administration to various animals is well understood, and the ordinarily skilled veterinary pharmacologist can design and/or perform such modification with merely ordinary, if any, experimentation. Subjects to which administration of the pharmaceutical compositions is contemplated include, but are not limited to, humans and/or other primates; mammals, including commercially relevant mammals such as cattle, pigs, horses, sheep, cats, dogs, mice, and/or rats; and/or birds, including commercially relevant birds such as poultry, chickens, ducks, geese, and/or turkeys.

[00848] In some embodiments, compositions are administered to humans, human patients or subjects. For the purposes of the present disclosure, the phrase "active ingredient" generally refers either to the viral vector carrying the payload or to the modulatory polynucleotide payload molecule delivered by a viral vector as described herein.

[00849] Formulations of the pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient into association with an excipient and/or one or more other accessory ingredients, and then, if necessary and/or desirable, dividing, shaping and/or packaging the product into a desired single- or multi-dose unit.

[00850] Relative amounts of the active ingredient, the pharmaceutically acceptable excipient, and/or any additional ingredients in a pharmaceutical composition in accordance with the invention will vary, depending upon the identity, size, and/or condition of the subject treated and further depending upon the route by which the composition is to be administered.

[00851] The modulatory polynucleotides or viral vectors encoding them can be formulated using one or more excipients to: (1) increase stability; (2) increase cell transfection or transduction; (3) permit the sustained or delayed release; or (4) alter the biodistribution (e.g., target the viral vector to specific tissues or cell types).

[00852] Formulations of the present invention can include, without limitation, saline, lipidoids, liposomes, lipid nanoparticles, polymers, lipoplexes, core-shell nanoparticles, peptides, proteins, cells transfected with viral vectors (e.g., for transplantation into a subject), nanoparticle mimics and combinations thereof. Further, the viral vectors of the present invention may be formulated using self-assembled nucleic acid nanoparticles.

[00853] Formulations of the pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of associating the active ingredient with an excipient and/or one or more other accessory ingredients.

[00854] A pharmaceutical composition in accordance with the present disclosure may be prepared, packaged, and/or sold in bulk, as a single unit dose, and/or as a plurality of single unit doses. As used herein, a "unit dose" refers to a discrete amount of the pharmaceutical composition comprising a predetermined amount of the active ingredient. The amount of the active ingredient is generally equal to the dosage of the active ingredient which would be administered to a subject and/or a convenient fraction of such a dosage such as, for example, one-half or one-third of such a dosage.

[00855] Relative amounts of the active ingredient, the pharmaceutically acceptable excipient, and/or any additional ingredients in a pharmaceutical composition in accordance with the present disclosure may vary, depending upon the identity, size, and/or condition of the subject being treated and further depending upon the route by which the composition is to be administered. For example, the composition may comprise between 0.1% and 99% (w/w) of the active ingredient. By way of example, the composition may comprise between 0.1% and 100%, e.g., between .5 and 50%, between 1-30%, between 5-80%, at least 80% (w/w) active ingredient.

[00856] In some embodiments, the formulations described herein may contain at least one payload molecule. As a non-limiting example, the formulations may contain 1, 2, 3, 4 or 5 modulatory polynucleotide payload molecules. In one embodiment the formulation may contain a modulatory polynucleotide payload construct targeting proteins selected from categories such as, but not limited to, human proteins, veterinary proteins, bacterial proteins, biological proteins, antibodies, immunogenic proteins, therapeutic peptides and proteins, secreted proteins, plasma membrane proteins, cytoplasmic and cytoskeletal proteins, intracellular membrane bound proteins, nuclear proteins, proteins associated with human disease and/or proteins associated with non-human diseases. In one embodiment, the formulation contains at least three payload construct targeting proteins.

[00857] In some embodiments, a pharmaceutically acceptable excipient may be at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% pure. In some embodiments, an excipient is approved for use for humans and for veterinary use. In some embodiments, an excipient may be approved by the United States Food and Drug Administration. In some embodiments, an excipient may be of pharmaceutical grade. In some embodiments, an excipient may meet the standards of the United States Pharmacopoeia (USP), the European Pharmacopoeia (EP), the British Pharmacopoeia, and/or the International Pharmacopoeia.

[00858] Excipients, which, as used herein, includes, but is not limited to, any and all solvents, dispersion media, diluents, or other liquid vehicles, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, and the like, as suited to the particular dosage form desired. Various excipients for formulating pharmaceutical compositions and techniques for preparing the composition are known in the art (see Remington: The Science and Practice of Pharmacy, 21st Edition, A. R. Gennaro, Lippincott, Williams & Wilkins, Baltimore, MD, 2006; incorporated herein by reference in its entirety). The use of a conventional excipient medium may be contemplated within the scope of the present disclosure, except insofar as any conventional excipient medium may be incompatible with a substance or its derivatives, such as by producing any undesirable biological effect or otherwise interacting in a deleterious manner with any other component(s) of the pharmaceutical composition.

[00859] Exemplary diluents include, but are not limited to, calcium carbonate, sodium carbonate, calcium phosphate, dicalcium phosphate, calcium sulfate, calcium hydrogen phosphate, sodium phosphate lactose, sucrose, cellulose, microcrystalline cellulose, kaolin, mannitol, sorbitol, inositol, sodium chloride, dry starch, cornstarch, powdered sugar, *etc.*, and/or combinations thereof.

Inactive Ingredients

[00860] In some embodiments, modulatory polynucleotide formulations may comprise at least one excipient which is an inactive ingredient. As used herein, the term “inactive ingredient” refers to one or more inactive agents included in formulations. In some embodiments, all, none or some of the inactive ingredients which may be used in the formulations of the present invention may be approved by the US Food and Drug Administration (FDA).

[00861] Formulations of viral vectors carrying modulatory polynucleotide disclosed herein may include cations or anions. In one embodiment, the formulations include metal cations such as, but not limited to, Zn2+, Ca2+, Cu2+, Mg+ and combinations thereof. As a non-limiting example, formulations may include polymers and modulatory polynucleotides complexed with a metal cation (See e.g., U.S. Pat. Nos. 6,265,389 and 6,555,525, each of which is herein incorporated by reference in its entirety).

Delivery

[00862] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for the delivery of AAV virions described in European Patent Application No. EP1857552, the contents of which are herein incorporated by reference in their entirety.

[00863] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering proteins using AAV vectors described in European Patent Application No. EP2678433, the contents of which are herein incorporated by reference in their entirety.

[00864] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering DNA molecules using AAV vectors described in US Patent No. US 5858351, the contents of which are herein incorporated by reference in their entirety.

[00865] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering DNA to the bloodstream described in US Patent No. US 6211163, the contents of which are herein incorporated by reference in their entirety.

[00866] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering AAV virions described in US Patent No. US 6325998, the contents of which are herein incorporated by reference in their entirety.

[00867] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering DNA to muscle cells described in US Patent No. US 6335011, the contents of which are herein incorporated by reference in their entirety.

[00868] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering DNA to muscle cells and tissues described in US Patent No. US 6610290, the contents of which are herein incorporated by reference in their entirety.

[00869] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering DNA to muscle cells described in US Patent No. US 7704492, the contents of which are herein incorporated by reference in their entirety.

[00870] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering a payload to skeletal muscles described in US Patent No. US 7112321, the contents of which are herein incorporated by reference in their entirety.

[00871] In one embodiment, the viral vector may be administered or delivered using the methods for delivering a payload to the central nervous system described in US Patent No. US 7588757, the contents of which are herein incorporated by reference in their entirety.

[00872] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering a payload described in US Patent No. US 8283151, the contents of which are herein incorporated by reference in their entirety.

[00873] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering a payload for the treatment of Alzheimer disease described in US Patent No. US 8318687, the contents of which are herein incorporated by reference in their entirety.

[00874] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering a payload described in International Patent Publication No. WO2012144446, the contents of which are herein incorporated by reference in their entirety.

[00875] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering a payload using a glutamic acid decarboxylase (GAD) delivery vector described in International Patent Publication No. WO2001089583, the contents of which are herein incorporated by reference in their entirety.

[00876] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering a payload described in International Patent Publication No. WO2001096587, the contents of which are herein incorporated by reference in their entirety.

[00877] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering a payload to muscle tissue described in International Patent Publication No. WO2002014487, the contents of which are herein incorporated by reference in their entirety.

[00878] In one embodiment, the viral vector comprising a modulatory polynucleotide may be administered or delivered using the methods for delivering a payload to neural cells described in International Patent Publication No. WO2012057363, the contents of which are herein incorporated by reference in their entirety.

[00879] The pharmaceutical compositions of viral vectors described herein may be characterized by one or more of bioavailability, therapeutic window and/or volume of distribution.

[00880] In one embodiment, the viral vectors comprising a modulatory polynucleotide may be formulated. As a non-limiting example the baricity and/or osmolality of the formulation may be optimized to ensure optimal drug distribution in the central nervous system or a region or component of the central nervous system.

[00881] In one embodiment, the viral vectors comprising a modulatory polynucleotide may be delivered to a subject via a single route administration.

[00882] In one embodiment, the viral vectors comprising a modulatory polynucleotide may be delivered to a subject via a multi-site route of administration. A subject may be administered the viral vectors comprising a modulatory polynucleotide at 2, 3, 4, 5 or more than 5 sites.

[00883] In one embodiment, a subject may be administered the viral vectors comprising a modulatory polynucleotide described herein using a bolus infusion.

[00884] In one embodiment, a subject may be administered the viral vectors comprising a modulatory polynucleotide described herein using sustained delivery over a period of minutes, hours or days. The infusion rate may be changed depending on the subject, distribution, formulation or another delivery parameter.

[00885] In one embodiment, the catheter may be located at more than one site in the spine for multi-site delivery. The viral vectors comprising a modulatory polynucleotide may be delivered in a continuous and/or bolus infusion. Each site of delivery may be a different dosing regimen or the same dosing regimen may be used for each site of delivery. As a non-limiting example, the sites of delivery may be in the cervical and the lumbar region. As another non-limiting example, the sites of delivery may be in the cervical region. As another non-limiting example, the sites of delivery may be in the lumbar region.

[00886] In one embodiment, a subject may be analyzed for spinal anatomy and pathology prior to delivery of the viral vectors comprising a modulatory polynucleotide described herein. As a non-limiting example, a subject with scoliosis may have a different dosing regimen and/or catheter location compared to a subject without scoliosis.

[00887] In one embodiment, the orientation of the spine subject during delivery of the viral vectors comprising a modulatory polynucleotide may be vertical to the ground.

[00888] In another embodiment, the orientation of the spine of the subject during delivery of the viral vectors comprising a modulatory polynucleotide may be horizontal to the ground.

[00889] In one embodiment, the spine of the subject may be at an angle as compared to the ground during the delivery of the viral vectors comprising a modulatory polynucleotide subject. The angle of the spine of the subject as compared to the ground may be at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150 or 180 degrees.

[00890] In one embodiment, the delivery method and duration is chosen to provide broad transduction in the spinal cord. As a non-limiting example, intrathecal delivery is used to provide broad transduction along the rostral-caudal length of the spinal cord. As another non-limiting example, multi-site infusions provide a more uniform transduction along the rostral-caudal length of the spinal cord. As yet another non-limiting example, prolonged infusions provide a more uniform transduction along the rostral-caudal length of the spinal cord.

Introduction into cells

[00891] The modulatory polynucleotides of the invention can be introduced into host cells using any of a variety of approaches. Infection with a viral vector comprising the modulatory polynucleotide can be affected. Examples of suitable viral vectors include replication defective retroviral vectors, adenoviral vectors, adeno-associated vectors and lentiviral vectors.

[00892] According to the present invention, viral vectors for use in therapeutics and/or diagnostics comprise a virus that has been distilled or reduced to the minimum components necessary for transduction of a nucleic acid payload or cargo of interest.

[00893] In this manner, viral vectors are engineered as vehicles for specific delivery while lacking the deleterious replication and/or integration features found in wild-type virus.

[00894] As used herein, a “vector” is any molecule or moiety which transports, transduces or otherwise acts as a carrier of a heterologous molecule such as the modulatory polynucleotides of the invention. A “viral vector” is a vector which comprises one or more polynucleotide regions encoding or comprising payload molecules of interest, e.g., a transgene, a polynucleotide encoding a polypeptide or multi-polypeptide or a modulatory nucleic acid. Viral vectors of the present invention may be produced recombinantly and may be based on adeno-associated virus (AAV) parent or reference sequences. Serotypes which may be useful in the present invention include any of those arising from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV9.47, AAV9(hu14), AAV10, AAV11, AAV12, AAVrh8, AAVrh10, AAV-DJ, AAV-DJ8, AAV-PHP.A and/or AAV-PHP.B.

[00895] In one embodiment, the serotype which may be useful in the present invention may be AAV-DJ8. The amino acid sequence of AAV-DJ8 may comprise two or more mutations in order to remove the heparin binding domain (HBD). As a non-limiting example, the AAV-DJ sequence described as SEQ ID NO: 1 in US Patent No. 7,588,772, the contents of which are herein incorporated by reference in their entirety, may comprise two mutations: (1) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (2) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr). As another non-limiting example, may comprise three mutations: (1) K406R where lysine (K; Lys) at amino acid 406 is changed to arginine (R; Arg), (2) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (3) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr).

[00896] AAV vectors may also comprise self-complementary AAV vectors (scAAVs). scAAV vectors contain both DNA strands which anneal together to form double stranded DNA. By skipping second strand synthesis, scAAVs allow for rapid expression in the cell.

[00897] In one embodiment, the AAV vector used in the present invention is a scAAV.

[00898] In one embodiment, the modulatory polynucleotides may be introduced into cells from any relevant species, such as, but not limited to, human, dog, mouse, rat or monkey.

[00899] In one embodiment, the modulatory polynucleotides may be introduced into cells which are relevant to the disease to be treated. As a non-limiting example, the disease is ALS and the target cells are motor neurons and astrocytes.

[00900] In one embodiment, the modulatory polynucleotides may be introduced into cells which have a high level of endogenous expression of the target sequence.

[00901] In another embodiment, the modulatory polynucleotides may be introduced into cells which have a low level of endogenous expression of the target sequence.

[00902] In one embodiment, the cells may be those which have a high efficiency of AAV transduction.

[00903] In one embodiment, the cells which may be used for *in vitro* analysis of the modulatory polynucleotides include, but are not limited to, HEK293, HeLa, human primary astrocytes, human astrocyte cell line (U251MG), SH-SY5Y-neurons and human iPSC-derived motor neuron progenitors.

III. ADMINISTRATION AND DOSING

Administration

[00904] The viral vectors comprising modulatory polynucleotides of the present invention may be administered by any route which results in a therapeutically effective outcome. These include, but are not limited to enteral (into the intestine), gastroenteral, epidural (into the dura matter), oral (by way of the mouth), transdermal, peridural, intracerebral (into the cerebrum), intracerebroventricular (into the cerebral ventricles), epicutaneous (application onto the skin), intradermal, (into the skin itself), subcutaneous (under the skin), nasal administration (through the nose), intravenous (into a vein), intravenous bolus, intravenous drip, intraarterial (into an artery), intramuscular (into a muscle), intracardiac (into the heart), intraosseous infusion (into the bone marrow), intrathecal (into the spinal canal), subpial (between the pia and the underlying tissue), intraperitoneal, (infusion or injection into the peritoneum), intravesical infusion, intravitreal, (through the eye), intracavernous injection (into a pathologic cavity) intracavitary (into the base of the penis), intravaginal administration, intrauterine, extra-amniotic administration, transdermal (diffusion through the intact skin for systemic distribution), transmucosal (diffusion through a mucous membrane), transvaginal, insufflation (snorting), sublingual, sublabial, enema, eye drops (onto the conjunctiva), in ear drops, auricular (in or by way of the ear), buccal (directed toward the cheek), conjunctival, cutaneous, dental (to a tooth or teeth), electro-osmosis, endocervical, endosinusial, endotracheal, extracorporeal, hemodialysis, infiltration, interstitial, intra-abdominal, intra-amniotic, intra-articular, intrabiliary, intrabronchial, intrabursal, intracartilaginous (within a cartilage), intracaudal (within the cauda equine), intracisternal (within the cisterna magna cerebellomedularis), intracorneal (within the cornea), dental intracornal, intracoronary (within the coronary arteries), intracorporus cavernosum (within the dilatable spaces of the corporus cavernosa of the penis), intradiscal (within a disc), intraductal (within a duct of a gland), intraduodenal (within the duodenum), intradural (within or beneath the dura), intraepidermal (to the epidermis), intraesophageal (to the esophagus), intragastric (within the stomach), intragingival (within the gingivae), intraileal (within the distal portion of the small intestine), intralesional (within or introduced directly to a localized lesion), intraluminal (within a lumen of a tube), intralymphatic (within the lymph), intramedullary (within the marrow cavity of a bone), intrameningeal (within the meninges), intraocular (within the eye), intraovarian (within the ovary), intrapericardial (within the pericardium), intrapleural (within the pleura), intraprostatic (within the prostate gland), intrapulmonary (within the lungs or its bronchi), intrasinal (within the nasal or periorbital sinuses), intraspinal (within the vertebral column), intrasynovial (within the synovial cavity of a joint), intratendinous (within a tendon), intratesticular (within the testicle), intrathecal (within the cerebrospinal fluid at any level of the cerebrospinal axis), intrathoracic (within the thorax), intratubular (within the tubules of an organ), intratumor (within a tumor), intratympanic (within the aurus media), intravascular (within a vessel or vessels), intraventricular (within a ventricle), iontophoresis (by means of electric current where ions of soluble salts migrate into the tissues of the body), irrigation (to bathe or flush open wounds or body cavities), laryngeal (directly upon the larynx), nasogastric (through the nose and into the stomach), occlusive dressing technique (topical route administration which is then covered by a dressing which occludes the area), ophthalmic (to the external eye), oropharyngeal (directly to the mouth and pharynx), parenteral, percutaneous, periarticular, peridural, perineural, periodontal, rectal, respiratory (within the respiratory tract by inhaling orally or nasally for local or systemic effect), retrobulbar (behind the pons or behind the eyeball), soft tissue, subarachnoid, subconjunctival, submucosal, topical, transplacental (through or across the placenta), transtracheal (through the wall of the trachea), transtympanic (across or through the tympanic cavity), ureteral (to the ureter), urethral (to the urethra), vaginal, caudal block, diagnostic, nerve block, biliary perfusion, cardiac perfusion, photopheresis or spinal. In specific embodiments, compositions may be administered in a way which allows them to cross the blood-brain barrier, vascular barrier, or other epithelial barrier. In one embodiment, a formulation for a route of administration may include at least one inactive ingredient.

Dosing

[00905] The present invention provides methods comprising administering viral vectors and their modulatory polynucleotide payload or complexes in accordance with the invention to a subject in need thereof. Viral vector pharmaceutical, imaging, diagnostic, or prophylactic compositions thereof, may be administered to a subject using any amount and any route of administration effective for preventing, treating, diagnosing, or imaging a disease, disorder, and/or condition (*e.g.*, a disease, disorder, and/or condition relating to working memory deficits). The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the severity of the disease, the particular composition, its mode of administration, its mode of activity, and the like. Compositions in accordance with the invention are typically formulated in unit dosage form for ease of administration and uniformity of dosage. It will be understood, however, that the total daily usage of the compositions of the present invention may be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective, prophylactically effective, or appropriate imaging dose level for any particular patient will depend upon a variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific compound employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific modulatory polynucleotide payload employed; the duration of the treatment; drugs used in combination or coincidental with the specific compound employed; and like factors well known in the medical arts.

[00906] In certain embodiments, viral vector pharmaceutical compositions in accordance with the present invention may be administered at modulatory polynucleotide dosage levels sufficient to deliver from about 0.0001 mg/kg to about 100 mg/kg, from about 0.001 mg/kg to about 0.05 mg/kg, from about 0.005 mg/kg to about 0.05 mg/kg, from about 0.001 mg/kg to about 0.005 mg/kg, from about 0.05 mg/kg to about 0.5 mg/kg, from about 0.01 mg/kg to about 50 mg/kg, from about 0.1 mg/kg to about 40 mg/kg, from about 0.5 mg/kg to about 30 mg/kg, from about 0.01 mg/kg to about 10 mg/kg, from about 0.1 mg/kg to about 10 mg/kg, or from about 1 mg/kg to about 25 mg/kg, of subject body weight per day, one or more times a day, to obtain the desired therapeutic, diagnostic, prophylactic, or imaging effect (see e.g., the range of unit doses described in International Publication No WO2013078199, herein incorporated by reference in its entirety). The desired modulatory polynucleotide dosage may be delivered more than once (e.g., more than one administration in a day). In certain embodiments, the desired modulatory polynucleotide dosage may be delivered using multiple administrations (*e.g.*, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, or more administrations). When multiple administrations are employed, split dosing regimens such as those described herein may be used. As used herein, a “split dose” is the division of single unit dose or total daily dose into two or more doses, e.g., two or more administrations of the single unit dose. As used herein, a “single unit dose” is a dose of any modulatory polynucleotide therapeutic administered in one dose/at one time/single route/single point of contact, i.e., single administration event. As used herein, a “total daily dose” is an amount given or prescribed in 24 hour period. It may be administered as a single unit dose. In one embodiment, the viral vectors comprising the modulatory polynucleotides of the present invention are administered to a subject in split doses. They may be formulated in buffer only or in a formulation described herein.

[00907] In one embodiment, delivery of the compositions in accordance with the present invention to cells comprises a rate of delivery defined by [VG/hour = mL/hour * VG/mL] wherein VG is viral genomes, VG/mL is composition concentration, and mL/hour is rate of prolonged delivery.

[00908] In one embodiment, delivery of compositions in accordance with the present invention to cells may comprise a total concentration per subject between about $1x10^6$ VG and about $1x10^{16}$ VG. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $1.1x10^{11}$, $1.2x10^{11}$, $1.3x10^{11}$, $1.4x10^{11}$, $1.5x10^{11}$, $1.6x10^{11}$, $1.7x10^{11}$, $1.8x10^{11}$, $1.9x10^{11}$, $2x10^{11}$, $2.1x10^{11}$, $2.2x10^{11}$, $2.3x10^{11}$, $2.4x10^{11}$, $2.5x10^{11}$, $2.6x10^{11}$, $2.7x10^{11}$, $2.8x10^{11}$, $2.9x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$,

$7.1x10^{11}$, $7.2x10^{11}$, $7.3x10^{11}$, $7.4x10^{11}$, $7.5x10^{11}$, $7.6x10^{11}$, $7.7x10^{11}$, $7.8x10^{11}$, $7.9x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1\ x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $2.1x10^{12}$, $2.2x10^{12}$, $2.3x10^{12}$, $2.4x10^{12}$, $2.5x10^{12}$, $2.6x10^{12}$, $2.7x10^{12}$, $2.8x10^{12}$, $2.9x10^{12}$, $3x10^{12}$, $3.1x10^{12}$, $3.2x10^{12}$, $3.3x10^{12}$, $3.4x10^{12}$, $3.5x10^{12}$, $3.6x10^{12}$, $3.7x10^{12}$, $3.8x10^{12}$, $3.9x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$,$4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $8.1x10^{12}$, $8.2x10^{12}$, $8.3x10^{12}$, $8.4x10^{12}$, $8.5x10^{12}$, $8.6x10^{12}$, $8.7x10^{12}$, $8.8\ x10^{12}$, $8.9x10^{12}$, $9x10^{12}$, $1x10^{13}$, $1.1x10^{13}$, $1.2x10^{13}$, $1.3x10^{13}$, $1.4x10^{13}$, $1.5x10^{13}$, $1.6x10^{13}$, $1.7x10^{13}$, $1.8x10^{13}$, $1.9x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/subject.

[00909] In one embodiment, delivery of compositions in accordance with the present invention to cells may comprise a total concentration per subject between about $1x10^{6}$ VG/kg and about $1x10^{16}$ VG/kg. In some embodiments, delivery may comprise a composition concentration of about $1x10^{6}$, $2x10^{6}$, $3x10^{6}$, $4x10^{6}$, $5x10^{6}$, $6x10^{6}$, $7x10^{6}$, $8x10^{6}$, $9x10^{6}$, $1x10^{7}$, $2x10^{7}$, $3x10^{7}$, $4x10^{7}$, $5x10^{7}$, $6x10^{7}$, $7x10^{7}$, $8x10^{7}$, $9x10^{7}$, $1x10^{8}$, $2x10^{8}$, $3x10^{8}$, $4x10^{8}$, $5x10^{8}$, $6x10^{8}$, $7x10^{8}$, $8x10^{8}$, $9x10^{8}$, $1x10^{9}$, $2x10^{9}$, $3x10^{9}$, $4x10^{9}$, $5x10^{9}$, $6x10^{9}$, $7x10^{9}$, $8x10^{9}$, $9x10^{9}$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $1.1x10^{11}$, $1.2x10^{11}$, $1.3x10^{11}$, $1.4x10^{11}$, $1.5x10^{11}$, $1.6x10^{11}$, $1.7x10^{11}$, $1.8x10^{11}$, $1.9x10^{11}$, $2x10^{11}$, $2.1x10^{11}$, $2.2x10^{11}$, $2.3x10^{11}$, $2.4x10^{11}$, $2.5x10^{11}$, $2.6x10^{11}$, $2.7x10^{11}$, $2.8x10^{11}$, $2.9x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $7.1x10^{11}$, $7.2x10^{11}$, $7.3x10^{11}$, $7.4x10^{11}$, $7.5x10^{11}$, $7.6x10^{11}$, $7.7x10^{11}$, $7.8x10^{11}$, $7.9x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1\ x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $2.1x10^{12}$, $2.2x10^{12}$, $2.3x10^{12}$, $2.4x10^{12}$, $2.5x10^{12}$, $2.6x10^{12}$, $2.7x10^{12}$, $2.8x10^{12}$, $2.9x10^{12}$, $3x10^{12}$, $3.1x10^{12}$, $3.2x10^{12}$, $3.3x10^{12}$, $3.4x10^{12}$, $3.5x10^{12}$, $3.6x10^{12}$, $3.7x10^{12}$, $3.8x10^{12}$, $3.9x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$,$4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $8.1x10^{12}$, $8.2x10^{12}$, $8.3x10^{12}$, $8.4x10^{12}$, $8.5x10^{12}$, $8.6x10^{12}$, $8.7x10^{12}$, $8.8\ x10^{12}$, $8.9x10^{12}$, $9x10^{12}$, $1x10^{13}$, $1.1x10^{13}$, $1.2x10^{13}$, $1.3x10^{13}$, $1.4x10^{13}$, $1.5x10^{13}$, $1.6x10^{13}$, $1.7x10^{13}$, $1.8x10^{13}$, $1.9x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/kg.

[00910] In one embodiment, about 10^{5} to 10^{6} viral genome (unit) may be administered per dose.

[00911] In one embodiment, delivery of the compositions in accordance with the present invention to cells may comprise a total concentration between about $1x10^6$ VG/mL and about $1x10^{16}$ VG/mL. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $1.1x10^{11}$, $1.2x10^{11}$, $1.3x10^{11}$, $1.4x10^{11}$, $1.5x10^{11}$, $1.6x10^{11}$, $1.7x10^{11}$, $1.8x10^{11}$, $1.9x10^{11}$, $2x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $2.1x10^{12}$, $2.2x10^{12}$, $2.3x10^{12}$, $2.4x10^{12}$, $2.5x10^{12}$, $2.6x10^{12}$, $2.7x10^{12}$, $2.8x10^{12}$, $2.9x10^{12}$, $3x10^{12}$, $3.1x10^{12}$, $3.2x10^{12}$, $3.3x10^{12}$, $3.4x10^{12}$, $3.5x10^{12}$, $3.6x10^{12}$, $3.7x10^{12}$, $3.8x10^{12}$, $3.9x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$, $4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $9x10^{12}$, $1x10^{13}$, $1.1x10^{13}$, $1.2x10^{13}$, $1.3x10^{13}$, $1.4x10^{13}$, $1.5x10^{13}$, $1.6x10^{13}$, $1.7x10^{13}$, $1.8x10^{13}$, $1.9x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/mL.

Bioavailability

[00912] Viral vectors comprising a modulatory polynucleotide of the present invention, when formulated into compositions with delivery/formulation agents or vehicles as described herein, may exhibit increased bioavailability as compared to compositions lacking delivery agents as described herein. As used herein, the term “bioavailability” refers to the systemic availability of a given amount of a particular agent administered to a subject. Bioavailability may be assessed by measuring the area under the curve (AUC) or the maximum serum or plasma concentration (C_{max}) of the unchanged form of a compound following administration of the compound to a mammal. AUC is a determination of the area under the curve plotting the serum or plasma concentration of a compound along the ordinate (Y-axis) against time along the abscissa (X-axis). Generally, the AUC for a particular compound may be calculated using methods known to those of ordinary skill in the art and as described in G. S. Banker, Modern Pharmaceutics, Drugs and the Pharmaceutical Sciences, v. 72, Marcel Dekker, New York, Inc., 1996, the contents of which are herein incorporated by reference in their entirety.

[00913] C_{max} values are maximum concentrations of compounds achieved in serum or plasma of a subject following administration of compounds to the subject. C_{max} values of particular compounds may be measured using methods known to those of ordinary skill in the art. As used herein, the phrases "increasing bioavailability" or "improving the pharmacokinetics," refer to actions that may increase the systemic availability of a viral vector of the present invention (as measured by AUC, C_{max}, or C_{min}) in a subject. In some embodiments, such actions may comprise co-administration with one or more delivery agents as described herein. In some embodiments, the bioavailability of viral vectors may increase by at least about 2%, at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95% or about 100%.

Therapeutic window

[00914] Viral vectors comprising a modulatory polynucleotide of the present invention, when formulated with one or more delivery agents as described herein, may exhibit increases in the therapeutic window of compound and/or composition administration as compared to the therapeutic window of viral vectors administered without one or more delivery agents as described herein. As used herein, the term "therapeutic window" refers to the range of plasma concentrations, or the range of levels of therapeutically active substance at the site of action, with a high probability of eliciting a therapeutic effect. In some embodiments, therapeutic windows of viral vectors when administered in a formulation may increase by at least about 2%, at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95% or about 100%.

Volume of distribution

[00915] Viral vectors comprising a modulatory polynucleotide of the present invention, when formulated with one or more delivery agents as described herein, may exhibit an improved volume of distribution (V_{dist}), e.g., reduced or targeted, relative to formulations lacking one or more delivery agents as described herein. V_{dist} relates the amount of an agent in the body to the concentration of the same agent in the blood or plasma. As used herein, the term "volume of distribution" refers to the fluid volume that would be required to contain the total amount of an agent in the body at the same concentration as in the blood or plasma: V_{dist} equals the amount of an agent in the body/concentration of the agent in blood or plasma. For example, for a 10 mg dose of a given agent and a plasma concentration of 10 mg/L, the volume of distribution would be 1 liter. The volume of distribution reflects the extent to which an agent is present in the extravascular tissue. Large volumes of distribution reflect the tendency of agents to bind to the tissue components as compared with plasma proteins. In clinical settings, V_{dist} may be used to determine loading doses to achieve steady state concentrations. In some embodiments, volumes of distribution of viral vector compositions of the present invention when co-administered with one or more delivery agents as described herein may decrease at least about 2%, at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%.

Combinations

[00916] The viral vectors comprising the modulatory polynucleotide may be used in combination with one or more other therapeutic, prophylactic, diagnostic, or imaging agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present disclosure. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent. In some embodiments, the present disclosure encompasses the delivery of pharmaceutical, prophylactic, diagnostic, or imaging compositions in combination with agents that may improve their bioavailability, reduce and/or modify their metabolism, inhibit their excretion, and/or modify their distribution within the body.

IV. METHODS OF USE

Reduce Expression of a Target Gene

[00917] In some embodiments, the present invention provides methods for inhibiting/silencing gene expression in a cell. Accordingly, the modulatory polynucleotides encoding siRNA duplexes or encoded dsRNA can be used to substantially inhibit gene expression in a cell, in particular in a neuron. In some aspects, the inhibition of gene expression refers to an inhibition by at least about 15%, such as by at least about 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-

95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. Accordingly, the protein product of the targeted gene may be inhibited by at least about 15%, preferably by at least about 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[00918] In some embodiments, the present invention provides methods for inhibiting/silencing gene expression in a cell, in particular in a medium spiny neuron. In some aspects, the inhibition of gene expression refers to an inhibition by at least about 15%, such as by at least about 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. Accordingly, the protein product of the targeted gene may be inhibited by at least about 15%, preferably by at least about 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[00919] In some embodiments, the present invention provides methods for inhibiting/silencing gene expression in a cell, in particular in a motor neuron. In some aspects, the inhibition of gene expression refers to an inhibition by at least about 15%, such as by at least about 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. Accordingly, the protein product of the targeted gene may be inhibited by at least about 15%, preferably by at least about 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[00920] In some embodiments, the present invention provides methods for inhibiting/silencing gene expression in a cell, in particular in an astrocyte. In some aspects, the inhibition of gene expression refers to an inhibition by at least about 15%, such as by at least about 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. Accordingly, the protein product of the targeted gene may be inhibited by at least about 15%, preferably by at least about 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[00921] In one embodiment, the siRNA duplexes or encoded dsRNA may be used to reduce the expression of protein by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of protein expression may be reduced by 50-90%. As a non-limiting example, the expression of protein expression may be reduced by 30-70%. As a non-limiting example, the expression of protein expression may be reduced by 20-70%. As a non-limting example, the expression of protein expression may be reduced by 15-30%.

[00922] In one embodiment, the modulatory polynucleotides encoding siRNA duplexes or encoded dsRNA may be used to reduce the expression of mRNA by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of mRNA expression may be reduced by 50-90%. As a non-limiting example, the expression of mRNA expression may be reduced by30-70%. As a non-limiting example, the expression of mRNA expression may be reduced by20-70%. As a non-limiting example, the expression of mRNA expression may be reduced by 15-30%.

[00923] In one embodiment, the siRNA duplexes or encoded dsRNA may be used to reduce the expression of protein and/or mRNA in at least one region of the CNS such as, but not limited to the midbrain. The expression of protein and/or mRNA is reduced by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-

95%, 90-100% or 95-100% in at least one region of the CNS. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 50-90%. As a non-limiting example, the expression of protein and mRNA in the striatum is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the striatum is reduced by 20-50%. As a non-limiting example, the expression of protein and mRNA in the striatum is reduced by 15-50%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 30-70%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 20-70%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 15-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 20-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 20-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 15-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 40-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 50-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 50-60%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 50%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 51%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 52%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 53%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 54%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 55%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 56%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 57%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 58%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 59%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 60%.

[00924] In one embodiment, the modulatory polynucleotides encoding siRNA duplexes or encoded dsRNA may be used to reduce the expression of protein and/or mRNA in at least one region of the CNS such as, but not limited to the forebrain. The expression of protein and/or mRNA is reduced by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in at least one region of the CNS. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 50-90%. As a non-limiting example, the expression of protein and mRNA in the striatum is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 30-70%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 20-70%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 15-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 20-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 15-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 40-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 50-70%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 50-60%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 50%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 51%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 52%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 53%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 54%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 55%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 56%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 57%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 58%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 59%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 60%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 61%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 62%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 63%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 64%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 65%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 66%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 67%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 68%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 69%. As a non-limiting example, the expression of protein and mRNA in the striatum and/or cortex is reduced by 70%.

[00925] In one embodiment, the modulatory polynucleotides encoding siRNA duplexes or encoded dsRNA may be used to reduce the expression of protein and/or mRNA in the putamen. The expression of protein and/or mRNA is reduced by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 55-60%, 55-70%, 55-80%, 55-90%, 55-95%, 55-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in at least one region of the CNS. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 40-70%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 50-70%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 50-60%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 50%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 51%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 52%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 53%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 54%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 55%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 56%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 57%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 58%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 59%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 60%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 61%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 62%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 63%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 64%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 65%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 66%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 67%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 68%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 69%. As a non-limiting example, the expression of protein and mRNA in the putamen is reduced by 70%.

[00926] In one embodiment, the modulatory polynucleotides encoding siRNA duplexes or encoded dsRNA may be used to reduce the expression of protein and/or mRNA in the cortex. The expression of protein and/or mRNA is reduced by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-

40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 30-70%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by at least 30%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 40-70%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 50-70%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 50-60%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 50%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 51%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 52%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 53%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 54%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 55%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 56%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 57%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 58%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 59%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 60%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 61%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 62%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 63%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 64%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 65%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 66%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 67%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 68%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 69%. As a non-limiting example, the expression of protein and mRNA in the cortex is reduced by 70%.

[00927] In one embodiment, the modulatory polynucleotides encoding siRNA duplexes or encoded dsRNA may be used to reduce the expression of protein and/or mRNA in the motor cortex. The expression of protein and/or mRNA is reduced by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 30-70%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 20-70%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 15-70%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by at least 30%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 40-70%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 50-70%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 50-60%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 50%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 51%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 52%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 53%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 54%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 55%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 56%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 57%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 58%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 59%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 60%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 61%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 62%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 63%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 64%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 65%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 66%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 67%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 68%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 69%. As a non-limiting example, the expression of protein and mRNA in the motor cortex is reduced by 70%.

[00928] In one embodiment, the modulatory polynucleotides encoding siRNA duplexes or encoded dsRNA may be used to reduce the expression of protein and/or mRNA in the somatosensory cortex. The expression of protein and/or mRNA is reduced by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 30-70%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 20-70%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 15-70%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by at least 30%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 40-70%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 50-70%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 50-60%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 50%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 51%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 52%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 53%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 54%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 55%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 56%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 57%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 58%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 59%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 60%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 61%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 62%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 63%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 64%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 65%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 66%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 67%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 68%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 69%. As a non-limiting example, the expression of protein and mRNA in the somatosensory cortex is reduced by 70%.

[00929] In one embodiment, the modulatory polynucleotides encoding siRNA duplexes or encoded dsRNA may be used to reduce the expression of protein and/or mRNA in the temporal cortex. The expression of protein and/or mRNA is reduced by at least about 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 85%, 90%, 95% and 100%, or at least 15-20%, 15-30%, 15-40%, 15-50%, 15-60%, 15-70%, 15-80%, 15-90%, 15-95%, 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 40-50%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 30-70%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 20-70%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 15-70%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by at least 30%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 40-70%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 50-70%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 50-60%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 50%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 51%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 52%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 53%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 54%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 55%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 56%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 57%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 58%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 59%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 60%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 61%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 62%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 63%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 64%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 65%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 66%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 67%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 68%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 69%. As a non-limiting example, the expression of protein and mRNA in the temporal cortex is reduced by 70%.

[00930] In some embodiments, the present invention provides methods for treating, or ameliorating a disease and/or disorder of the central nervous system by inhibiting the expression of a gene and/or protein in a subject in need of treatment, the method comprising administering to the subject a pharmaceutically effective amount of at least one modulatory polynucleotides encoding siRNA duplex or a nucleic acid encoding an siRNA duplex targeting the gene, delivering the modulatory polynucleotides encoding siRNA duplex (or encoded duplex) into targeted cells, inhibiting gene expression and protein production, and ameliorating symptoms of the disease and/or disorder of the central nervous system in the subject.

V. KITS AND DEVICES

Kits

[00931] The invention provides a variety of kits for conveniently and/or effectively carrying out methods of the present invention. Typically kits will comprise sufficient amounts and/or numbers of components to allow a user to perform multiple treatments of a subject(s) and/or to perform multiple experiments.

[00932] Any of the vectors, constructs, modulatory polynucleotides, polynucleotides or polypeptides of the present invention may be comprised in a kit. In some embodiments, kits may further include reagents and/or instructions for creating and/or synthesizing compounds and/or compositions of the present invention. In some embodiments, kits may also include one or more buffers. In some embodiments, kits of the invention may include components for making protein or nucleic acid arrays or libraries and thus, may include, for example, solid supports.

[00933] In some embodiments, kit components may be packaged either in aqueous media or in lyophilized form. The container means of the kits will generally include at least one vial, test tube, flask, bottle, syringe or other container means, into which a component may be placed, and preferably, suitably aliquotted. Where there are more than one kit component, (labeling reagent and label may be packaged together), kits may also generally contain second, third or other additional containers into which additional components may be separately placed. In some embodiments, kits may also comprise second container means for containing sterile, pharmaceutically acceptable buffers and/or other diluents. In some embodiments, various combinations of components may be comprised in one or more vial. Kits of the present invention may also typically include means for containing compounds and/or compositions of the present invention, e.g., proteins, nucleic acids, and any other reagent containers in close confinement for commercial sale. Such containers may include injection or blow-molded plastic containers into which desired vials are retained.

[00934] In some embodiments, kit components are provided in one and/or more liquid solutions. In some embodiments, liquid solutions are aqueous solutions, with sterile aqueous solutions being particularly preferred. In some embodiments, kit components may be provided as dried powder(s). When reagents and/or components are provided as dry powders, such powders may be reconstituted by the addition of suitable volumes of solvent. In some embodiments, it is envisioned that solvents may also be provided in another container means. In some embodiments, labeling dyes are provided as dried powders. In some embodiments, it is contemplated that 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400, 500, 600, 700, 800, 900, 1000 micrograms or at least or at most those amounts of dried dye are provided in kits of the invention. In such embodiments, dye may then be resuspended in any suitable solvent, such as DMSO.

[00935] In some embodiments, kits may include instructions for employing kit components as well the use of any other reagent not included in the kit. Instructions may include variations that may be implemented.

Devices

[00936] In some embodiments, compounds and/or compositions of the present invention may be combined with, coated onto or embedded in a device. Devices may include, but are not limited to, dental implants, stents, bone replacements, artificial joints, valves, pacemakers and/or other implantable therapeutic device.

[00937] The present invention provides for devices which may incorporate viral vectors that encode one or more modulatory polynucleotide payload molecules. These devices contain in a stable formulation the viral vectors which may be immediately delivered to a subject in need thereof, such as a human patient.

[00938] Devices for administration may be employed to deliver the viral vectors comprising a modulatory polynucleotide of the present invention according to single, multi- or split-dosing regimens taught herein.

[00939] Method and devices known in the art for multi-administration to cells, organs and tissues are contemplated for use in conjunction with the methods and compositions disclosed herein as embodiments of the present invention. These include, for example, those methods and devices having multiple needles, hybrid devices employing for example lumens or catheters as well as devices utilizing heat, electric current or radiation driven mechanisms.

[00940] The modulatory polynucleotides of the present invention may be used in the treatment, prophylaxis or amelioration of any disease or disorder characterized by aberrant or undesired target expression.

VI. DEFINITIONS

[00941] At various places in the present specification, substituents of compounds of the present disclosure are disclosed in groups or in ranges. It is specifically intended that the present disclosure include each and every individual subcombination of the members of such groups and ranges.

[00942] *About:* As used herein, the term "about" means +/- 10% of the recited value.

[00943] *Administered in combination:* As used herein, the term "administered in combination" or "combined administration" means that two or more agents are administered to a subject at the same time or within an interval such that there may be an overlap of an effect of each agent on the patient. In some embodiments, they are administered within about 60, 30, 15, 10, 5, or 1 minute of one another. In some embodiments, the administrations of the agents are spaced sufficiently closely together such that a combinatorial (*e.g.*, a synergistic) effect is achieved.

[00944] *Animal:* As used herein, the term "animal" refers to any member of the animal kingdom. In some embodiments, "animal" refers to humans at any stage of development. In some embodiments, "animal" refers to non-human animals at any stage of development. In certain embodiments, the non-human animal is a mammal (*e.g.*, a rodent, a mouse, a rat, a rabbit, a monkey, a dog, a cat, a sheep, cattle, a primate, or a pig). In some embodiments, animals include, but are not limited to, mammals, birds, reptiles, amphibians, fish, and worms. In some embodiments, the animal is a transgenic animal, genetically-engineered animal, or a clone.

[00945] *Approximately:* As used herein, the term "approximately" or "about," as applied to one or more values of interest, refers to a value that is similar to a stated reference value. In certain embodiments, the term "approximately" or "about" refers to a range of values that fall within 25%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context (except where such number would exceed 100% of a possible value).

[00946] *Associated with:* As used herein, the terms "associated with," "conjugated," "linked," "attached," and "tethered," when used with respect to two or more moieties, means that the moieties are physically associated or connected with one another, either directly or via one or more additional moieties that serves as a linking agent, to form a structure that is sufficiently stable so that the moieties remain physically associated under the conditions in which the structure is used, *e.g.*, physiological conditions. An “association” need not be strictly through direct covalent chemical bonding. It may also suggest ionic or hydrogen bonding or a hybridization based connectivity sufficiently stable such that the “associated” entities remain physically associated.

[00947] *Bifunctional:* As used herein, the term “bifunctional” refers to any substance, molecule or moiety which is capable of or maintains at least two functions. The functions may affect the same outcome or a different outcome. The structure that produces the function may be the same or different.

[00948] *Biocompatible*: As used herein, the term “biocompatible” means compatible with living cells, tissues, organs or systems posing little to no risk of injury, toxicity or rejection by the immune system.

[00949] *Biodegradable*: As used herein, the term “biodegradable” means capable of being broken down into innocuous products by the action of living things.

[00950] *Biologically active*: As used herein, the phrase “biologically active” refers to a characteristic of any substance that has activity in a biological system and/or organism. For instance, a substance that, when administered to an organism, has a biological effect on that organism, is considered to be biologically active. In particular embodiments, a modulatory polynucleotide of the present invention may be considered biologically active if even a portion of the polynucleotides is biologically active or mimics an activity considered biologically relevant.

[00951] *Induced pluripotent stem cells*: As used herein, “induced pluripotent stem cells” are cells that may be induced to form any of several distinct cell types.

[00952] *Compound:* As used herein, the term “compound,” is meant to include all stereoisomers, geometric isomers, tautomers, and isotopes of the structures depicted.

[00953] The compounds described herein can be asymmetric (*e.g.*, having one or more stereocenters). All stereoisomers, such as enantiomers and diastereomers, are intended unless otherwise indicated. Compounds of the present disclosure that contain asymmetrically substituted carbon atoms can be isolated in optically active or racemic forms. Methods on how to prepare optically active forms from optically active starting materials are known in the art, such as by resolution of racemic mixtures or by stereoselective synthesis. Many geometric isomers of olefins, C=N double bonds, and the like can also be present in the compounds described herein, and all such stable isomers are contemplated in the present disclosure. Cis and trans geometric isomers of the compounds of the present disclosure are described and may be isolated as a mixture of isomers or as separated isomeric forms.

[00954] Compounds of the present disclosure also include tautomeric forms. Tautomeric forms result from the swapping of a single bond with an adjacent double bond and the concomitant migration of a proton. Tautomeric forms include prototropic tautomers which are isomeric protonation states having the same empirical formula and total charge.

[00955] Compounds of the present disclosure also include all of the isotopes of the atoms occurring in the intermediate or final compounds. "Isotopes" refers to atoms having the same atomic number but different mass numbers resulting from a different number of neutrons in the nuclei. For example, isotopes of hydrogen include tritium and deuterium.

[00956] The compounds and salts of the present disclosure can be prepared in combination with solvent or water molecules to form solvates and hydrates by routine methods.

[00957] *Conserved*: As used herein, the term "conserved" refers to nucleotides or amino acid residues of a polynucleotide sequence or polypeptide sequence, respectively, that are those that occur unaltered in the same position of two or more sequences being compared. Nucleotides or amino acids that are relatively conserved are those that are conserved amongst more related sequences than nucleotides or amino acids appearing elsewhere in the sequences.

[00958] In some embodiments, two or more sequences are said to be "completely conserved" if they are 100% identical to one another. In some embodiments, two or more sequences are said to be "highly conserved" if they are at least 70% identical, at least 80% identical, at least 90% identical, or at least 95% identical to one another. In some embodiments, two or more sequences are said to be "highly conserved" if they are about 70% identical, about 80% identical, about 90% identical, about 95%, about 98%, or about 99% identical to one another. In some embodiments, two or more sequences are said to be "conserved" if they are at least 30% identical, at least 40% identical, at least 50% identical, at least 60% identical, at least 70% identical, at least 80% identical, at least 90% identical, or at least 95% identical to one another. In some embodiments, two or more sequences are said to be "conserved" if they are about 30% identical, about 40% identical, about 50% identical, about 60% identical, about 70% identical, about 80% identical, about 90% identical, about 95% identical, about 98% identical, or about 99% identical to one another. Conservation of sequence may apply to the entire length of a polynucleotide or polypeptide or may apply to a portion, region or feature thereof.

[00959] *Controlled Release:* As used herein, the term "controlled release" refers to a pharmaceutical composition or compound release profile that conforms to a particular pattern of release to effect a therapeutic outcome.

[00960] *Cyclic or Cyclized:* As used herein, the term "cyclic" refers to the presence of a continuous loop. Cyclic molecules need not be circular, only joined to form an unbroken chain of subunits.

[00961] *Cytostatic*: As used herein, "cytostatic" refers to inhibiting, reducing, suppressing the growth, division, or multiplication of a cell (*e.g.*, a mammalian cell (*e.g.*, a human cell)), bacterium, virus, fungus, protozoan, parasite, prion, or a combination thereof.

[00962] *Cytotoxic*: As used herein, "cytotoxic" refers to killing or causing injurious, toxic, or deadly effect on a cell (*e.g.*, a mammalian cell (*e.g.*, a human cell)), bacterium, virus, fungus, protozoan, parasite, prion, or a combination thereof.

[00963] *Delivery:* As used herein, "delivery" refers to the act or manner of delivering a compound, substance, entity, moiety, cargo or payload.

[00964] *Delivery Agent*: As used herein, "delivery agent" refers to any substance which facilitates, at least in part, the *in vivo* delivery of a modulatory polynucleotide to targeted cells.

[00965] *Destabilized:* As used herein, the term "destable," "destabilize," or "destabilizing region" means a region or molecule that is less stable than a starting, wild-type or native form of the same region or molecule.

[00966] *Detectable label:* As used herein, "detectable label" refers to one or more markers, signals, or moieties which are attached, incorporated or associated with another entity that is readily detected by methods known in the art including radiography, fluorescence, chemiluminescence, enzymatic activity, absorbance and the like. Detectable labels include radioisotopes, fluorophores, chromophores, enzymes, dyes, metal ions, ligands such as biotin, avidin, streptavidin and haptens, quantum dots, and the like. Detectable labels may be located at any position in the peptides or proteins disclosed herein. They may be within the amino acids, the peptides, or proteins, or located at the N- or C- termini.

[00967] *Diastereomer:* As used herein, the term "diastereomer," means stereoisomers that are not mirror images of one another and are non-superimposable on one another.

[00968] *Digest*: As used herein, the term "digest" means to break apart into smaller pieces or components. When referring to polypeptides or proteins, digestion results in the production of peptides.

[00969] *Distal:* As used herein, the term "distal" means situated away from the center or away from a point or region of interest.

[00970] *Dosing regimen*: As used herein, a "dosing regimen" is a schedule of administration or physician determined regimen of treatment, prophylaxis, or palliative care.

[00971] *Enantiomer:* As used herein, the term "enantiomer" means each individual optically active form of a compound of the invention, having an optical purity or enantiomeric excess (as determined by methods standard in the art) of at least 80% (i.e., at least 90% of one enantiomer and at most 10% of the other enantiomer), preferably at least 90% and more preferably at least 98%.

[00972] *Encapsulate:* As used herein, the term "encapsulate" means to enclose, surround or encase.

[00973] *Engineered:* As used herein, embodiments of the invention are "engineered" when they are designed to have a feature or property, whether structural or chemical, that varies from a starting point, wild type or native molecule.

[00974] *Effective Amount:* As used herein, the term "effective amount" of an agentis that amount sufficient to effect beneficial or desired results, for example, clinical results, and, as such, an "effective amount" depends upon the context in which it is being applied. For example, in the context of administering an agent that treats cancer, an effective amount of an agent is, for example, an amount sufficient to achieve treatment, as defined herein, of cancer, as compared to the response obtained without administration of the agent.

[00975] *Exosome:* As used herein, "exosome" is a vesicle secreted by mammalian cells or a complex involved in RNA degradation.

[00976] *Expression*: As used herein, "expression" of a nucleic acid sequence refers to one or more of the following events: (1) production of an RNA template from a DNA sequence (*e.g.*, by transcription); (2) processing of an RNA transcript (*e.g.*, by splicing, editing, 5′ cap formation, and/or 3′ end processing); (3) translation of an RNA into a polypeptide or protein; and (4) post-translational modification of a polypeptide or protein.

[00977] *Feature:* As used herein, a "feature" refers to a characteristic, a property, or a distinctive element.

[00978] *Formulation*: As used herein, a "formulation" includes at least one modulatory polynucleotide and a delivery agent.

[00979] *Fragment:* A "fragment," as used herein, refers to a portion. For example, fragments of proteins may comprise polypeptides obtained by digesting full-length protein isolated from cultured cells.

[00980] *Functional*: As used herein, a "functional" biological molecule is a biological molecule in a form in which it exhibits a property and/or activity by which it is characterized.

[00981] *Homology*: As used herein, the term "homology" refers to the overall relatedness between polymeric molecules, *e.g.* between nucleic acid molecules (*e.g.* DNA molecules and/or

RNA molecules) and/or between polypeptide molecules. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identical or similar. The term "homologous" necessarily refers to a comparison between at least two sequences (polynucleotide or polypeptide sequences). In accordance with the invention, two polynucleotide sequences are considered to be homologous if the polypeptides they encode are at least about 50%, 60%, 70%, 80%, 90%, 95%, or even 99% for at least one stretch of at least about 20 amino acids. In some embodiments, homologous polynucleotide sequences are characterized by the ability to encode a stretch of at least 4–5 uniquely specified amino acids. For polynucleotide sequences less than 60 nucleotides in length, homology is determined by the ability to encode a stretch of at least 4–5 uniquely specified amino acids. In accordance with the invention, two protein sequences are considered to be homologous if the proteins are at least about 50%, 60%, 70%, 80%, or 90% identical for at least one stretch of at least about 20 amino acids.

[00982] *Identity*: As used herein, the term "identity" refers to the overall relatedness between polymeric molecules, *e.g.*, between polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of the percent identity of two polynucleotide sequences, for example, can be performed by aligning the two sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in one or both of a first and a second nucleic acid sequences for optimal alignment and non-identical sequences can be disregarded for comparison purposes). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or 100% of the length of the reference sequence. The nucleotides at corresponding nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which needs to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. For example, the percent identity between two nucleotide sequences can be determined using methods such as those described in Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Sequence Analysis in Molecular Biology, von Heinje, G., Academic

Press, 1987; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; each of which is incorporated herein by reference. For example, the percent identity between two nucleotide sequences can be determined using the algorithm of Meyers and Miller (CABIOS, 1989, 4:11-17), which has been incorporated into the ALIGN program (version 2.0) using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. The percent identity between two nucleotide sequences can, alternatively, be determined using the GAP program in the GCG software package using an NWSgapdna.CMP matrix. Methods commonly employed to determine percent identity between sequences include, but are not limited to those disclosed in Carillo, H., and Lipman, D., SIAM J Applied Math., 48:1073 (1988); incorporated herein by reference. Techniques for determining identity are codified in publicly available computer programs. Exemplary computer software to determine homology between two sequences include, but are not limited to, GCG program package, Devereux, J., *et al.*, *Nucleic Acids Research*, 12(1), 387 (1984)), BLASTP, BLASTN, and FASTA Altschul, S. F. *et al.*, *J. Molec. Biol.*, 215, 403 (1990)).

[00983] *Inhibit expression of a gene:* As used herein, the phrase "inhibit expression of a gene" means to cause a reduction in the amount of an expression product of the gene. The expression product can be an RNA transcribed from the gene (*e.g.*, an mRNA) or a polypeptide translated from an mRNA transcribed from the gene. Typically a reduction in the level of an mRNA results in a reduction in the level of a polypeptide translated therefrom. The level of expression may be determined using standard techniques for measuring mRNA or protein.

[00984] *Isomer:* As used herein, the term "isomer" means any tautomer, stereoisomer, enantiomer, or diastereomer of any compound of the invention. It is recognized that the compounds of the invention can have one or more chiral centers and/or double bonds and, therefore, exist as stereoisomers, such as double-bond isomers (i.e., geometric E/Z isomers) or diastereomers (e.g., enantiomers (i.e., (+) or (-)) or cis/trans isomers). According to the invention, the chemical structures depicted herein, and therefore the compounds of the invention, encompass all of the corresponding stereoisomers, that is, both the stereomerically pure form (e.g., geometrically pure, enantiomerically pure, or diastereomerically pure) and enantiomeric and stereoisomeric mixtures, e.g., racemates. Enantiomeric and stereoisomeric mixtures of compounds of the invention can typically be resolved into their component enantiomers or stereoisomers by well-known methods, such as chiral-phase gas chromatography, chiral-phase high performance liquid chromatography, crystallizing the compound as a chiral salt complex, or crystallizing the compound in a chiral solvent. Enantiomers and stereoisomers can also be obtained from stereomerically or enantiomerically pure intermediates, reagents, and catalysts by well-known asymmetric synthetic methods.

[00985] *In vitro*: As used herein, the term "*in vitro*" refers to events that occur in an artificial environment, *e.g.*, in a test tube or reaction vessel, in cell culture, in a Petri dish, *etc.*, rather than within an organism (*e.g.*, animal, plant, or microbe).

[00986] *In vivo*: As used herein, the term "*in vivo*" refers to events that occur within an organism (*e.g.*, animal, plant, or microbe or cell or tissue thereof).

[00987] *Isolated*: As used herein, the term "isolated" refers to a substance or entity that has been separated from at least some of the components with which it was associated (whether in nature or in an experimental setting). Isolated substances may have varying levels of purity in reference to the substances from which they have been associated. Isolated substances and/or entities may be separated from at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or more of the other components with which they were initially associated. In some embodiments, isolated agents are more than about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more than about 99% pure. As used herein, a substance is "pure" if it is substantially free of other components.

[00988] *Substantially isolated*: By "substantially isolated" is meant that the compound is substantially separated from the environment in which it was formed or detected. Partial separation can include, for example, a composition enriched in the compound of the present disclosure. Substantial separation can include compositions containing at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 97%, or at least about 99% by weight of the compound of the present disclosure, or salt thereof. Methods for isolating compounds and their salts are routine in the art.

[00989] *Linker:* As used herein, a linker refers to a group of atoms, e.g., 10-1,000 atoms, and can be comprised of the atoms or groups such as, but not limited to, carbon, amino, alkylamino, oxygen, sulfur, sulfoxide, sulfonyl, carbonyl, and imine. The linker can be attached to a modified nucleoside or nucleotide on the nucleobase or sugar moiety at a first end, and to a payload, e.g., a detectable or therapeutic agent, at a second end. The linker may be of sufficient length as to not interfere with incorporation into a nucleic acid sequence. The linker can be used for any useful purpose, such as to form modulatory polynucleotide multimers (e.g., through linkage of two or more modulatory polynucleotides molecules) or modulatory polynucleotides conjugates, as well as to administer a payload, as described herein. Examples of chemical groups that can be incorporated into the linker include, but are not limited to, alkyl, alkenyl, alkynyl, amido, amino, ether, thioether, ester, alkylene, heteroalkylene, aryl, or heterocyclyl, each of which can be optionally substituted, as described herein. Examples of linkers include, but are not limited to, unsaturated alkanes, polyethylene glycols (e.g., ethylene or propylene glycol monomeric units, e.g., diethylene glycol, dipropylene glycol, triethylene glycol, tripropylene glycol, tetraethylene glycol, or tetraethylene glycol), and dextran polymers and derivatives thereof., Other examples include, but are not limited to, cleavable moieties within the linker, such as, for example, a disulfide bond (-S-S-) or an azo bond (-N=N-), which can be cleaved using a reducing agent or photolysis. Non-limiting examples of a selectively cleavable bond include an amido bond can be cleaved for example by the use of tris(2-carboxyethyl)phosphine (TCEP), or other reducing agents, and/or photolysis, as well as an ester bond can be cleaved for example by acidic or basic hydrolysis.

[00990] *MicroRNA (miRNA) binding site:* As used herein, a microRNA (miRNA) binding site represents a nucleotide location or region of a nucleic acid transcript to which at least the "seed" region of a miRNA binds.

[00991] *Modified:* As used herein "modified" refers to a changed state or structure of a molecule of the invention. Molecules may be modified in many ways including chemically, structurally, and functionally.

[00992] *Naturally occurring:* As used herein, "naturally occurring" means existing in nature without artificial aid.

[00993] *Neutralizing antibody*: As used herein, a "neutralizing antibody" refers to an antibody which binds to its antigen and defends a cell from an antigen or infectious agent by neutralizing or abolishing any biological activity it has.

[00994] *Non-human vertebrate:* As used herein, a "non human vertebrate" includes all vertebrates except *Homo sapiens*, including wild and domesticated species. Examples of non-human vertebrates include, but are not limited to, mammals, such as alpaca, banteng, bison, camel, cat, cattle, deer, dog, donkey, gayal, goat, guinea pig, horse, llama, mule, pig, rabbit, reindeer, sheep water buffalo, and yak.

[00995] *Off-target:* As used herein, "off target" refers to any unintended effect on any one or more target, gene, or cellular transcript.

[00996] *Open reading frame:* As used herein, "open reading frame" or "ORF" refers to a sequence which does not contain a stop codon in a given reading frame.

[00997] *Operably linked:* As used herein, the phrase "operably linked" refers to a functional connection between two or more molecules, constructs, transcripts, entities, moieties or the like.

[00998] *Optionally substituted:* Herein a phrase of the form "optionally substituted X" (*e.g.*, optionally substituted alkyl) is intended to be equivalent to "X, wherein X is optionally substituted" (*e.g.*, "alkyl, wherein the alkyl is optionally substituted"). It is not intended to mean that the feature "X" (*e.g.* alkyl) *per se* is optional.

[00999] *Peptide:* As used herein, "peptide" is less than or equal to 50 amino acids long, e.g., about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acids long.

[001000] *Patient:* As used herein, "patient" refers to a subject who may seek or be in need of treatment, requires treatment, is receiving treatment, will receive treatment, or a subject who is under care by a trained professional for a particular disease or condition.

[001001] *Pharmaceutically acceptable*: The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

[001002] *Pharmaceutically acceptable excipients:* The phrase "pharmaceutically acceptable excipient," as used herein, refers any ingredient other than the compounds described herein (for example, a vehicle capable of suspending or dissolving the active compound) and having the properties of being substantially nontoxic and non-inflammatory in a patient. Excipients may include, for example: antiadherents, antioxidants, binders, coatings, compression aids, disintegrates, dyes (colors), emollients, emulsifiers, fillers (diluents), film formers or coatings, flavors, fragrances, glidants (flow enhancers), lubricants, preservatives, printing inks, sorbents, suspensing or dispersing agents, sweeteners, and waters of hydration. Exemplary excipients include, but are not limited to: butylated hydroxytoluene (BHT), calcium carbonate, calcium phosphate (dibasic), calcium stearate, croscarmellose, crosslinked polyvinyl pyrrolidone, citric acid, crospovidone, cysteine, ethylcellulose, gelatin, hydroxypropyl cellulose, hydroxypropyl methylcellulose, lactose, magnesium stearate, maltitol, mannitol, methionine, methylcellulose, methyl paraben, microcrystalline cellulose, polyethylene glycol, polyvinyl pyrrolidone, povidone, pregelatinized starch, propyl paraben, retinyl palmitate, shellac, silicon dioxide, sodium carboxymethyl cellulose, sodium citrate, sodium starch glycolate, sorbitol, starch (corn), stearic acid, sucrose, talc, titanium dioxide, vitamin A, vitamin E, vitamin C, and xylitol.

[001003] *Pharmaceutically acceptable salts*: The present disclosure also includes pharmaceutically acceptable salts of the compounds described herein. As used herein, "pharmaceutically acceptable salts" refers to derivatives of the disclosed compounds wherein the parent compound is modified by converting an existing acid or base moiety to its salt form (e.g., by reacting the free base group with a suitable organic acid). Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or organic acid salts of basic residues such as amines; alkali or organic salts of acidic residues such as carboxylic acids; and the like. Representative acid addition salts include acetate, acetic acid, adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzene sulfonic acid, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate, citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, glucoheptonate, glycerophosphate, hemisulfate, heptonate, hexanoate, hydrobromide, hydrochloride, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like, as well as nontoxic ammonium, quaternary ammonium, and amine cations, including, but not limited to ammonium, tetramethylammonium, tetraethylammonium, methylamine, dimethylamine, trimethylamine, triethylamine, ethylamine, and the like. The pharmaceutically acceptable salts of the present disclosure include the conventional non-toxic salts of the parent compound formed, for example, from non-toxic inorganic or organic acids. The pharmaceutically acceptable salts of the present disclosure can be synthesized from the parent compound which contains a basic or acidic moiety by conventional chemical methods. Generally, such salts can be prepared by reacting the free acid or base forms of these compounds with a stoichiometric amount of the appropriate base or acid in water or in an organic solvent, or in a mixture of the two; generally, nonaqueous media like ether, ethyl acetate, ethanol, isopropanol, or acetonitrile are preferred. Lists of suitable salts are found in *Remington's Pharmaceutical Sciences*, 17th ed., Mack Publishing Company, Easton, Pa., 1985, p. 1418, *Pharmaceutical Salts: Properties, Selection, and Use*, P.H. Stahl and C.G. Wermuth (eds.), Wiley-VCH, 2008, and Berge et al., *Journal of Pharmaceutical Science*, 66, 1-19 (1977), each of which is incorporated herein by reference in its entirety.

[001004] *Pharmaceutically acceptable solvate*: The term "pharmaceutically acceptable solvate," as used herein, means a compound of the invention wherein molecules of a suitable solvent are incorporated in the crystal lattice. A suitable solvent is physiologically tolerable at the dosage administered. For example, solvates may be prepared by crystallization, recrystallization, or precipitation from a solution that includes organic solvents, water, or a mixture thereof. Examples of suitable solvents are ethanol, water (for example, mono-, di-, and tri-hydrates), *N*-

methylpyrrolidinone (NMP), dimethyl sulfoxide (DMSO), *N,N'*-dimethylformamide (DMF), *N,N'*-dimethylacetamide (DMAC), 1,3-dimethyl-2-imidazolidinone (DMEU), 1,3-dimethyl-3,4,5,6-tetrahydro-2-(1H)-pyrimidinone (DMPU), acetonitrile (ACN), propylene glycol, ethyl acetate, benzyl alcohol, 2-pyrrolidone, benzyl benzoate, and the like. When water is the solvent, the solvate is referred to as a "hydrate."

[001005] *Pharmacokinetic:* As used herein, "pharmacokinetic" refers to any one or more properties of a molecule or compound as it relates to the determination of the fate of substances administered to a living organism. Pharmacokinetics is divided into several areas including the extent and rate of absorption, distribution, metabolism and excretion. This is commonly referred to as ADME where: (A) Absorption is the process of a substance entering the blood circulation; (D) Distribution is the dispersion or dissemination of substances throughout the fluids and tissues of the body; (M) Metabolism (or Biotransformation) is the irreversible transformation of parent compounds into daughter metabolites; and (E) Excretion (or Elimination) refers to the elimination of the substances from the body. In rare cases, some drugs irreversibly accumulate in body tissue.

[001006] *Physicochemical:* As used herein, "physicochemical" means of or relating to a physical and/or chemical property.

[001007] *Preventing*: As used herein, the term "preventing" refers to partially or completely delaying onset of an infection, disease, disorder and/or condition; partially or completely delaying onset of one or more symptoms, features, or clinical manifestations of a particular infection, disease, disorder, and/or condition; partially or completely delaying onset of one or more symptoms, features, or manifestations of a particular infection, disease, disorder, and/or condition; partially or completely delaying progression from an infection, a particular disease, disorder and/or condition; and/or decreasing the risk of developing pathology associated with the infection, the disease, disorder, and/or condition.

[001008] *Prodrug*: The present disclosure also includes prodrugs of the compounds described herein. As used herein, "prodrugs" refer to any substance, molecule or entity which is in a form predicate for that substance, molecule or entity to act as a therapeutic upon chemical or physical alteration. Prodrugs may by covalently bonded or sequestered in some way and which release or are converted into the active drug moiety prior to, upon or after administered to a mammalian subject. Prodrugs can be prepared by modifying functional groups present in the compounds in such a way that the modifications are cleaved, either in routine manipulation or *in vivo*, to the parent compounds. Prodrugs include compounds wherein hydroxyl, amino, sulfhydryl, or carboxyl groups are bonded to any group that, when administered to a mammalian subject, cleaves to form a free hydroxyl, amino, sulfhydryl, or carboxyl group respectively. Preparation and use of prodrugs is discussed in T. Higuchi and V. Stella, "Pro-drugs as Novel Delivery Systems," Vol. 14 of the A.C.S. Symposium Series, and in *Bioreversible Carriers in Drug Design*, ed. Edward B. Roche, American Pharmaceutical Association and Pergamon Press, 1987, both of which are hereby incorporated by reference in their entirety. In some embodiments, the pri-miRs of the invention may be prodrugs of the pre-miRs. Likewise either pri- or pre-miRs may be prodrugs of the artificial miRs which are processed from them.

[001009] *Proliferate:* As used herein, the term "proliferate" means to grow, expand or increase or cause to grow, expand or increase rapidly. "Proliferative" means having the ability to proliferate. "Anti-proliferative" means having properties counter to or inapposite to proliferative properties.

[001010] *Prophylactic*: As used herein, "prophylactic" refers to a therapeutic or course of action used to prevent the spread of disease.

[001011] *Prophylaxis:* As used herein, a "prophylaxis" refers to a measure taken to maintain health and prevent the spread of disease.

[001012] *Protein cleavage site*: As used herein, "protein cleavage site" refers to a site where controlled cleavage of the amino acid chain can be accomplished by chemical, enzymatic or photochemical means.

[001013] *Protein cleavage signal:* As used herein "protein cleavage signal" refers to at least one amino acid that flags or marks a polypeptide for cleavage.

[001014] *Protein of interest:* As used herein, the terms "proteins of interest" or "desired proteins" include those provided herein and fragments, mutants, variants, and alterations thereof.

[001015] *Proximal:* As used herein, the term "proximal" means situated nearer to the center or to a point or region of interest.

[001016] *Purified:* As used herein, "purify," "purified," "purification" means to make substantially pure or clear from unwanted components, material defilement, admixture or imperfection.

[001017] *Sample:* As used herein, the term "sample" or "biological sample" refers to a subset of its tissues, cells or component parts (e.g. body fluids, including but not limited to blood, mucus, lymphatic fluid, synovial fluid, cerebrospinal fluid, saliva, amniotic fluid, amniotic cord blood, urine, vaginal fluid and semen). A sample further may include a homogenate, lysate or extract prepared from a whole organism or a subset of its tissues, cells or component parts, or a fraction or portion thereof, including but not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, tumors, organs. A sample further refers to a medium, such as a nutrient broth or gel, which may contain cellular components, such as proteins or nucleic acid molecule.

[001018] *Signal Sequences:* As used herein, the phrase "signal sequences" refers to a sequence which can direct the transport or localization of a protein.

[001019] *Single unit dose*: As used herein, a "single unit dose" is a dose of any therapeutic administered in one dose/at one time/single route/single point of contact, i.e., single administration event.

[001020] *Similarity*: As used herein, the term "similarity" refers to the overall relatedness between polymeric molecules, *e.g.* between polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of percent similarity of polymeric molecules to one another can be performed in the same manner as a calculation of percent identity, except that calculation of percent similarity takes into account conservative substitutions as is understood in the art.

[001021] *Split dose*: As used herein, a "split dose" is the division of single unit dose or total daily dose into two or more doses.

[001022] *Stable:* As used herein "stable" refers to a compound that is sufficiently robust to survive isolation to a useful degree of purity from a reaction mixture, and preferably capable of formulation into an efficacious therapeutic agent.

[001023] *Stabilized:* As used herein, the term "stabilize", "stabilized," "stabilized region" means to make or become stable.

[001024] *Stereoisomer:* As used herein, the term "stereoisomer" refers to all possible different isomeric as well as conformational forms which a compound may possess (e.g., a compound of any formula described herein), in particular all possible stereochemically and conformationally isomeric forms, all diastereomers, enantiomers and/or conformers of the basic molecular structure. Some compounds of the present invention may exist in different tautomeric forms, all of the latter being included within the scope of the present invention.

[001025] *Subject:* As used herein, the term "subject" or "patient" refers to any organism to which a composition in accordance with the invention may be administered, *e.g.*, for experimental, diagnostic, prophylactic, and/or therapeutic purposes. Typical subjects include animals (*e.g.*, mammals such as mice, rats, rabbits, non-human primates, and humans) and/or plants.

[001026] *Substantially*: As used herein, the term "substantially" refers to the qualitative condition of exhibiting total or near-total extent or degree of a characteristic or property of interest. One of ordinary skill in the biological arts will understand that biological and chemical phenomena rarely, if ever, go to completion and/or proceed to completeness or achieve or avoid an absolute result. The term “substantially” is therefore used herein to capture the potential lack of completeness inherent in many biological and chemical phenomena.

[001027] *Substantially equal*: As used herein as it relates to time differences between doses, the term means plus/minus 2%.

[001028] *Substantially simultaneously*: As used herein and as it relates to plurality of doses, the term means within 2 seconds.

[001029] *Suffering from*: An individual who is “suffering from” a disease, disorder, and/or condition has been diagnosed with or displays one or more symptoms of a disease, disorder, and/or condition.

[001030] *Susceptible to*: An individual who is “susceptible to” a disease, disorder, and/or condition has not been diagnosed with and/or may not exhibit symptoms of the disease, disorder, and/or condition but harbors a propensity to develop a disease or its symptoms. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition (for example, cancer) may be characterized by one or more of the following: (1) a genetic mutation associated with development of the disease, disorder, and/or condition; (2) a genetic polymorphism associated with development of the disease, disorder, and/or condition; (3) increased and/or decreased expression and/or activity of a protein and/or nucleic acid associated with the disease, disorder, and/or condition; (4) habits and/or lifestyles associated with development of the disease, disorder, and/or condition; (5) a family history of the disease, disorder, and/or condition; and (6) exposure to and/or infection with a microbe associated with development of the disease, disorder, and/or condition. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition will develop the disease, disorder, and/or condition. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition will not develop the disease, disorder, and/or condition.

[001031] *Sustained release:* As used herein, the term “sustained release” refers to a pharmaceutical composition or compound release profile that conforms to a release rate over a specific period of time.

[001032] *Synthetic*: The term “synthetic” means produced, prepared, and/or manufactured by the hand of man. Synthesis of polynucleotides or polypeptides or other molecules of the present invention may be chemical or enzymatic.

[001033] *Targeted Cells:* As used herein, “targeted cells” refers to any one or more cells of interest. The cells may be found *in vitro*, *in vivo*, *in situ* or in the tissue or organ of an organism.

The organism may be an animal, preferably a mammal, more preferably a human and most preferably a patient.

[001034] *Therapeutic Agent:* The term “therapeutic agent” refers to any agent that, when administered to a subject, has a therapeutic, diagnostic, and/or prophylactic effect and/or elicits a desired biological and/or pharmacological effect.

[001035] *Therapeutically effective amount:* As used herein, the term “therapeutically effective amount” means an amount of an agent to be delivered (*e.g.*, nucleic acid, drug, therapeutic agent, diagnostic agent, prophylactic agent, *etc.*) that is sufficient, when administered to a subject suffering from or susceptible to an infection, disease, disorder, and/or condition, to treat, improve symptoms of, diagnose, prevent, and/or delay the onset of the infection, disease, disorder, and/or condition.

[001036] *Therapeutically effective outcome*: As used herein, the term “therapeutically effective outcome” means an outcome that is sufficient in a subject suffering from or susceptible to an infection, disease, disorder, and/or condition, to treat, improve symptoms of, diagnose, prevent, and/or delay the onset of the infection, disease, disorder, and/or condition.

[001037] *Total daily dose:* As used herein, a “total daily dose” is an amount given or prescribed in 24 hour period. It may be administered as a single unit dose.

[001038] *Transfection*: As used herein, the term “transfection” refers to methods to introduce exogenous nucleic acids into a cell. Methods of transfection include, but are not limited to, chemical methods, physical treatments and cationic lipids or mixtures.

[001039] *Treating*: As used herein, the term “treating” refers to partially or completely alleviating, ameliorating, improving, relieving, delaying onset of, inhibiting progression of, reducing severity of, and/or reducing incidence of one or more symptoms or features of a particular infection, disease, disorder, and/or condition. For example, “treating” cancer may refer to inhibiting survival, growth, and/or spread of a tumor. Treatment may be administered to a subject who does not exhibit signs of a disease, disorder, and/or condition and/or to a subject who exhibits only early signs of a disease, disorder, and/or condition for the purpose of decreasing the risk of developing pathology associated with the disease, disorder, and/or condition.

[001040] *Unmodified*: As used herein, “unmodified” refers to any substance, compound or molecule prior to being changed in any way. Unmodified may, but does not always, refer to the wild type or native form of a biomolecule. Molecules may undergo a series of modifications whereby each modified molecule may serve as the “unmodified” starting molecule for a subsequent modification.

VII. EQUIVALENTS AND SCOPE

[001041] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments in accordance with the invention described herein. The scope of the present invention is not intended to be limited to the above Description, but rather is as set forth in the appended claims.

[001042] In the claims, articles such as "a," "an," and "the" may mean one or more than one unless indicated to the contrary or otherwise evident from the context. Claims or descriptions that include "or" between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. The invention includes embodiments in which exactly one member of the group is present in, employed in, or otherwise relevant to a given product or process. The invention includes embodiments in which more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process.

[001043] It is also noted that the term "comprising" is intended to be open and permits but does not require the inclusion of additional elements or steps. When the term "comprising" is used herein, the term "consisting of" is thus also encompassed and disclosed.

[001044] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Methods and materials are described herein for use in the present disclosure; other, suitable methods and materials known in the art can also be used.

[001045] Where ranges are given, endpoints are included. Furthermore, it is to be understood that unless otherwise indicated or otherwise evident from the context and understanding of one of ordinary skill in the art, values that are expressed as ranges can assume any specific value or subrange within the stated ranges in different embodiments of the invention, to the tenth of the unit of the lower limit of the range, unless the context clearly dictates otherwise.

[001046] In addition, it is to be understood that any particular embodiment of the present invention that falls within the prior art may be explicitly excluded from any one or more of the claims. Since such embodiments are deemed to be known to one of ordinary skill in the art, they may be excluded even if the exclusion is not set forth explicitly herein. Any particular embodiment of the compositions of the invention (*e.g.*, any nucleic acid or protein encoded thereby; any method of production; any method of use; *etc.*) can be excluded from any one or more claims, for any reason, whether or not related to the existence of prior art.

[001047] All cited sources, for example, references, publications, databases, database entries, and art cited herein, are incorporated into this application by reference, even if not expressly stated in the citation. In case of conflicting statements of a cited source and the instant application, the statement in the instant application shall control.

[001048] Section and table headings are not intended to be limiting.

VIII. EXAMPLES

Example 1. Design of modulatory polynucleotides (artificial pri- or pre-microRNAs)

[001049] Artificial pri- or pre-microRNAs are designed to contain shRNA or stem loop structures encoding an artificial miR (or artificial siRNA or mature miRNA) having at least one strand that can at least partially hybridize with a target nucleic acid, e.g., RNA or DNA and one or more of the following features (a) UG motif at the base of basal stem, (b) a UGUG motif at the 5' end of the miRNA loop, (c) Uridine at the 5' end of guide strand, (d) a loop structure derived from a canonical microRNA such as miR-22, (e) a CNNC at the 3' flanking sequence, (f) flanking regions from a canonical microRNA such as let-7b, (g) one or more wobble base-pairs, bulges and mismatches in the stem after guide and passenger stands, and/or (h) one or more wobble base-pairs, bulges and mismatches between the passenger and guide strand.

[001050] Once designed, the sequence is engineered or synthesized or inserted in a plasmid or vector and administered to a cell or organism. Suitable plasmids or vectors are any which transfect or transduce the target cell.

[001051] Adeno-associated viral vectors (AAV), viral particles or entire viruses may be used.

[001052] Administration results in the processing of the modulatory polynucleotide to generate the artificial microRNA which alters expression levels of the target nucleic acid.

[001053] Effective knockdown of a target may be determined by methods in the art and will show little if any off-target effects.

[001054] Effective passenger-guide strand duplexes of the modulatory polynucleotides, e.g., pri- or pre-microRNAs demonstrate greater than 8-10-fold guide to passenger strand ratio when processing is measured.

Example 2. Passenger-Guide strand optimization

[001055] In order to achieve target knockdown or modulation of target expression which is specific and potent, the passenger and guide strands that will form the duplex stem of the stem-loop structure of the pri- or pre-microRNA of the invention may be optimized separately, for example as siRNA (small interfering RNAs).

[001056] siRNAs are designed against a target nucleic acid of choice as canonical siRNAs having a 19 base pair central duplex with a dinucleotide overhang on the 3' end of the strands of the duplex and where the antisense strand (guide strand) has perfect complementarity to the target nucleic acid over the 19 nucleotide region.

[001057] Alternatively, siRNAs are designed whereby the sense strand (passenger strand) comprises less than 19 nucleotide identity to the target nucleic acid.

[001058] Modifications to the sense-antisense (passenger-guide) strand duplex base pairing is made to introduce wobbles, bulges or mismatches. Insertions or deletions or mismatches may be incorporated at the 5' or 3' terminus of the sense strand (passenter strand) and these insertions or deletions may or may not be mirrored on the antisense strand (guide strand).

[001059] The resulting siRNA are tested by standard methods known in the art for target knockdown and other relevant physiologic and pharmacokinetic properties and for degree of off-target effects.

[001060] siRNA exhibiting sufficient target knockdown with few off target effects are then engineered, either with or without further modifications, as the passenger and guide strands of the pri- or pre-microRNAs of the invention.

Example 3. Pri and pre-microRNAs targeting HTT

[001061] The passenger-guide strand duplexes found to be efficacious are engineered into expression vectors and transfected into cells of the central nervous system or neuronal cell lines or immortalized cell lines of other origins. Even though overhang utilized in the siRNA knockdown study is a canonical dTdT for siRNA, the overhang in the synthetic pri- or pre-miR may comprise any dinucleotide overhang.

[001062] The cells used may be primary cells or derived from induced pluripotent stem cells (iPS cells).

[001063] The knockdown of the target is then measured and deep sequencing performed to determine the exact passenger and guide strand processed from each pri- or pre-microRNA administered in the expression vector.

[001064] A guide to passenger strand ratio is calculated to determine the efficiency of assembly, e.g., assembly into RNA Induced Silencing Complex (RISC).

[001065] The 5' end of guide and passenger strands are sequenced to determine the cleavage site and to determine the 5' end processing prcision. It is expected that processing precision will be higher than 85 percent.

[001066] HeLa cells are co-transfected in a parallel study to analyze in vitro knockdown of the target. In parallel, a cell-base luciferase reporter assay is established; a luciferase construct containing guide strand target site is used to assess on-target effect and a construct with passenger strand target site is used to determine off-target (passenger strand) effects.

[001067] Deep sequencing is again performed.

Example 4. Pri-miRNA constructs in AAV-miRNA vectors

[001068] Passenger-guide strand duplexes of the designed siRNA are engineered into AAV-miRNA expression vectors. The construct from ITR to ITR, recited 5' to 3', comprises a mutant or wild-type ITR, a promoter (either a CMV, a H1, a U6 or the CBA promoter (which includes a CMVie enhancer, a CB promoter and an SV40 or a human betaGlobin intron)), the pri-miRNA construct for the target, a rabbit globin or human growth hormone polyA and wildtype ITR. *In vitro* and *in vivo* studies are performed to test the efficacy of the AAV-miRNA expression vectors.

[001069] While the present invention has been described at some length and with some particularity with respect to the several described embodiments, it is not intended that it should be limited to any such particulars or embodiments or any particular embodiment, but it is to be construed with references to the appended claims so as to provide the broadest possible interpretation of such claims in view of the prior art and, therefore, to effectively encompass the intended scope of the invention.

[001070] All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, section headings, the materials, methods, and examples are illustrative only and not intended to be limiting.

In the claims which follow and in the preceding description of the invention, except where the context requires otherwise due to express language or necessary implication, the word “comprise” or variations such as “comprises” or “comprising” is used in an inclusive sense, i.e. to specify the presence of the stated features but not to preclude the presence or addition of further features in various embodiments of the invention.

It is to be understood that, if any prior art publication is referred to herein, such reference does not constitute an admission that the publication forms a part of the common general knowledge in the art, in Australia or any other country.

CLAIMS

We claim:

1. A modulatory polynucleotide comprising:

(a) a 5’ flanking region comprising the nucleotide sequence of SEQ ID NO: 7;

(b) a loop region comprising the nucleotide sequence of SEQ ID NO: 16; and

(c) a 3’ flanking region comprising the nucleotide sequence of SEQ ID NO: 26.

2. The modulatory polynucleotide of claim 1, further comprising a passenger strand and a guide strand.

3. The modulatory polynucleotide of claim 2, wherein the passenger strand is located between the 5’ flanking region and the loop region and the guide strand is located between the loop region and the 3’ flanking region.

4. The modulatory polynucleotide of claim 2, wherein the guide strand is located between the 5’ flanking region and the loop region and the passenger strand is located between the loop region and the 3’ flanking region.

5. The modulatory polynucleotide of any one of claims 2-5, wherein the guide strand, the passenger strand, or both the guide strand and the passenger strand are between 15-30 or 21-25 nucleotides in length.

6. The modulatory polynucleotide of any one of claims 2-5, wherein the guide strand and the passenger strand are each 21 nucleotides in length.

7. The modulatory polynucleotide of any one of claims 2-6, wherein:

(i) the passenger strand is at least 70% complementary to the guide strand; and/or

(ii) the guide strand is at least 60% complementary to a target RNA, wherein said target RNA is expressed in a neurologic cell, tissue or organ.

8. The modulatory polynucleotide of any one of claims 1-7, wherein the modulatory polynucleotide targets the expression of a SOD1 gene.

9. The modulatory polynucleotide of any one of claims 1-8, wherein the modulatory polynucleotide targets the expression of an HTT gene.

10. A viral genome which comprises a nucleic acid sequence positioned between two inverted terminal repeats (ITRs), wherein the nucleic acid sequence encodes the modulatory polynucleotide of any one of claims 1-9.

11. The viral genome of claim 10, which further comprises one, two, three, or all of:

(i) a promoter operably linked to the nucleotide sequence encoding the modulatory polynucleotide;

(ii) an enhancer;

(iii) an intron region; and

(iv) a poly A signal region.

12. The viral genome of claim 11, wherein:

(i) the promoter is a CBA promoter, an H1 promoter, a PGK promoter, a synapsin promoter, a GFAP promoter, or an EF-1α promoter;

(ii) the enhancer is a CMV enhancer; or

(iii) the intron is an SV40 intron.

13. The viral genome of any one of claims 10-12, wherein the viral genome is single stranded or self-complementary.

14. A recombinant adeno-associated virus (rAAV) comprising the viral genome of any one of claims 10-13, and an AAV capsid protein.

15. The rAAV of claim 14, comprising an AAV1 capsid protein or variant thereof, an AAV5 capsid protein or variant thereof, an AAVrh10 capsid protein or a variant thereof, or AAV9 capsid protein or a variant thereof.

16. A vector encoding the modulatory polynucleotide of any of claims 1-9 or comprising the viral genome of any one of claims 10-13.

17. A cell comprising the modulatory polynucleotide of any one of claims 1-9, the viral genome of any one of claims 10-13, the rAAV of claim 14 or 25, or the vector of claim 16.

18. The cell of claim 17, which is a mammalian cell, an HEK293 cell, an insect cell, an Sf9 cell, a cell of the central nervous system, a neuron, medium spiny neuron, a motor neuron, or an astrocyte.

19. A pharmaceutical composition comprising the modulatory polynucleotide of any one of claims 1-9, the viral genome of any one of claims 10-13, or the rAAV of claim 14 or 15, and a pharmaceutically acceptable excipient.

20. A composition comprising the modulatory polynucleotide of any one of claims 1-9, the viral genome of any one of claims 10-13, the rAAV of claim 14 or 15, or the pharmaceutical composition of claim 19, for use in treating a disease of the central nervous system.

21. A method of treating a disease of the central nervous system in a subject, the method comprising administering an effective amount of a composition comprising the modulatory polynucleotide of any one of claims 1-9, the viral genome of any one of claims 10-13, the rAAV of claim 14 or 15, or the pharmaceutical composition of claim 19 to the subject, thereby treating the disease of the central nervous system in the subject.

22. The composition for use of claim 20, or the method of claim 21, wherein the disease of the central nervous system is ALS.

23. The composition for use of any one of claims 20-22, or the method of any one of claims 21-22, where the composition is administered via intravenous administration or via intracisternal administration.

24. A method of producing a recombinant AAV, comprising providing a cell with a polynucleotide comprising the viral genome of any one of claims 10-13, at least one polynucleotide encoding AAV rep genes, and at least one polynucleotide encoding AAV cap genes; and harvesting the recombinant AAV from the cell.

25. Use of the modulatory polynucleotide of any one of claims 1-9, the viral genome of any one of claims 10-13, the rAAV of claim 14 or 15, or the pharmaceutical composition of claim 19, in the manufacture of a medicament for treating a disease of the central nervous system in a subject.

26. Use of the modulatory polynucleotide of any one of claims 1-9, the viral genome of any one of claims 10-13, the rAAV of claim 14 or 15, or the pharmaceutical composition of claim 19, in the manufacture of a medicament for treating a disease of the central nervous system in a subject.

FIG. 1

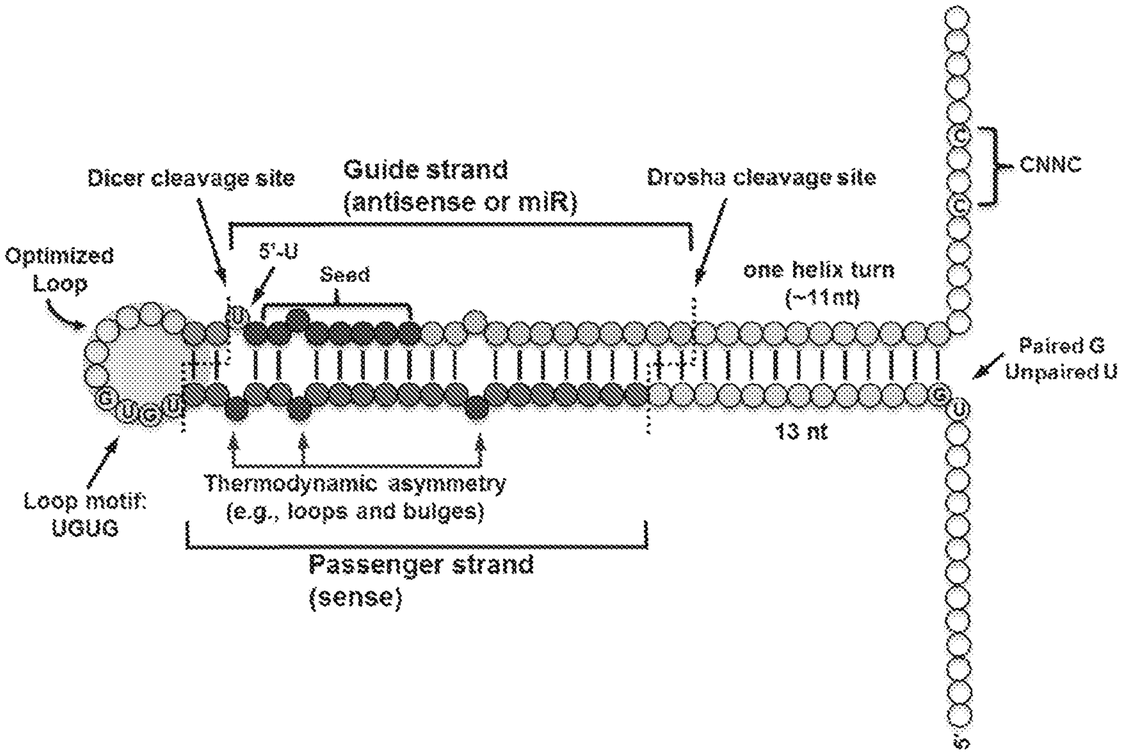
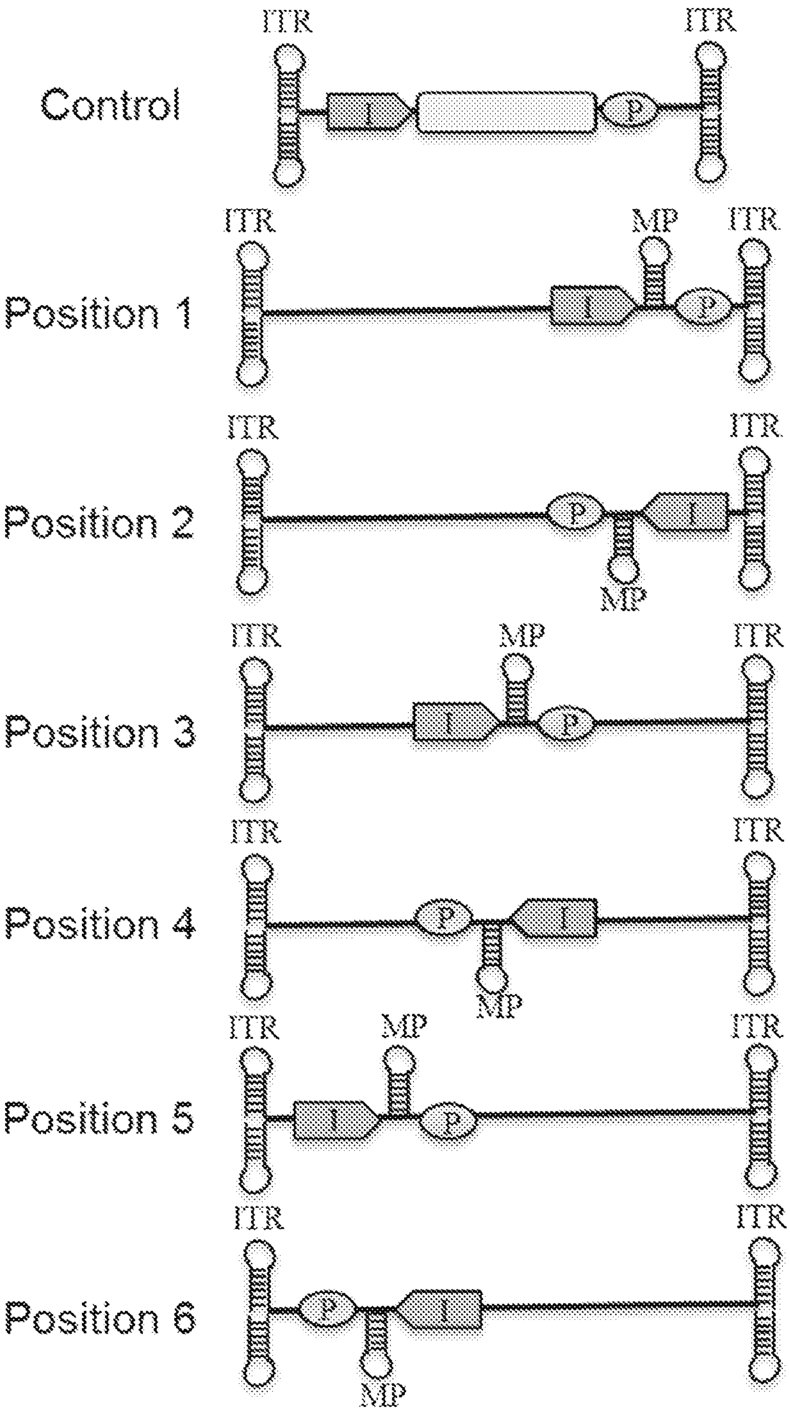

Dicer cleavage site
Guide strand
(antisense or miR)
Drosha cleavage site
Optimized
Loop
5'-U
Seed
one helix turn
(~11nt)
CNNC
C
C
U
Paired G
Unpaired U
G
U
G
U
G
U
13 nt
Loop motif:
UGUG
Thermodynamic asymmetry
(e.g., loops and bulges)
Passenger strand
(sense)
5'

FIG. 2


ITR
ITR
Control
I
P
ITR
MP
ITR
Position 1
I
P
ITR
ITR
Position 2
P
I
MP
ITR
MP
ITR
Position 3
I
P
ITR
ITR
Position 4
P
I
MP
ITR
MP
ITR
Position 5
I
P
ITR
ITR
Position 6
P
I
MP

SEQUENCE LISTING

<110> VOYAGER THERAPEUTICS, INC.

<120> MODULATORY POLYNUCLEOTIDES

<130> 2057.1039PCT

<140> PCT/US2017/XXXXXX
<141> 2017-05-18

<150> 62/485,050
<151> 2017-04-13

<150> 62/338,137
<151> 2016-05-18

<160> 943

<170> PatentIn version 3.5

<210> 1
<211> 50
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 1
uuuaugccuc auccucugag ugcugaaggc uugcuguagg cuguaugcug   50

<210> 2
<211> 54
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 2
gugcugggcg gggggcggcg ggcccucccg cagaacacca ugcgcucuuc ggaa   54

<210> 3
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 3
gaagcaaaga aggggcagag ggagcccgug agcugagugg gccagggacu gggagaagga   60

gugaggaggc agggccggca ugccucugcu gcuggccaga   100

<210> 4
<211> 54
<212> RNA
<213> Artificial Sequence

<220>

```
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 4
gugcugggcg gggggcggcg ggcccucccg cagaacacca ugcgcucuuc ggga             54


<210> 5
<211> 54
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 5
gugcugggcg gggggcggcg ggcccucccg cagaacacca ugcgcuccac ggaa             54


<210> 6
<211> 35
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 6
gggcccuccc gcagaacacc augcgcucca cggaa                                  35


<210> 7
<211> 30
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 7
cuccegcaga acaccaugcg cuccacggaa                                        30


<210> 8
<211> 55
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 8
gugcugggcg gggggcggcg ggcccucccg cagaacacca ugcgcuccac ggaag            55


<210> 9
<211> 54
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide
```

```
<400> 9
gugcugggcg gggggcggcg ggcccucccg cagaacacca ugcgcuccuc ggaa             54


<210> 10
<211> 10
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 10
ugugaccugg                                                              10


<210> 11
<211> 10
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 11
ugugauuugg                                                              10


<210> 12
<211> 10
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 12
uauaauuugg                                                              10


<210> 13
<211> 11
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 13
ccugacccag u                                                            11


<210> 14
<211> 18
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 14
gucugcaccu gucacuag                                                     18
```

```
<210> 15
<211> 10
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 15
gugacccaag                                                            10


<210> 16
<211> 15
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 16
guggccacug agaag                                                      15


<210> 17
<211> 10
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 17
gugacccaau                                                            10


<210> 18
<211> 10
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 18
gugacccaac                                                            10


<210> 19
<211> 15
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 19
guggccacug agaaa                                                      15


<210> 20
<211> 50
```

<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 20
aguguaugau gccuguuacu agcauucaca uggaacaaau ugcugccgug   50

<210> 21
<211> 52
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 21
cugaggagcg ccuugacagc agccauggga gggccgcccc cuaccucagu ga   52

<210> 22
<211> 52
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 22
cuguggagcg ccuugacagc agccauggga gggccgcccc cuaccucagu ga   52

<210> 23
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 23
uggccgugua gugcuaccca gcgcuggcug ccuccucagc auugcaauuc cucucccauc   60

ugggcaccag ucagcuaccc uggugggaau cuggguagcc   100

<210> 24
<211> 99
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 24
ggccguguag ugcuacccag cgcuggcugc cuccucagca uugcaauucc ucucccaucu   60

gggcaccagu cagcuacccu ggugggaauc uggguagcc   99

<210> 25

<211> 54
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 25
uccugaggag cgccuugaca gcagccaugg gagggccgcc cccuaccuca guga 54

<210> 26
<211> 35
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 26
cugaggagcg ccuugacagc agccauggga gggcc 35

<210> 27
<211> 52
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 27
cugcggagcg ccuugacagc agccauggga gggccgcccc cuaccucagu ga 52

<210> 28
<211> 2211
<212> DNA
<213> Adeno-associated virus 1

<400> 28
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

```
accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc      780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg      840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc      900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa      960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg     1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag     1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg     1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct     1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct     1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac     1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac     1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct     1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat     1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct     1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt     1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga     1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc     1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt accttaccc gtcccctgta a               2211


<210> 29
<211> 736
<212> PRT
<213> Adeno-associated virus 1

<400> 29
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590
```

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 30
<211> 4718
<212> DNA
<213> Adeno-associated virus 1

<400> 30
ttgcccactc cctctctgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60

agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcag agagggagtg 120

ggcaactcca tcactagggg taatcgcgaa gcgcctccca cgctgccgcg tcagcgctga 180

cgtaaattac gtcatagggg agtggtcctg tattagctgt cacgtgagtg cttttgcgac 240

attttgcgac accacgtggc catttagggt atatatggcc gagtgagcga gcaggatctc 300

cattttgacc gcgaaatttg aacgagcagc agccatgccg ggcttctacg agatcgtgat 360

caaggtgccg agcgacctgg acgagcacct gccgggcatt tctgactcgt ttgtgagctg 420

ggtggccgag aaggaatggg agctgccccc ggattctgac atggatctga atctgattga 480

gcaggcaccc ctgaccgtgg ccgagaagct gcagcgcgac ttcctggtcc aatggcgccg 540

cgtgagtaag gccccggagg ccctcttctt tgttcagttc gagaagggcg agtcctactt 600

ccacctccat attctggtgg agaccacggg ggtcaaatcc atggtgctgg gccgcttcct 660

gagtcagatt agggacaagc tggtgcagac catctaccgc gggatcgagc cgaccctgcc 720

caactggttc gcggtgacca agacgcgtaa tggcgccgga ggggggaaca aggtggtgga 780

```
cgagtgctac atccccaact acctcctgcc caagactcag cccgagctgc agtgggcgtg      840
gactaacatg gaggagtata taagcgcctg tttgaacctg gccgagcgca aacggctcgt      900
ggcgcagcac ctgacccacg tcagccagac ccaggagcag aacaaggaga atctgaaccc      960
caattctgac gcgcctgtca tccggtcaaa aacctccgcg cgctacatgg agctggtcgg     1020
gtggctggtg gaccggggca tcacctccga gaagcagtgg atccaggagg accaggcctc     1080
gtacatctcc ttcaacgccg cttccaactc gcggtcccag atcaaggccg ctctggacaa     1140
tgccggcaag atcatggcgc tgaccaaatc cgcgcccgac tacctggtag gccccgctcc     1200
gcccgcggac attaaaacca accgcatcta ccgcatcctg gagctgaacg gctacgaacc     1260
tgcctacgcc ggctccgtct ttctcggctg ggcccagaaa aggttcggga agcgcaacac     1320
catctggctg tttgggccgg ccaccacggg caagaccaac atcgcggaag ccatcgccca     1380
cgccgtgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaatgattg     1440
cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc     1500
cgccaaggcc attctcggcg gcagcaaggt gcgcgtggac caaaagtgca agtcgtccgc     1560
ccagatcgac cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga     1620
cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga     1680
actcacccgc cgtctggagc atgactttgg caaggtgaca aagcaggaag tcaaagagtt     1740
cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttctacg tcagaaaggg     1800
tggagccaac aaaagacccg cccccgatga cgcggataaa agcgagccca agcgggcctg     1860
cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga     1920
caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa     1980
gacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga cgagagactg     2040
ttcagagtgc ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg     2100
gaaactctgt gccattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg     2160
cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag     2220
gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc     2280
gcgagtggtg ggacttgaaa cctggagccc cgaagcccaa agccaaccag caaaagcagg     2340
acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg     2400
acaaggggga gcccgtcaac gcggcggacg cagcggccct cgagcacgac aaggcctacg     2460
accagcagct caaagcgggt gacaatccgt acctgcggta taaccacgcc gacgccgagt     2520
ttcaggagcg tctgcaagaa gatacgtctt ttgggggcaa cctcgggcga gcagtcttcc     2580
aggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc     2640
ctggaaagaa acgtccggta gagcagtcgc cacaagagcc agactcctcc tcgggcatcg     2700
gcaagacagg ccagcagccc gctaaaaaga gactcaattt tggtcagact ggcgactcag     2760
agtcagtccc cgatccacaa cctctcggag aacctccagc aacccccgct gctgtgggac     2820
```

ctactacaat ggcttcaggc ggtggcgcac caatggcaga caataacgaa ggcgccgacg 2880

gagtgggtaa tgcctcagga aattggcatt gcgattccac atggctgggc gacagagtca 2940

tcaccaccag cacccgcacc tgggccttgc ccacctacaa taaccacctc tacaagcaaa 3000

tctccagtgc ttcaacgggg gccagcaacg acaaccacta cttcggctac agcacccccт 3060

gggggtattt tgatttcaac agattccact gccacttttc accacgtgac tggcagcgac 3120

tcatcaacaa caattgggga ttccggccca agagactcaa cttcaaactc ttcaacatcc 3180

aagtcaagga ggtcacgacg aatgatggcg tcacaaccat cgctaataac cttaccagca 3240

cggttcaagt cttctcggac tcggagtacc agcttccgta cgtcctcggc tctgcgcacc 3300

agggctgcct ccctccgttc ccggcggacg tgttcatgat tccgcaatac ggctacctga 3360

cgctcaacaa tggcagccaa gccgtgggac gttcatcctt ttactgcctg gaatatttcc 3420

cttctcagat gctgagaacg ggcaacaact ttaccttcag ctacaccttt gaggaagtgc 3480

ctttccacag cagctacgcg cacagccaga gcctggaccg gctgatgaat cctctcatcg 3540

accaatacct gtattacctg aacagaactc aaaatcagtc cggaagtgcc caaaacaagg 3600

acttgctgtt tagccgtggg tctccagctg gcatgtctgt tcagcccaaa aactggctac 3660

ctggaccctg ttatcggcag cagcgcgttt ctaaaacaaa aacagacaac aacaacagca 3720

attttacctg gactggtgct tcaaaatata acctcaatgg gcgtgaatcc atcatcaacc 3780

ctggcactgc tatggcctca cacaaagacg acgaagacaa gttctttccc atgagcggtg 3840

tcatgatttt tggaaaagag agcgccggag cttcaaacac tgcattggac aatgtcatga 3900

ttacagacga agaggaaatt aaagccacta accctgtggc caccgaaaga tttgggaccg 3960

tggcagtcaa tttccagagc agcagcacag accctgcgac cggagatgtg catgctatgg 4020

gagcattacc tggcatggtg tggcaagata gagacgtgta cctgcagggt cccatttggg 4080

ccaaaattcc tcacacagat ggacactttc acccgtctcc tcttatgggc ggctttggac 4140

tcaagaaccc gcctcctcag atcctcatca aaaacacgcc tgttcctgcg aatcctccgg 4200

cggagttttc agctacaaag tttgcttcat tcatcaccca atactccaca ggacaagtga 4260

gtgtggaaat tgaatgggag ctgcagaaag aaaacagcaa gcgctggaat cccgaagtgc 4320

agtacacatc caattatgca aaatctgcca acgttgattt tactgtggac aacaatggac 4380

tttatactga gcctcgcccc attggcaccc gttaccttac ccgtcccctg taattacgtg 4440

ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctcctgtc cttcttatct 4500

tatcggttac catggttata gcttacacat taactgcttg gttgcgcttc gcgataaaag 4560

acttacgtca tcgggttacc cctagtgatg gagttgccca ctccctctct gcgcgctcgc 4620

tcgctcggtg gggcctgcgg accaaaggtc cgcagacggc agagctctgc tctgccggcc 4680

ccaccgagcg agcgagcgcg cagagaggga gtgggcaa 4718

<210> 31
<211> 3131

<212> DNA
<213> Adeno-associated virus

<400> 31
gcggccgcga attcgccctt ggctgcgtca actggaccaa tgagaacttt cccttcaatg 60

attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc aaggtcgtgg 120

agtccgccaa ggccattctc ggcggcagca aggtgcgcgt ggaccaaaag tgcaagtcgt 180

ccgcccagat cgaccccacc cccgtgatcg tcacctccaa caccaacatg tgcgccgtga 240

ttgacgggaa cagcaccacc ttcgagcacc agcagcctct ccaggaccgg atgtttaagt 300

tcgaactcac ccgccgtctg gagcacgact ttggcaaggt gacaaagcag gaagtcaaag 360

agttcttccg ctgggccagt gatcacgtga ccgaggtggc gcatgagttt tacgtcagaa 420

agggcggagc cagcaaaaga cccgcccccg atgacgcgga taaaagcgag cccaagcggg 480

cctgcccctc agtcgcggat ccatcgacgt cagacgcgga aggagctccg gtggactttg 540

ccgacaggta ccaaaacaaa tgttctcgtc acgcgggcat gcttcagatg ctgtttccct 600

gcaaaacgtg cgagagaatg aatcggaatt tcaacatttg cttcacacac ggggtcagag 660

actgctcaga gtgtttcccc ggcgtgtcag aatctcaacc ggtcgtcaga aagaggacgt 720

atcggaaact ccgtgcgatt catcatctgc tggggcgggc tcccgagatt gcttgctcgg 780

cctgcgatct ggtcaacgtg gacctggatg actgtgtttc tgagcaataa atgacttaaa 840

ccaggtatgg ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc 900

attcgcgagt ggtgggcgct gaaacctgga gccccgaagc ccaaagccaa ccagcaaaag 960

caggacgacg gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga 1020

ctcgacaagg gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggct 1080

tacgaccagc agctgcaggc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc 1140

gagtttcagg agcgtctgca agaagatacg tcttttgggg gcaacctcgg gcgagcagtc 1200

ttccaggcca agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg 1260

gctcctggaa agaagagacc ggtagagcca tcaccccagc gttctccaga ctcctctacg 1320

ggcatcggca agaaaggcca acagcccgcc agaaaaagac tcaattttgg tcagactggc 1380

gactcagagt cagttccaga ccctcaacct ctcggagaac ctccagcagc gccctctggt 1440

gtgggaccta atacaatggc tgcaggcggt ggcgcaccaa tggcagacaa taacgaaggc 1500

gccgacggag tgggtagttc ctcgggaaat tggcattgcg attccacatg gctgggcgac 1560

agagtcatca ccaccagcac ccgaacctgg gccctgccca cctacaacaa ccacctctac 1620

aagcaaatct ccaacgggac atcgggagga gccaccaacg acaacaccta cttcggctac 1680

agcacccccct gggggtattt tgactttaac agattccact gccacctttc accacgtgac 1740

tggcagcgac tcatcaacaa caactgggga ttccgaccca agagactcag cttcaagctc 1800

ttcaacatcc aggtcaagga ggtcacgcag aatgaaggca ccaagaccat cgccaataac 1860

ctcaccagca ccatccaggt gtttacggac tcggagtacc agctgccgta cgttctcggc 1920 tctgtccacc agggctgcct gcctccgttc ccggcggacg tgttcatgat tccccagtac 1980

ggctacctaa cactcaacaa cggtagtcag gccgtgggac gctcctcctt ctactgcctg 2040

gaatactttc cttcgcagat gctgagaacc ggcaacaact tccagtttac ttacaccttc 2100

gaggacgtgc ctttccacag cagctacgcc cacagctaga gcttggaccg gctgatgaat 2160

cctctgattg accagtacct gtactacttg tctcggactc aaacaacagg aggcacggca 2220

aatacgcaga ctctgggctt cagccaaggt gggcctaata caatggccaa tcaggcaaag 2280

aactggctgc caggaccctg ttaccgccaa caacgcgtct caacgacaac cgggcaaaac 2340

aacaatagca actttgcctg gactgctggg accaaatacc atctgaatgg aagaaattca 2400

ttggctaatc ctggcatcgc tatggcaaca cacaaagacg acgaggagcg ttttttttccc 2460

agtaacggga tcctgatttt tggcaaacaa aatgctgcca gagacaatgc ggattacagc 2520

gatgtcatgc tcaccagcga ggaagaaatc aaaaccacta accctgtggc tacagaggaa 2580

tacggtatcg tggcagataa cttgcagcag caaaacacgg ctcctcaaat tggaactgtc 2640

aacagccagg gggccttacc cggtatggtc tggcagaacc gggacgtgta cctgcagggt 2700

cccatctggg ccaagattcc tcacacggac ggcaacttcc acccgtctcc gctgatgggc 2760

ggctttggcc tgaaacatcc tccgcctcag atcctgatca agaacacgcc tgtacctgcg 2820

gatcctccga ccaccttcaa ccagtcaaag ctgaactctt tcatcacgca atacagcacc 2880

ggacaggtca gcgtggaaat tgaatgggag ctgcagaagg aaaacagcaa gcgctggaac 2940

cccgagatcc agtacacctc caactactac aaatctataa gtgtggactt tgctgttaat 3000

acagaaggcg tgtactctga accccgcccc attggcaccc gttacctcac ccgtaatctg 3060

taattgcctg ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga 3120

agggcgaatt c 3131

<210> 32
<211> 255
<212> DNA
<213> Adeno-associated virus 10

<400> 32
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 60

accagcaccc gaacctgggt cctgcccacc tacaacaacc acatctacaa gcaaatctcc 120

agcgagacag gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 180

tttgacttta acagattcca ctgccacttt tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattc 255

<210> 33
<211> 738
<212> PRT
<213> Adeno-associated virus 10

<400> 33
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Glu Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly
            580                 585                 590


Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 34
<211> 738
<212> PRT
<213> Adeno-associated virus 10

<400> 34
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590
```

```
Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

```
<210> 35
<211> 258
<212> DNA
<213> Adeno-associated virus 11

<400> 35
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc       60

accagcaccc gaacctgggc cctgccaacc tacaacaacc acctctacaa acaaatctcc      120

agcgcttcaa cgggggccag caacgacaac cactactttg gctacagcac cccctggggg      180

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc      240

aacaacaact ggggattc                                                    258


<210> 36
<211> 255
<212> DNA
<213> Adeno-associated virus 12

<400> 36
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgaccg agtcattacc       60

accagcaccc ggacttgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc      120

agccaatcgg gtgccaccaa cgacaaccac tacttcggct acagcacccc ttgggggtat      180
```

tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattc 255

<210> 37
<211> 2208
<212> DNA
<213> Adeno-associated virus 2

<400> 37
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

```
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa     1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 38
<211> 735
<212> PRT
<213> Adeno-associated virus 2

<400> 38
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

```
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 39
<211> 621
<212> PRT
<213> Adeno-associated virus 2

<400> 39
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1   5   10   15

Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20   25   30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35   40   45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50   55   60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65   70   75   80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85   90   95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100   105   110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115   120   125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130   135   140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145   150   155   160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165   170   175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180   185   190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195   200   205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210   215   220

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

```
225                 230                 235                 240


Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255


Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270


Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275                 280                 285


Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300


Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320


Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335


Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340                 345                 350


Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365


Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380


Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400


Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415


Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430


Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445


Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460


Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                 470                 475                 480


Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495


Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
```

```
            500                 505                 510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515                 520                 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545                 550                 555                 560

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565                 570                 575

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580                 585                 590

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
        595                 600                 605

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610                 615                 620
```

```
<210> 40
<211> 4675
<212> DNA
<213> Adeno-associated virus 2

<400> 40
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc       60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg      120

gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag      180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat      240

gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga      300

ggtttgaacg cgcagccgcc atgccggggt tttacgagat tgtgattaag gtccccagcg      360

accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg      420

aatgggagtt gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga      480

ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc      540

cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc      600

tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg      660

aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg      720

tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc      780

ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac      840

agtatttaag cgcctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga      900

cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc      960
```

cggtgatcag atcaaaaact tcagccaggt acatggagct ggtcgggtgg ctcgtggaca 1020

aggggattac ctcggagaag cagtggatcc aggaggacca ggcctcatac atctccttca 1080

atgcggcctc caactcgcgg tcccaaatca aggctgcctt ggacaatgcg ggaaagatta 1140

tgagcctgac taaaaccgcc cccgactacc tggtgggcca gcagcccgtg gaggacattt 1200

ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt 1260

ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg 1320

ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct 1380

acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg 1440

tgatctggtg ggaggagggg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc 1500

tcggaggaag caaggtgcgc gtggaccaga aatgcaagtc ctcggcccag atagacccga 1560

ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga 1620

ccttcgaaca ccagcagccg ttgcaagacc ggatgttcaa atttgaactc acccgccgtc 1680

tggatcatga ctttgggaag gtcaccaagc aggaagtcaa agactttttc cggtgggcaa 1740

aggatcacgt ggttgaggtg gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa 1800

gacccgcccc cagtgacgca gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc 1860

agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat 1920

gttctcgtca cgtgggcatg aatctgatgc tgtttccctg cagacaatgc gagagaatga 1980

atcagaattc aaatatctgc ttcactcacg gacagaaaga ctgtttagag tgctttcccg 2040

tgtcagaatc tcaacccgtt tctgtcgtca aaaaggcgta tcagaaactg tgctacattc 2100

atcatatcat gggaaaggtg ccagacgctt gcactgcctg cgatctggtc aatgtggatt 2160

tggatgactg catctttgaa caataaatga tttaaatcag gtatggctgc cgatggttat 2220

cttccagatt ggctcgagga cactctctct gaaggaataa gacagtggtg gaagctcaaa 2280

cctggcccac caccaccaaa gcccgcagag cggcataagg acgacagcag gggtcttgtg 2340

cttcctgggt acaagtacct cggacccttc aacggactcg acaagggaga gccggtcaac 2400

gaggcagacg ccgcggccct cgagcacgta caaagcctac gaccggcagc tcgacagcgg 2460

agacaacccg tacctcaagt acaaccacgc cgacgcggag tttcaggagc gccttaaaga 2520

agatacgtct tttgggggca acctcggacg agcagtcttc caggcgaaaa agagggttct 2580

tgaacctctg ggcctggttg aggaacctgt taagacggct ccgggaaaaa agaggccggt 2640

agagcactct cctgtggagc cagactcctc ctcgggaacc ggaaaggcgg gccagcagcc 2700

tgcaagaaaa agattgaatt ttggtcagac tggagacgca gactcagtac ctgaccccca 2760

gcctctcgga cagccaccag cagccccctc tggtctggga actaatacga tggctacagg 2820

cagtggcgca ccaatggcag acaataacga gggcgccgac ggagtgggta attcctccgg 2880

aaattggcat tgcgattcca catggatggg cgacagagtc atcaccacca gcacccgaac 2940

ctgggccctg cccacctaca acaaccacct ctacaaacaa atttccagcc aatcaggagc 3000 ctcgaacgac aatcactact ttggctacag cacccccttgg gggtattttg acttcaacag 3060

attccactgc cacttttcac cacgtgactg gcaaagactc atcaacaaca actggggatt 3120

ccgacccaag agactcaact tcaagctctt taacattcaa gtcaaagagg tcacgcagaa 3180

tgacggtacg acgacgattg ccaataacct taccagcacg gttcaggtgt ttactgactc 3240

ggagtaccag ctcccgtacg tcctcggctc ggcgcatcaa ggatgcctcc cgccgttccc 3300

agcagacgtc ttcatggtgc cacagtatgg atacctcacc ctgaacaacg ggagtcaggc 3360

agtaggacgc tcttcatttt actgcctgga gtactttcct tctcagatgc tgcgtaccgg 3420

aaacaacttt accttcagct acacttttga ggacgttcct ttccacagca gctacgctca 3480

cagccagagt ctggaccgtc tcatgaatcc tctcatcgac cagtacctgt attacttgag 3540

cagaacaaac actccaagtg gaaccaccac gcagtcaagg cttcagtttt ctcaggccgg 3600

agcgagtgac attcgggacc agtctaggaa ctggcttcct ggaccctgtt accgccagca 3660

gcgagtatca aagacatctg cggataacaa caacagtgaa tactcgtgga ctggagctac 3720

caagtaccac ctcaatggca gagactctct ggtgaatccg gccatggcaa gccacaagga 3780

cgatgaagaa aagtttttc ctcagagcgg ggttctcatc tttgggaagc aaggctcaga 3840

gaaaacaaat gtgaacattg aaaaggtcat gattacagac gaagaggaaa tcggaacaac 3900

caatcccgtg gctacggagc agtatggttc tgtatctacc aacctccaga gaggcaacag 3960

acaagcagct accgcagatg tcaacacaca aggcgttctt ccaggcatgg tctggcagga 4020

cagagatgtg taccttcagg ggcccatctg ggcaaagatt ccacacacgg acggacattt 4080

tcacccctct cccctcatgg gtggattcgg acttaaacac cctcctccac agattctcat 4140

caagaacacc ccggtacctg cgaatccttc gaccaccttc agtgcggcaa agtttgcttc 4200

cttcatcaca cagtactcca cgggacacgg tcagcgtgga gatcgagtgg gagctgcaga 4260

aggaaaacag caaacgctgg aatcccgaaa ttcagtacac ttccaactac aacaagtctg 4320

ttaatcgtgg acttaccgtg gatactaatg gcgtgtattc agagcctcgc cccattggca 4380

ccagatacct gactcgtaat ctgtaattgc ttgttaatca ataaaccgtt taattcgttt 4440

cagttgaact ttggtctctg cgtatttctt tcttatctag tttccatggc tacgtagata 4500

agtagcatgg cgggttaatc attaactaca aggaacccct agtgatggag ttggccactc 4560

cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc cgacgcccgg 4620

gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg gccaa 4675

<210> 41
<211> 4679
<212> DNA
<213> Adeno-associated virus 2

<400> 41
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

```
gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag      180
ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat      240
gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga      300
ggtttgaacg cgcagccgcc atgccggggt tttacgagat tgtgattaag gtccccagcg      360
accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg      420
aatgggagtt gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga      480
ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc      540
cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc      600
tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg      660
aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg      720
tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc      780
ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac      840
agtatttaag cgcctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga      900
cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc      960
cggtgatcag atcaaaaact tcagccaggt acatggagct ggtcgggtgg ctcgtggaca     1020
aggggattac ctcggagaag cagtggatcc aggaggacca ggcctcatac atctccttca     1080
atgcggcctc caactcgcgg tcccaaatca aggctgcctt ggacaatgcg ggaaagatta     1140
tgagcctgac taaaaccgcc cccgactacc tggtgggcca gcagcccgtg gaggacattt     1200
ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt     1260
ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg     1320
ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct     1380
acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg     1440
tgatctggtg ggaggagggg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc     1500
tcggaggaag caaggtgcgc gtggaccaga aatgcaagtc ctcggcccag atagacccga     1560
ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga     1620
ccttcgaaca ccagcagccg ttgcaagacc ggatgttcaa atttgaactc acccgccgtc     1680
tggatcatga ctttgggaag gtcaccaagc aggaagtcaa agactttttc cggtgggcaa     1740
aggatcacgt ggttgaggtg gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa     1800
gacccgcccc cagtgacgca gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc     1860
agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat     1920
gttctcgtca cgtgggcatg aatctgatgc tgtttccctg cagacaatgc gagagaatga     1980
atcagaattc aaatatctgc ttcactcacg gacagaaaga ctgtttagag tgctttcccg     2040
tgtcagaatc tcaacccgtt tctgtcgtca aaaaggcgta tcagaaactg tgctacattc     2100
atcatatcat gggaaaggtg ccagacgctt gcactgcctg cgatctggtc aatgtggatt     2160
```

```
tggatgactg catctttgaa caataaatga tttaaatcag gtatggctgc cgatggttat     2220
cttccagatt ggctcgagga cactctctct gaaggaataa gacagtggtg gaagctcaaa     2280
cctggcccac caccaccaaa gcccgcagag cggcataagg acgacagcag gggtcttgtg     2340
cttcctgggt acaagtacct cggacccttc aacggactcg acaagggaga gccggtcaac     2400
gaggcagacg ccgcggccct cgagcacgac aaagcctacg accggcagct cgacagcgga     2460
gacaacccgt acctcaagta caaccacgcc gacgcggagt ttcaggagcg ccttaaagaa     2520
gatacgtctt ttgggggcaa cctcggacga gcagtcttcc aggcgaaaaa gagggttctt     2580
gaacctctgg gcctggttga ggaacctgtt aagacggctc cgggaaaaaa gaggccggta     2640
gagcactctc ctgtggagcc agactcctcc tcgggaaccg gaaaggcggg ccagcagcct     2700
gcaagaaaaa gattgaattt tggtcagact ggagacgcag actcagtacc tgacccccag     2760
cctctcggac agccaccagc agccccctct ggtctgggaa ctaatacgat ggctacaggc     2820
agtggcgcac caatggcaga caataacgag ggcgccgacg gagtgggtaa ttcctccgga     2880
aattggcatt gcgattccac atggatgggc gacagagtca tcaccaccag cacccgaacc     2940
tgggccctgc ccacctacaa caaccacctc tacaaacaaa tttccagcca atcaggagcc     3000
tcgaacgaca atcactactt tggctacagc accccttggg ggtattttga cttcaacaga     3060
ttccactgcc acttttcacc acgtgactgg caaagactca tcaacaacaa ctggggattc     3120
cgacccaaga gactcaactt caagctcttt aacattcaag tcaaagaggt cacgcagaat     3180
gacggtacga cgacgattgc caataacctt accagcacgg ttcaggtgtt tactgactcg     3240
gagtaccagc tcccgtacgt cctcggctcg gcgcatcaag gatgcctccc gccgttccca     3300
gcagacgtct tcatggtgcc acagtatgga tacctcaccc tgaacaacgg gagtcaggca     3360
gtaggacgct cttcatttta ctgcctggag tactttcctt ctcagatgct gcgtaccgga     3420
aacaacttta ccttcagcta cacttttgag gacgttcctt tccacagcag ctacgctcac     3480
agccagagtc tggaccgtct catgaatcct ctcatcgacc agtacctgta ttacttgagc     3540
agaacaaaca ctccaagtgg aaccaccacg cagtcaaggc ttcagttttc tcaggccgga     3600
gcgagtgaca ttcgggacca gtctaggaac tggcttcctg gaccctgtta ccgccagcag     3660
cgagtatcaa agacatctgc ggataacaac aacagtgaat actcgtggac tggagctacc     3720
aagtaccacc tcaatggcag agactctctg gtgaatccgg gcccggccat ggcaagccac     3780
aaggacgatg aagaaaagtt ttttcctcag agcggggttc tcatctttgg gaagcaaggc     3840
tcagagaaaa caaatgtgga cattgaaaag gtcatgatta cagacgaaga ggaaatcagg     3900
acaaccaatc ccgtggctac ggagcagtat ggttctgtat ctaccaacct ccagagaggc     3960
aacagacaag cagctaccgc agatgtcaac acacaaggcg ttcttccagg catggtctgg     4020
caggacagag atgtgtacct tcaggggccc atctgggcaa agattccaca cacggacgga     4080
cattttcacc cctctcccct catgggtgga ttcggactta aacaccctcc tccacagatt     4140
ctcatcaaga acaccccggt acctgcgaat ccttcgacca ccttcagtgc ggcaaagttt     4200
```

```
gcttccttca tcacacagta ctccacggga caggtcagcg tggagatcga gtgggagctg     4260

cagaaggaaa acagcaaacg ctggaatccc gaaattcagt acacttccaa ctacaacaag     4320

tctgttaatg tggactttac tgtggacact aatggcgtgt attcagagcc tcgccccatt     4380

ggcaccagat acctgactcg taatctgtaa ttgcttgtta atcaataaac cgtttaattc     4440

gtttcagttg aactttggtc tctgcgtatt tctttcttat ctagtttcca tggctacgta     4500

gataagtagc atggcgggtt aatcattaac tacaaggaac ccctagtgat ggagttggcc     4560

actccctctc tgcgcgctcg ctcgctcact gaggccgggc gaccaaaggt cgcccgacgc     4620

ccgggctttg cccgggcggc ctcagtgagc gagcgagcgc gcagagaggg agtggccaa      4679


<210> 42
<211> 725
<212> PRT
<213> Adeno-associated virus 5

<400> 42
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg
    130                 135                 140


Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145                 150                 155                 160


Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
                165                 170                 175


Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
```

```
            180                 185                 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
        195                 200                 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
    210                 215                 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225                 230                 235                 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
                245                 250                 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305                 310                 315                 320

Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
                325                 330                 335

Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
            340                 345                 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
        355                 360                 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
    370                 375                 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
                405                 410                 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
            420                 425                 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
        435                 440                 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
```

```
    450                 455                 460


Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465                 470                 475                 480


Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
                485                 490                 495


Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
            500                 505                 510


Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
        515                 520                 525


Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
    530                 535                 540


Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545                 550                 555                 560


Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
                565                 570                 575


Ser Thr Thr Ala Pro Thr Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val
            580                 585                 590


Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
        595                 600                 605


Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
    610                 615                 620


Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625                 630                 635                 640


Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
                645                 650                 655


Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
            660                 665                 670


Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
        675                 680                 685


Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro
    690                 695                 700


Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr
705                 710                 715                 720


Leu Thr Arg Pro Leu
```

725

<210> 43
<211> 644
<212> PRT
<213> Adeno-associated virus

<220>
<221> MOD_RES
<222> (434)..(434)
<223> Any amino acid

<400> 43
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1   5   10   15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20   25   30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35   40   45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50   55   60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65   70   75   80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85   90   95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100   105   110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115   120   125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130   135   140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145   150   155   160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165   170   175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180   185   190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195   200   205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn

```
    210                 215                 220


Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300


Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335


Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365


Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380


Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400


Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415


Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430


Asn Xaa Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445


Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460


Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480


Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
```

485 490 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 44
<211> 1933
<212> DNA
<213> Adeno-associated virus

<400> 44
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagt gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gttgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg 600 ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttctccc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacgccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 45
<211> 644
<212> PRT
<213> Adeno-associated virus

<400> 45
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Cys Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

```
Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Val Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Ser Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620


Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640


Tyr Ser Glu Pro



<210> 46
<211> 1933
<212> DNA
<213> Adeno-associated virus

<400> 46
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc        60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg       120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc       180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg       240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga       300

gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc       360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg       420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat       480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat       540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcaccccctg       600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact       660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca       720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac       780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca       840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac       900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc       960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc      1020

tttccacagc agctacgcgc acagccagag tctgggccgg ctgatgaatc ccctcatcga      1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg      1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct      1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag      1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa      1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg      1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat      1440
```

```
gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt     1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg     1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc     1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact     1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga     1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag     1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca     1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt     1920

ttactctgag cct                                                        1933


<210> 47
<211> 644
<212> PRT
<213> Adeno-associated virus

<400> 47
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1               5                   10                  15


Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30


Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45


Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60


Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80


Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95


Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110


Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140


Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145                 150                 155                 160


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220


Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300


Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335


Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
            340                 345                 350


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365


Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380


Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400


Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415


Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430


Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445
```

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450   455   460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465   470   475   480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485   490   495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500   505   510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515   520   525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530   535   540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545   550   555   560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565   570   575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
            580   585   590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595   600   605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610   615   620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625   630   635   640

Tyr Ser Glu Pro

<210> 48
<211> 1933
<212> DNA
<213> Adeno-associated virus

<400> 48
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc   60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg   120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc   180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg   240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga   300 gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcaccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctgggccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 49
<211> 644
<212> PRT
<213> Adeno-associated virus

<400> 49
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

```
Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 50
<211> 1933
<212> DNA
<213> Adeno-associated virus

<400> 50
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aatagcgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcaccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

```
ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct     1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag     1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa     1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg     1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat     1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt     1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg     1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc     1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact     1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga     1740

agtgtttact cctgccaagc ttgcttcctt catcacgcag tacagcaccg ggcaagtcag     1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca     1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt     1920

ttactctgag cct                                                        1933


<210> 51
<211> 644
<212> PRT
<213> Adeno-associated virus

<400> 51
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1               5                   10                  15


Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30


Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45


Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60


Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80


Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110


Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125


Ala Pro Met Ala Asp Asn Ser Glu Gly Ala Asp Gly Val Gly Asn Ala
```

```
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
```

```
                405                 410                 415


Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430


Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445


Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460


Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480


Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495


Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510


Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575


Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Leu Ala Ser Phe Ile Thr
            580                 585                 590


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620


Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640


Tyr Ser Glu Pro


<210> 52
<211> 1933
<212> DNA
<213> Adeno-associated virus
```

<400> 52
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcaccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggacc cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaaga ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

```
<210> 53
<211> 644
<212> PRT
<213> Adeno-associated virus

<400> 53
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1               5                   10                  15


Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30


Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45


Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60


Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80


Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110


Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175


Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220


Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Pro Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525
```

```
Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575


Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Ile Ala Ser Phe Ile Thr
            580                 585                 590


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620


Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640


Tyr Ser Glu Pro



<210> 54
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 54
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Thr Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala Arg Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Gly Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

```
Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 55
<211> 3121
<212> DNA
<213> Adeno-associated virus

<400> 55

```
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgactg       60

tgtcgacaag atggtgatct ggtgggagga ggggaagatg accgccaagg tcgtggagtc      120

ggccaaagcc attctcggag gaagcaaggt gcgcgtggac cagaaatgca agtcctcggc      180

ccagatagac ccgactcccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga      240

cgggaactca acgaccttcg aacaccagca gccgttgcaa gaccggatgt tcaaatttga      300

actcacccgc cgtctggatc atgactttgg gaaggtcacc aagcaggaag tcaaagactt      360

tttccggtgg gcaaaggatc acgtggttga ggtggagcac gaattctacg tcaaaaaggg      420

tggagccaag aaaagacccg cccccagtga cgcagatata agtgagccca aacgggtgcg      480

cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgatcaact acgcagacag      540

gtaccaaaac aaatgttctc gtcacgcggg catgaatctg atgctgtttc cctgcagaca      600

atgcgagaga atgaatcaga attcaaatat ctgcttcact cacggacaga aagactgttt      660

agagtgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcaaaaagg cgtatcagaa      720

actgtgctac attcatcata tcatgggaaa ggtgccagac gcttgcactg cctgcgatct      780

ggtcgatgtg gatttggatg actgcatctt tgaacaataa atgatttaaa tcaggtatgg      840

ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt      900

ggtgggcgct gaaacctgga gccccgaagc ccaaagccaa ccagcaaaag caggacggcg      960

gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga ctcgacaagg     1020

gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc     1080

agctcaaagc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg     1140
```

agcgtctgca agaagatacg tcttttgggg gcaacctcgg gcgagcagtc ttccaggcca 1200

agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg gctcctggaa 1260

agaagagacc ggtagagcca tcaccccagc gttctccaga ctcctctacg ggcatcggca 1320

agaaaggcca gcagcccgcg aaaaagagac tcaactttgg gcagactggc gactcagagt 1380

cagtgcccga ccctcaacca atcggagaac cccccgcagg cccctctggt ctgggatctg 1440

gtacaatggc tgcaggcggt ggcgctccaa tggcagacaa taacgaaggc gccgacggag 1500

tgggtagttc ctcaggaaat tggcattgcg attccacatg gctgggcgac tgagtcatca 1560

ccaccagcac ccgaacctgg gccctcccca cctacaacaa ccacctctac aagcaaatct 1620

ccaacgggac ttcgggagga agcaccaacg acaacaccta cttcggctac agcacccccct 1680

gggggtattt tgactttaac agattccact gccacttctc accacgtgac tggcagcgac 1740

tcatcaacaa caactgggga ttccggccca agagactcaa cttcaagctc ttcaacatcc 1800

aggtcaagga ggtcacgcag aatgaaggca ccaagaccat cgccaataac cttaccagca 1860

cgattcaggt ctttacggac tcggaatacc agctcccgta cgtcctcggc tctgcgcacc 1920

agggctgcct gcctccgttc ccggcggacg tcttcatgat tcctcagtac gggtacctga 1980

ctctgaacaa tggcagtcag gccgtgggcc gttcctcctt ctactgcctg gagtactttc 2040

cttctcaaat gctgagaacg ggcaacaact ttgagttcag ctaccagttt gaggacgtgc 2100

cttttcacag cagctacgcg cacagccaaa gcctggaccg gctgatgaac cccctcatcg 2160

accagtacct gtactacctg tctcggactc agtccacggg aggtaccgca ggaactcagc 2220

agttgctatt ttctcaggcc gggcctaata acatgtcggc tcaggccaaa aactggctac 2280

ccgggccctg ctaccggcag taacgcgtct ccacgacact gtcgcaaaat aacaacagca 2340

actttgtctg gaccggtgcc accaagtatc atctgaatgg cagagactct ctggtagatc 2400

ccggtgtcgc tatggcaacc cacaaggacg acgaagagcg atttttttccg tccagcggag 2460

tcataatgtt tgggaaacag ggagctggaa aagacaacgt ggactatagc agcgtcatgc 2520

taaccagtga ggaagaaatt aaaaccacca acccagtggc cacagaacag tacggcgtgg 2580

tggccgataa cctgcaacag caaaacgccg ctcctattgt aggggccgtc aacagtcaag 2640

gagccttacc tggcatggtc tggcagaacc gggacgtgta cctgcagggt cctacctggg 2700

ccaagattcc tcacacggac ggaaactttc atccctcgcc gctgatggga ggctttggac 2760

tgaaacaccc gcctcctcag atcctgatta agaatacacc tgttcccgcg gatcctccaa 2820

ctaccttcag tcaagctaag ctggcgtcgt tcatcacgca gtacagcacc ggacaggtca 2880

gcgtggaaat tgaatgggag ctgcaggaag aaaacagcaa acgctggaac ccagagattc 2940

aatacacttc caactactac aaatctacaa atgtggactt tgctgttaac acagatggca 3000

cttattctga gcctcgcccc atcggcaccc gttacctcac ccgtaatctg taattgcttg 3060

ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga agggcgaatt 3120

c 3121

```
<210> 56
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 56
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Gly Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
```

```
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Ser Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asp Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
```

```
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 57
<211> 3121
<212> DNA
<213> Adeno-associated virus

<400> 57
gaattcgccc ttcgcgagac caaagttcaa ctgaaacgaa tcaaccggtt tattgattaa       60

caagcaatta cagattacgg gtgaggtaac gggtgccgat ggggcgaggc tcagaataag      120
```

tgccatctgt gttaacagca aagtccacat ttgtagattt gtagtagttg gaagtgtatt 180

gaatctctgg gttccagcgt ttgctgtttt ctttctgcag ctcccattca atttccacgc 240

tgacctgtcc ggtgctgtac tgcgtgatga acgacgccag cttagcttga ctgaaggtag 300

ttggaggatc cgcgggaaca ggtgtattct taatcaggat ctgaggaggc gggtgtttca 360

gtccaaagcc tcccatcagc ggcgagggat gaaagtttcc gtccgtgtga ggaatcttgg 420

cccagatagg accctgcagg tacacgtccc ggttctgcca gaccatgcca ggtaaggctc 480

cttgactgtt gacggcccct acaataggag cggcgttttg ctgttgcagg ttatcggcca 540

ccacgccgta ctgttctgtg gccactgggt tggtggtttt aatttcttcc tcactggtta 600

gcataacgct gctatagtcc acgttgtctt ttccagctcc ctgtttccca aacattaaga 660

ctccgctgga cggaaaaaat cgctcttcgt cgtccttgtg ggttgccata gcgacaccgg 720

gatttaccag agagtctctg ccattcagat gatacttggt ggcaccggtc caggcaaagt 780

tgctgttgtc attttgcgac agtgtcgtgg agacgcgttg ctgccggtag cagggcccgg 840

gtagccagtt tttggcctga gccgacatgt tattaggccc ggcctgagaa aatagcaact 900

gctgagttcc tgcggtacct cccgtggact gagtccgaga caggtagtac aggtactggt 960

cgatgagggg gttcatcagc cggtccaggc tttggctgtg cgcgtagctg ctgtgaaaag 1020

gcacgtcctc aaactggtag ctgaactcaa agttgttgcc cgttctcagc atttgagaag 1080

gaaagtactc caggcagtag aaggaggaac ggcccacggc ctgactgcca ttgttcagag 1140

tcaggtaccc gtactgagga atcatgaaga cgtccgccgg gaacggaggc aggcagccct 1200

ggtgcgcaga gccgaggacg tacgggagct ggtattccga gtccgtaaag acctgaatcg 1260

tgctggtaag gttattggcg atggtcttgg tgccttcatt ctgcgtgacc tccttgacct 1320

ggatgttgaa gagcttgaag ttgaggctct tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttaaagtca aaataccccc 1440

agggggtgct gtagccgaag taggtgttgt cgttggtgct tcctcccgaa gtcccgttgg 1500

agatttgctt gtagaggtgg ttgttgtagg tggggagggc ccaggttcgg gtgctggtgg 1560

tgatgactcc gtcgcccagc catgtggaat cgcaatgcca atttcctgag gaactaccca 1620

ctccgtcggc gccttcgtta ttgtctgcca ttggagcgcc accgcctgca gccattgtac 1680

cagatcccag accagagggg cctgcggggg gttctccgat tggttgaggg tcgggcactg 1740

actctgagtc gccagtctgc ccaaagttga gtctcttttt cgcgggctgc tggcctttct 1800

tgccgatgcc cgtagaggag tctggagaac gctggggtga tggctctacc ggtctcttct 1860

ttccaggagc cgtcttagcg ccttcctcaa ccagaccgag aggttcgaga acccgcttct 1920

tggcctggaa gactgctcgc ccgaggttgc ccccaaaaga cgtatcttct tgcagacgct 1980

cctgaaactc ggcgtcggcg tggttatacc gcaggtacgg attgtcaccc gctttgagct 2040

gctggtcgta ggccttgtcg tgctcgaggg ccgctgcgtc cgccgcgttg acgggctccc 2100

ccttgtcgag tccgttgaag ggtccgaggt acttgtagcc aggaagcacc agaccccggc 2160 cgtcgtcctg cttttgctgg ttggctttgg gcttcggggc tccaggtttc agcgcccacc 2220

actcgcgaat gccctcagag aggttgtcct cgagccaatc tggaagataa ccatcggcag 2280

ccatacctga tttaaatcat ttattgttca aagatgcagt catccaaatc cacattgacc 2340

agatcgcagg cagtgcaagc gtctggcacc tttcccatga tatgatgaat gtagcacagt 2400

ttctgatacg cctttttgac gacagaaacg ggttgagatt ctgacacggg aaagcactct 2460

aaacagtctt tctgtccgtg agtgaagcag atatttgaat tctgattcat tctctcgcat 2520

tgtctgcagg gaaacagcat cagattcatg cccacgtgac gagaacattt gttttggtac 2580

ctgtctgcgt agttgatcga agcttccgcg tctgacgtcg atggctgcgc aactgactcg 2640

cgcacccgtt tgggctcact tatatctgcg tcactggggg cgggtctttt cttggctcca 2700

cccttttga cgtagaattc atgctccacc tcaaccacgt gatcctttgc ccaccggaaa 2760

aagtctttga cttcctgctt ggtgaccttc ccaaagtcat gatccagacg gcgggtgagt 2820

tcaaatttga acatccggtc ttgcaacggc tgctggtgtt cgaaggtcgt tgagttcccg 2880

tcaatcacgg cgcacatgtt ggtgttggag gtgacgatca cgggagtcgg gtctatctgg 2940

gccgaggact tgcatttctg gtccacgcgc accttgcttc ctccgagaat ggctttggcc 3000

gactccacga ccttggcggt catcttcccc tcctcccacc agatcaccat cttgtcgaca 3060

cagtcgttga agggaaagtt ctcattggtc cagttgacgc agccgtagaa agggcgaatt 3120

c 3121

<210> 58
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 58
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaagg gggctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg agactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780 tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgactg gaactgtcaa tcatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgtg a 2211

<210> 59
<211> 736
<212> PRT
<213> Adeno-associated virus 3

<400> 59
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140


Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
```

```
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445


Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460


Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
```

```
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 60
<211> 4726
<212> DNA
<213> Adeno-associated virus 3

<400> 60
ttggccactc cctctatgcg cactcgctcg ctcggtgggg cctggcgacc aaaggtcgcc       60

agacggacgt gctttgcacg tccggcccca ccgagcgagc gagtgcgcat agagggagtg      120

gccaactcca tcactagagg tatggcagtg acgtaacgcg aagcgcgcga agcgagacca      180

cgcctaccag ctgcgtcagc agtcaggtga cccttttgcg acagtttgcg acaccacgtg      240

gccgctgagg gtatatattc tcgagtgagc gaaccaggag ctccattttg accgcgaaat      300

ttgaacgagc agcagccatg ccggggttct acgagattgt cctgaaggtc ccgagtgacc      360

tggacgagcg cctgccgggc atttctaact cgtttgttaa ctgggtggcc gagaaggaat      420

gggacgtgcc gccggattct gacatggatc cgaatctgat tgagcaggca cccctgaccg      480

tggccgaaaa gcttcagcgc gagttcctgg tggagtggcg ccgcgtgagt aaggccccgg      540

aggccctctt ttttgtccag ttcgaaaagg gggagaccta cttccacctg cacgtgctga      600

ttgagaccat cggggtcaaa tccatggtgg tcggccgcta cgtgagccag attaaagaga      660

agctggtgac ccgcatctac cgcggggtcg agccgcagct tccgaactgg ttcgcggtga      720

ccaaaacgcg aaatggcgcc gggggcggga acaaggtggt ggacgactgc tacatcccca      780

actacctgct ccccaagacc cagcccgagc tccagtgggc gtggactaac atggaccagt      840
```

atttaagcgc ctgtttgaat ctcgcggagc gtaaacggct ggtggcgcag catctgacgc 900

acgtgtcgca gacgcaggag cagaacaaag agaatcagaa ccccaattct gacgcgccgg 960

tcatcaggtc aaaaacctca gccaggtaca tggagctggt cgggtggctg gtggaccgcg 1020

ggatcacgtc agaaaagcaa tggattcagg aggaccaggc ctcgtacatc tccttcaacg 1080

ccgcctccaa ctcgcggtcc cagatcaagg ccgcgctgga caatgcctcc aagatcatga 1140

gcctgacaaa gacggctccg gactacctgg tgggcagcaa cccgccggag gacattacca 1200

aaaatcggat ctaccaaatc ctggagctga acgggtacga tccgcagtac gcggcctccg 1260

tcttcctggg ctgggcgcaa aagaagttcg ggaagaggaa caccatctgg ctctttgggc 1320

cggccacgac gggtaaaacc aacatcgcgg aagccatcgc ccacgccgtg cccttctacg 1380

gctgcgtaaa ctggaccaat gagaactttc ccttcaacga ttgcgtcgac aagatggtga 1440

tctggtggga ggagggcaag atgacggcca aggtcgtgga gagcgccaag gccattctgg 1500

gcggaagcaa ggtgcgcgtg gaccaaaagt gcaagtcatc ggcccagatc gaacccactc 1560

ccgtgatcgt cacctccaac accaacatgt gcgccgtgat tgacgggaac agcaccacct 1620

tcgagcatca gcagccgctg caggaccgga tgtttgaatt tgaacttacc cgccgtttgg 1680

accatgactt tgggaaggtc accaaacagg aagtaaagga ctttttccgg tgggcttccg 1740

atcacgtgac tgacgtggct catgagttct acgtcagaaa gggtggagct aagaaacgcc 1800

ccgcctccaa tgacgcggat gtaagcgagc caaaacggga gtgcacgtca cttgcgcagc 1860

cgacaacgtc agacgcggaa gcaccggcgg actacgcgga caggtaccaa aacaaatgtt 1920

ctcgtcacgt gggcatgaat ctgatgcttt ttccctgtaa aacatgcgag agaatgaatc 1980

aaatttccaa tgtctgtttt acgcatggtc aaagagactg tggggaatgc ttccctggaa 2040

tgtcagaatc tcaacccgtt tctgtcgtca aaaagaagac ttatcagaaa ctgtgtccaa 2100

ttcatcatat cctgggaagg gcacccgaga ttgcctgttc ggcctgcgat ttggccaatg 2160

tggacttgga tgactgtgtt tctgagcaat aaatgactta aaccaggtat ggctgctgac 2220

ggttatcttc cagattggct cgaggacaac ctttctgaag gcattcgtga gtggtgggct 2280

ctgaaacctg gagtccctca acccaaagcg aaccaacaac accaggacaa ccgtcggggt 2340

cttgtgcttc cgggttacaa atacctcgga cccggtaacg gactcgacaa aggagagccg 2400

gtcaacgagg cggacgcggc agccctcgaa cacgacaaag cttacgacca gcagctcaag 2460

gccggtgaca acccgtacct caagtacaac cacgccgacg ccgagtttca ggagcgtctt 2520

caagaagata cgtcttttgg gggcaacctt ggcagagcag tcttccaggc caaaaagagg 2580

atccttgagc ctcttggtct ggttgaggaa gcagctaaaa cggctcctgg aaagaagggg 2640

gctgtagatc agtctcctca ggaaccggac tcatcatctg gtgttggcaa atcgggcaaa 2700

cagcctgcca gaaaaagact aaatttcggt cagactggag actcagagtc agtcccagac 2760

cctcaacctc tcggagaacc accagcagcc cccacaagtt tgggatctaa tacaatggct 2820

tcaggcggtg gcgcaccaat ggcagacaat aacgagggtg ccgatggagt gggtaattcc 2880 tcaggaaatt ggcattgcga ttcccaatgg ctgggcgaca gagtcatcac caccagcacc 2940

agaacctggg ccctgcccac ttacaacaac catctctaca agcaaatctc cagccaatca 3000

ggagcttcaa acgacaacca ctactttggc tacagcaccc cttgggggta ttttgacttt 3060

aacagattcc actgccactt ctcaccacgt gactggcagc gactcattaa caacaactgg 3120

ggattccggc ccaagaaact cagcttcaag ctcttcaaca tccaagttag aggggtcacg 3180

cagaacgatg gcacgacgac tattgccaat aaccttacca gcacggttca agtgtttacg 3240

gactcggagt atcagctccc gtacgtgctc gggtcggcgc accaaggctg tctcccgccg 3300

tttccagcgg acgtcttcat ggtccctcag tatggatacc tcaccctgaa caacggaagt 3360

caagcggtgg gacgctcatc cttttactgc ctggagtact tcccttcgca gatgctaagg 3420

actggaaata acttccaatt cagctatacc ttcgaggatg taccttttca cagcagctac 3480

gctcacagcc agagtttgga tcgcttgatg aatcctctta ttgatcagta tctgtactac 3540

ctgaacagaa cgcaaggaac aacctctgga acaaccaacc aatcacggct gctttttagc 3600

caggctgggc ctcagtctat gtctttgcag gccagaaatt ggctacctgg gccctgctac 3660

cggcaacaga gactttcaaa gactgctaac gacaacaaca acagtaactt tccttggaca 3720

gcggccagca aatatcatct caatggccgc gactcgctgg tgaatccagg accagctatg 3780

gccagtcaca aggacgatga agaaaaattt ttccctatgc acggcaatct aatatttggc 3840

aaagaaggga caacggcaag taacgcagaa ttagataatg taatgattac ggatgaagaa 3900

gagattcgta ccaccaatcc tgtggcaaca gagcagtatg gaactgtggc aaataacttg 3960

cagagctcaa atacagctcc cacgactgga actgtcaatc atcagggggc cttacctggc 4020

atggtgtggc aagatcgtga cgtgtacctt caaggaccta tctgggcaaa gattcctcac 4080

acggatggac actttcatcc ttctcctctg atgggaggct ttggactgaa acatccgcct 4140

cctcaaatca tgatcaaaaa tactccggta ccggcaaatc ctccgacgac tttcagcccg 4200

gccaagtttg cttcatttat cactcagtac tccactggac aggtcagcgt ggaaattgag 4260

tgggagctac agaaagaaaa cagcaaacgt tggaatccag agattcagta cacttccaac 4320

tacaacaagt ctgttaatgt ggactttact gtagacacta atggtgttta tagtgaacct 4380

cgccctattg gaacccggta tctcacacga aacttgtgaa tcctggttaa tcaataaacc 4440

gtttaattcg tttcagttga actttggctc ttgtgcactt ctttatcttt atcttgtttc 4500

catggctact gcgtagataa gcagcggcct gcggcgcttg cgcttcgcgg tttacaactg 4560

ctggttaata tttaactctc gccatacctc tagtgatgga gttggccact ccctctatgc 4620

gcactcgctc gctcggtggg gcctggcgac caaaggtcgc cagacggacg tgctttgcac 4680

gtccggcccc accgagcgag cgagtgcgca tagagggagt ggccaa 4726

<210> 61
<211> 737
<212> PRT
<213> Adeno-associated virus

```
<400> 61
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Asn Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Glu Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270
```

```
Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asp Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540
```

```
Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560


Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 62
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 62
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt      60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac     120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac     180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac     240
```

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaagg gggctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg agactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgactg gaactgtcaa tcatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 63

```
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 63
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140


Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445


Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460


Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 64
<211> 736
<212> PRT
<213> Adeno-associated virus 3A

<400> 64
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
```

305 310 315 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
435 440 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
450 455 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
485 490 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
530 535 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr

```
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 65
<211> 624
<212> PRT
<213> Adeno-associated virus 3A

<400> 65
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15

Glu Arg Leu Pro Gly Ile Ser Asn Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Asp Val Pro Pro Asp Ser Asp Met Asp Pro Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60

Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Thr Tyr Phe His Leu His Val Leu Ile Glu
                85                  90                  95
```

```
Thr Ile Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Leu
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Ser Asn
        275                 280                 285

Pro Pro Glu Asp Ile Thr Lys Asn Arg Ile Tyr Gln Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365
```

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370   375   380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385   390   395   400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Glu Pro Thr Pro Val
                405   410   415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420   425   430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Glu Phe
        435   440   445

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450   455   460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Asp Val
465   470   475   480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485   490   495

Ser Asn Asp Ala Asp Val Ser Glu Pro Lys Arg Glu Cys Thr Ser Leu
            500   505   510

Ala Gln Pro Thr Thr Ser Asp Ala Glu Ala Pro Ala Asp Tyr Ala Asp
        515   520   525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530   535   540

Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Ile Ser Asn Val Cys
545   550   555   560

Phe Thr His Gly Gln Arg Asp Cys Gly Glu Cys Phe Pro Gly Met Ser
                565   570   575

Glu Ser Gln Pro Val Ser Val Val Lys Lys Lys Thr Tyr Gln Lys Leu
            580   585   590

Cys Pro Ile His His Ile Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser
        595   600   605

Ala Cys Asp Leu Ala Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610   615   620

<210> 66
<211> 736
<212> PRT

<213> Adeno-associated virus 3B

<400> 66
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145   150   155   160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr

```
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
```

530 535 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
580 585 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 67
<211> 624
<212> PRT
<213> Adeno-associated virus 3B

<400> 67
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1 5 10 15

Glu His Leu Pro Gly Ile Ser Asn Ser Phe Val Asn Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Pro Asn Leu Ile
35 40 45

```
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60


Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Glu Thr Tyr Phe His Leu His Val Leu Ile Glu
                85                  90                  95


Thr Ile Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110


Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125


Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140


Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160


Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Leu
                165                 170                 175


Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190


Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205


Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220


Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240


Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255


Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270


Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Ser Asn
        275                 280                 285


Pro Pro Glu Asp Ile Thr Lys Asn Arg Ile Tyr Gln Ile Leu Glu Leu
    290                 295                 300


Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320
```

```
Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Glu Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Asp Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495

Ser Asn Asp Ala Asp Val Ser Glu Pro Lys Arg Gln Cys Thr Ser Leu
            500                 505                 510

Ala Gln Pro Thr Thr Ser Asp Ala Glu Ala Pro Ala Asp Tyr Ala Asp
        515                 520                 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540

Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Ile Ser Asn Val Cys
545                 550                 555                 560

Phe Thr His Gly Gln Arg Asp Cys Gly Glu Cys Phe Pro Gly Met Ser
                565                 570                 575

Glu Ser Gln Pro Val Ser Val Val Lys Lys Lys Thr Tyr Gln Lys Leu
            580                 585                 590
```

```
Cys Pro Ile His His Ile Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser
        595                 600                 605


Ala Cys Asp Leu Ala Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620


<210> 68
<211> 4722
<212> DNA
<213> Adeno-associated virus 3B

<400> 68
tggccactcc ctctatgcgc actcgctcgc tcggtggggc ctggcgacca aaggtcgcca       60

gacggacgtg ctttgcacgt ccggccccac cgagcgagcg agtgcgcata gagggagtgg      120

ccaactccat cactagaggt atggcagtga cgtaacgcga agcgcgcgaa gcgagaccac      180

gcctaccagc tgcgtcagca gtcaggtgac ccttttgcga cagtttgcga caccacgtgg      240

ccgctgaggg tatatattct cgagtgagcg aaccaggagc tccattttga ccgcgaaatt      300

tgaacgagca gcagccatgc cggggttcta cgagattgtc ctgaaggtcc cgagtgacct      360

ggacgagcac ctgccgggca tttctaactc gtttgttaac tgggtggccg agaaggaatg      420

ggagctgccg ccggattctg acatggatcc gaatctgatt gagcaggcac ccctgaccgt      480

ggccgaaaag cttcagcgcg agttcctggt ggagtggcgc cgcgtgagta aggccccgga      540

ggccctcttt tttgtccagt tcgaaaaggg ggagacctac ttccacctgc acgtgctgat      600

tgagaccatc ggggtcaaat ccatggtggt cggccgctac gtgagccaga ttaaagagaa      660

gctggtgacc cgcatctacc gcggggtcga gccgcagctt ccgaactggt tcgcggtgac      720

caaaacgcga aatggcgccg gggcgggaa caaggtggtg gacgactgct acatccccaa       780

ctacctgctc cccaagaccc agcccgagct ccagtgggcg tggactaaca tggaccagta      840

tttaagcgcc tgtttgaatc tcgcggagcg taaacggctg gtggcgcagc atctgacgca      900

cgtgtcgcag acgcaggagc agaacaaaga gaatcagaac cccaattctg acgcgccggt      960

catcaggtca aaaacctcag ccaggtacat ggagctggtc gggtggctgg tggaccgcgg     1020

gatcacgtca gaaaagcaat ggattcagga ggaccaggcc tcgtacatct ccttcaacgc     1080

cgcctccaac tcgcggtccc agatcaaggc cgcgctggac aatgcctcca agatcatgag     1140

cctgacaaag acggctccgg actacctggt gggcagcaac ccgccggagg acattaccaa     1200

aaatcggatc taccaaatcc tggagctgaa cgggtacgat ccgcagtacg cggcctccgt     1260

cttcctgggc tgggcgcaaa agaagttcgg gaagaggaac accatctggc tctttgggcc     1320

ggccacgacg ggtaaaacca acatcgcgga agccatcgcc cacgccgtgc ccttctacgg     1380

ctgcgtaaac tggaccaatg agaactttcc cttcaacgat tgcgtcgaca agatggtgat     1440

ctggtgggag gagggcaaga tgacggccaa ggtcgtggag agcgccaagg ccattctggg     1500

cggaagcaag gtgcgcgtgg accaaaagtg caagtcatcg gcccagatcg aacccactcc     1560

cgtgatcgtc acctccaaca ccaacatgtg cgccgtgatt gacgggaaca gcaccacctt     1620
```

cgagcatcag cagccgctgc aggaccggat gtttaaattt gaacttaccc gccgtttgga 1680

ccatgacttt gggaaggtca ccaaacagga agtaaaggac tttttccggt gggcttccga 1740

tcacgtgact gacgtggctc atgagttcta cgtcagaaag ggtggagcta agaaacgccc 1800

cgcctccaat gacgcggatg taagcgagcc aaaacggcag tgcacgtcac ttgcgcagcc 1860

gacaacgtca gacgcggaag caccggcgga ctacgcggac aggtaccaaa acaaatgttc 1920

tcgtcacgtg ggcatgaatc tgatgctttt tccctgtaaa acatgcgaga gaatgaatca 1980

aatttccaat gtctgtttta cgcatggtca aagagactgt ggggaatgct tccctggaat 2040

gtcagaatct caacccgttt ctgtcgtcaa aaagaagact tatcagaaac tgtgtccaat 2100

tcatcatatc ctgggaaggg cacccgagat tgcctgttcg gcctgcgatt tggccaatgt 2160

ggacttggat gactgtgttt ctgagcaata aatgacttaa accaggtatg gctgctgacg 2220

gttatcttcc agattggctc gaggacaacc tttctgaagg cattcgtgag tggtgggctc 2280

tgaaacctgg agtccctcaa cccaaagcga accaacaaca ccaggacaac cgtcggggtc 2340

ttgtgcttcc gggttacaaa tacctcggac ccggtaacgg actcgacaaa ggagagccgg 2400

tcaacgaggc ggacgcggca gccctcgaac acgacaaagc ttacgaccag cagctcaagg 2460

ccggtgacaa cccgtacctc aagtacaacc acgccgacgc cgagtttcag gagcgtcttc 2520

aagaagatac gtcttttggg ggcaaccttg gcagagcagt cttccaggcc aaaaagagga 2580

tccttgagcc tcttggtctg gttgaggaag cagctaaaac ggctcctgga aagaagaggc 2640

ctgtagatca gtctcctcag gaaccggact catcatctgg tgttggcaaa tcgggcaaac 2700

agcctgccag aaaaagacta aatttcggtc agactggcga ctcagagtca gtcccagacc 2760

ctcaacctct cggagaacca ccagcagccc ccacaagttt gggatctaat acaatggctt 2820

caggcggtgg cgcaccaatg gcagacaata acgagggtgc cgatggagtg ggtaattcct 2880

caggaaattg gcattgcgat tcccaatggc tgggcgacag agtcatcacc accagcacca 2940

gaacctgggc cctgcccact tacaacaacc atctctacaa gcaaatctcc agccaatcag 3000

gagcttcaaa cgacaaccac tactttggct acagcacccc ttgggggtat tttgacttta 3060

acagattcca ctgccacttc tcaccacgtg actggcagcg actcattaac aacaactggg 3120

gattccggcc caagaaactc agcttcaagc tcttcaacat ccaagttaaa gaggtcacgc 3180

agaacgatgg cacgacgact attgccaata accttaccag cacggttcaa gtgtttacgg 3240

actcggagta tcagctcccg tacgtgctcg ggtcggcgca ccaaggctgt ctcccgccgt 3300

ttccagcgga cgtcttcatg gtccctcagt atggatacct caccctgaac aacggaagtc 3360

aagcggtggg acgctcatcc ttttactgcc tggagtactt cccttcgcag atgctaagga 3420

ctggaaataa cttccaattc agctatacct tcgaggatgt acctttttcac agcagctacg 3480

ctcacagcca gagtttggat cgcttgatga atcctcttat tgatcagtat ctgtactacc 3540

tgaacagaac gcaaggaaca acctctggaa caaccaacca atcacggctg ctttttagcc 3600

aggctgggcc tcagtctatg tctttgcagg ccagaaattg gctacctggg ccctgctacc 3660 ggcaacagag actttcaaag actgctaacg acaacaacaa cagtaacttt ccttggacag 3720

cggccagcaa atatcatctc aatggccgcg actcgctggt gaatccagga ccagctatgg 3780

ccagtcacaa ggacgatgaa gaaaaatttt tccctatgca cggcaatcta atatttggca 3840

aagaagggac aacggcaagt aacgcagaat tagataatgt aatgattacg gatgaagaag 3900

agattcgtac caccaatcct gtggcaacag agcagtatgg aactgtggca aataacttgc 3960

agagctcaaa tacagctccc acgactagaa ctgtcaatga tcaggggggcc ttacctggca 4020

tggtgtggca agatcgtgac gtgtaccttc aaggacctat ctgggcaaag attcctcaca 4080

cggatggaca ctttcatcct tctcctctga tgggaggctt tggactgaaa catccgcctc 4140

ctcaaatcat gatcaaaaat actccggtac cggcaaatcc tccgacgact ttcagcccgg 4200

ccaagtttgc ttcatttatc actcagtact ccactggaca ggtcagcgtg gaaattgagt 4260

gggagctaca gaaagaaaac agcaaacgtt ggaatccaga gattcagtac acttccaact 4320

acaacaagtc tgttaatgtg gactttactg tagacactaa tggtgtttat agtgaacctc 4380

gccctattgg aacccggtat ctcacacgaa acttgtaatc ctggttaatc aataaaccgt 4440

ttaattcgtt tcagttgaac tttggctctt gtgcacttct tatcttatct tgtttccatg 4500

gctactgcgt agataagcag cggcctgcgg cgcttgcgct tcgcggttta caactgctgg 4560

ttaatattta actctcgcca tacctctagt gatggagttg gccactccct ctatgcgcac 4620

tcgctcgctc ggtggggccg gacgtgcaaa gcacgtccgt ctggcgacct ttggtcgcca 4680

ggccccaccg agcgagcgag tgcgcataga gggagtggcc aa 4722

<210> 69
<211> 1800
<212> DNA
<213> Adeno-associated virus 4

<220>
<221> modified_base
<222> (342)..(342)
<223> a, c, t or g

<400> 69
acggctcctg gaaagaagag accgttgatt gaatcccccc agcagcccga ctcctccacg 60

ggtatcggca aaaaaggcaa gcagccggct aaaaagaagc tcgttttcga agacgaaact 120

ggagcaggcg acggaccccc tgagggatca acttccggag ccatgtctga tgacagtgag 180

atgcgtgcag cagctggcgg agctgcagtc gagggsggac aaggtgccga tggagtgggt 240

aatgcctcgg gtgattggca ttgcgattcc acctggtctg agggccacgt cacgaccacc 300

agcaccagaa cctgggtctt gcccacctac aacaaccacc tntacaagcg actcggagag 360

agcctgcagt ccaacaccta caacggattc tccacccccct ggggatactt tgacttcaac 420

cgcttccact gccacttctc accacgtgac tggcagcgac tcatcaacaa caactggggc 480

atgcgaccca aagccatgcg ggtcaaaatc ttcaacatcc aggtcaagga ggtcacgacg 540 tcgaacggcg agacaacggt ggctaataac cttaccagca cggttcagat ctttgcggac 600

tcgtcgtacg aactgccgta cgtgatggat gcgggtcaag agggcagcct gcctcctttt 660

cccaacgacg tctttatggt gccccagtac ggctactgtg gactggtgac cggcaacact 720

tcgcagcaac agactgacag aaatgccttc tactgcctgg agtactttcc ttcgcagatg 780

ctgcggactg gcaacaactt tgaaattacg tacagttttg agaaggtgcc tttccactcg 840

atgtacgcgc acagccagag cctggaccgg ctgatgaacc ctctcatcga ccagtacctg 900

tggggactgc aatcgaccac caccggaacc accctgaatg ccgggactgc caccaccaac 960

tttaccaagc tgcggcctac caacttttcc aactttaaaa agaactggct gcccgggcct 1020

tcaatcaagc agcagggctt ctcaaagact gccaatcaaa actacaagat ccctgccacc 1080

gggtcagaca gtctcatcaa atacgagacg cacagcactc tggacggaag atggagtgcc 1140

ctgacccccg gacctccaat ggccacggct ggacctgcgg acagcaagtt cagcaacagc 1200

cagctcatct ttgcggggcc taaacagaac ggcaacacgg ccaccgtacc cgggactctg 1260

atcttcacct ctgaggagga gctggcagcc accaacgcca ccgatacgga catgtggggc 1320

aacctacctg gcggtgacca gagcaacagc aacctgccga ccgtggacag actgacagcc 1380

ttgggagccg tgcctggaat ggtctggcaa aacagagaca tttactacca gggtcccatt 1440

tgggccaaga ttcctcatac cgatggacac tttcacccct caccgctgat tggtgggttt 1500

gggctgaaac acccgcctcc tcaaattttt atcaagaaca ccccggtacc tgcgaatcct 1560

gcaacgacct tcagctctac tccggtaaac tccttcatta ctcagtacag cactggccag 1620

gtgtcggtgc agattgactg ggagatccag aaggagcggt ccaaacgctg gaaccccgag 1680

gtccagttta cctccaacta cggacagcaa aactctctgt tgtgggctcc cgatgcggct 1740

gggaaataca ctgagcctag ggctatcggt acccgctacc tcacccacca cctgtaataa 1800

<210> 70
<211> 2208
<212> DNA
<213> Adeno-associated virus 4

<220>
<221> modified_base
<222> (750)..(750)
<223> a, c, t or g

<400> 70
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggsggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctn tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc caccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaataa 2208

<210> 71
<211> 1872
<212> DNA
<213> Adeno-associated virus 4

<400> 71

atgccggggt tctacgagat cgtgctgaag gtgcccagcg acctggacga gcacctgccc 60

ggcatttctg actcttttgt gagctgggtg gccgagaagg aatgggagct gccgccggat 120

tctgacatgg acttgaatct gattgagcag gcacccctga ccgtggccga aaagctgcaa 180

cgcgagttcc tggtcgagtg gcgccgcgtg agtaaggccc cggaggccct cttctttgtc 240

cagttcgaga agggggacag ctacttccac ctgcacatcc tggtggagac cgtgggcgtc 300

aaatccatgg tggtgggccg ctacgtgagc cagattaaag agaagctggt gacccgcatc 360

taccgcgggg tcgagccgca gcttccgaac tggttcgcgg tgaccaagac gcgtaatggc 420

gccggaggcg ggaacaaggt ggtggacgac tgctacatcc ccaactacct gctccccaag 480

acccagcccg agctccagtg ggcgtggact aacatggacc agtatataag cgcctgtttg 540

aatctcgcgg agcgtaaacg gctggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aggaaaacca gaaccccaat tctgacgcgc cggtcatcag gtcaaaaacc 660

tccgccaggt acatggagct ggtcgggtgg ctggtggacc gcgggatcac gtcagaaaag 720

caatggatcc aggaggacca ggcgtcctac atctccttca acgccgcctc caactcgcgg 780

tcacaaatca aggccgcgct ggacaatgcc tccaaaatca tgagcctgac aaagacggct 840

ccggactacc tggtgggcca gaacccgccg gaggacattt ccagcaaccg catctaccga 900

atcctcgaga tgaacgggta cgatccgcag tacgcggcct ccgtcttcct gggctgggcg 960

caaaagaagt tcgggaagag gaacaccatc tggctctttg ggccggccac gacgggtaaa 1020

accaacatcg cggaagccat cgcccacgcc gtgcccttct acggctgcgt gaactggacc 1080

aatgagaact ttccgttcaa cgattgcgtc gacaagatgg tgatctggtg ggaggagggc 1140

aagatgacgg ccaaggtcgt agagagcgcc aaggccatcc tgggcggaag caaggtgcgc 1200

gtggaccaaa agtgcaagtc atcggcccag atcgacccaa ctcccgtgat cgtcacctcc 1260

aacaccaaca tgtgcgcggt catcgacgga aactcgacca ccttcgagca ccaacaacca 1320

ctccaggacc ggatgttcaa gttcgagctc accaagcgcc tggagcacga ctttggcaag 1380

gtcaccaagc aggaagtcaa agactttttc cggtgggcgt cagatcacgt gaccgaggtg 1440

actcacgagt tttacgtcag aaagggtgga gctagaaaga ggcccgcccc caatgacgca 1500

gatataagtg agcccaagcg ggcctgtccg tcagttgcgc agccatcgac gtcagacgcg 1560

gaagctccgg tggactacgc ggacaggtac caaaacaaat gttctcgtca cgtgggtatg 1620

aatctgatgc tttttccctg ccggcaatgc gagagaatga atcagaatgt ggacatttgc 1680

ttcacgcacg gggtcatgga ctgtgccgag tgcttccccg tgtcagaatc tcaacccgtg 1740

tctgtcgtca gaaagcggac gtatcagaaa ctgtgtccga ttcatcacat catggggagg 1800

gcgcccgagg tggcctgctc ggcctgcgaa ctggccaatg tggacttgga tgactgtgac 1860

atggaacaat aa 1872

<210> 72
<211> 1611
<212> DNA

<213> Adeno-associated virus 4

<400> 72
atgccggggt tctacgagat cgtgctgaag gtgcccagcg acctggacga gcacctgccc 60

ggcatttctg actcttttgt gagctgggtg gccgagaagg aatgggagct gccgccggat 120

tctgacatgg acttgaatct gattgagcag gcacccctga ccgtggccga aaagctgcaa 180

cgcgagttcc tggtcgagtg gcgccgcgtg agtaaggccc cggaggccct cttctttgtc 240

cagttcgaga agggggacag ctacttccac ctgcacatcc tggtggagac cgtgggcgtc 300

aaatccatgg tggtgggccg ctacgtgagc cagattaaag agaagctggt gacccgcatc 360

taccgcgggg tcgagccgca gcttccgaac tggttcgcgg tgaccaagac gcgtaatggc 420

gccggaggcg ggaacaaggt ggtggacgac tgctacatcc ccaactacct gctccccaag 480

acccagcccg agctccagtg ggcgtggact aacatggacc agtatataag cgcctgtttg 540

aatctcgcgg agcgtaaacg gctggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aggaaaacca gaaccccaat tctgacgcgc cggtcatcag gtcaaaaacc 660

tccgccaggt acatggagct ggtcgggtgg ctggtggacc gcgggatcac gtcagaaaag 720

caatggatcc aggaggacca ggcgtcctac atctccttca acgccgcctc caactcgcgg 780

tcacaaatca aggccgcgct ggacaatgcc tccaaaatca tgagcctgac aaagacggct 840

ccggactacc tggtgggcca gaacccgccg gaggacattt ccagcaaccg catctaccga 900

atcctcgaga tgaacgggta cgatccgcag tacgcggcct ccgtcttcct gggctgggcg 960

caaaagaagt tcgggaagag gaacaccatc tggctctttg ggccggccac gacgggtaaa 1020

accaacatcg cggaagccat cgcccacgcc gtgcccttct acggctgcgt gaactggacc 1080

aatgagaact ttccgttcaa cgattgcgtc gacaagatgg tgatctggtg ggaggagggc 1140

aagatgacgg ccaaggtcgt agagagcgcc aaggccatcc tgggcggaag caaggtgcgc 1200

gtggaccaaa agtgcaagtc atcggcccag atcgacccaa ctcccgtgat cgtcacctcc 1260

aacaccaaca tgtgcgcggt catcgacgga aactcgacca ccttcgagca ccaacaacca 1320

ctccaggacc ggatgttcaa gttcgagctc accaagcgcc tggagcacga ctttggcaag 1380

gtcaccaagc aggaagtcaa agactttttc cggtgggcgt cagatcacgt gaccgaggtg 1440

actcacgagt tttacgtcag aaagggtgga gctagaaaga ggcccgcccc caatgacgca 1500

gatataagtg agcccaagcg ggcctgtccg tcagttgcgc agccatcgac gtcagacgcg 1560

gaagctccgg tggactacgc ggacagattg gctagaggac aacctctctg a 1611

<210> 73
<211> 1872
<212> DNA
<213> Adeno-associated virus 4

<400> 73
atgccggggt tctacgagat cgtgctgaag gtgcccagcg acctggacga gcacctgccc 60

ggcatttctg actcttttgt gagctgggtg gccgagaagg aatgggagct gccgccggat 120 tctgacatgg acttgaatct gattgagcag gcacccctga ccgtggccga aaagctgcaa 180

cgcgagttcc tggtcgagtg gcgccgcgtg agtaaggccc cggaggccct cttctttgtc 240

cagttcgaga agggggacag ctacttccac ctgcacatcc tggtggagac cgtgggcgtc 300

aaatccatgg tggtgggccg ctacgtgagc cagattaaag agaagctggt gacccgcatc 360

taccgcgggg tcgagccgca gcttccgaac tggttcgcgg tgaccaagac gcgtaatggc 420

gccggaggcg ggaacaaggt ggtggacgac tgctacatcc ccaactacct gctccccaag 480

acccagcccg agctccagtg ggcgtggact aacatggacc agtatataag cgcctgtttg 540

aatctcgcgg agcgtaaacg gctggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aggaaaacca gaaccccaat tctgacgcgc cggtcatcag gtcaaaaacc 660

tccgccaggt acatggagct ggtcgggtgg ctggtggacc gcgggatcac gtcagaaaag 720

caatggatcc aggaggacca ggcgtcctac atctccttca acgccgcctc caactcgcgg 780

tcacaaatca aggccgcgct ggacaatgcc tccaaaatca tgagcctgac aaagacggct 840

ccggactacc tggtgggcca gaacccgccg gaggacattt ccagcaaccg catctaccga 900

atcctcgaga tgaacgggta cgatccgcag tacgcggcct ccgtcttcct gggctgggcg 960

caaaagaagt tcgggaagag gaacaccatc tggctctttg ggccggccac gacgggtaaa 1020

accaacatcg cggaagccat cgcccacgcc gtgcccttct acggctgcgt gaactggacc 1080

aatgagaact ttccgttcaa cgattgcgtc gacaagatgg tgatctggtg ggaggagggc 1140

aagatgacgg ccaaggtcgt agagagcgcc aaggccatcc tgggcggaag caaggtgcgc 1200

gtggaccaaa agtgcaagtc atcggcccag atcgacccaa ctcccgtgat cgtcacctcc 1260

aacaccaaca tgtgcgcggt catcgacgga aactcgacca ccttcgagca ccaacaacca 1320

ctccaggacc ggatgttcaa gttcgagctc accaagcgcc tggagcacga ctttggcaag 1380

gtcaccaagc aggaagtcaa agactttttc cggtgggcgt cagatcacgt gaccgaggtg 1440

actcacgagt tttacgtcag aaagggtgga gctagaaaga ggcccgcccc caatgacgca 1500

gatataagtg agcccaagcg ggcctgtccg tcagttgcgc agccatcgac gtcagacgcg 1560

gaagctccgg tggactacgc ggacaggtac caaaacaaat gttctcgtca cgtgggtatg 1620

aatctgatgc tttttccctg ccggcaatgc gagagaatga atcagaatgt ggacatttgc 1680

ttcacgcacg ggtcatgga ctgtgccgag tgcttccccg tgtcagaatc tcaacccgtg 1740

tctgtcgtca gaaagcggac gtatcagaaa ctgtgtccga ttcatcacat catggggagg 1800

gcgcccgagg tggcctgctc ggcctgcgaa ctggccaatg tggacttgga tgactgtgac 1860

atggaacaat aa 1872

<210> 74
<211> 1617
<212> DNA
<213> Adeno-associated virus 4

<220>

<221> modified_base
<222> (162)..(162)
<223> a, c, t or g

<400> 74
atgcgtgcag cagctggcgg agctgcagtc gagggsggac aaggtgccga tggagtgggt 60

aatgcctcgg gtgattggca ttgcgattcc acctggtctg agggccacgt cacgaccacc 120

agcaccagaa cctgggtctt gcccacctac aacaaccacc tntacaagcg actcggagag 180

agcctgcagt ccaacaccta caacggattc tccacccct ggggatactt tgacttcaac 240

cgcttccact gccacttctc accacgtgac tggcagcgac tcatcaacaa caactggggc 300

atgcgaccca aagccatgcg ggtcaaaatc ttcaacatcc aggtcaagga ggtcacgacg 360

tcgaacggcg agacaacggt ggctaataac cttaccagca cggttcagat ctttgcggac 420

tcgtcgtacg aactgccgta cgtgatggat gcgggtcaag agggcagcct gcctcctttt 480

cccaacgacg tctttatggt gccccagtac ggctactgtg gactggtgac cggcaacact 540

tcgcagcaac agactgacag aaatgccttc tactgcctgg agtactttcc ttcgcagatg 600

ctgcggactg gcaacaactt tgaaattacg tacagttttg agaaggtgcc tttccactcg 660

atgtacgcgc acagccagag cctggaccgg ctgatgaacc ctctcatcga ccagtacctg 720

tggggactgc aatcgaccac caccggaacc accctgaatg ccgggactgc caccaccaac 780

tttaccaagc tgcggcctac caacttttcc aactttaaaa agaactggct gcccgggcct 840

tcaatcaagc agcagggctt ctcaaagact gccaatcaaa actacaagat ccctgccacc 900

gggtcagaca gtctcatcaa atacgagacg cacagcactc tggacggaag atggagtgcc 960

ctgacccccg gacctccaat ggccacggct ggacctgcgg acagcaagtt cagcaacagc 1020

cagctcatct ttgcggggcc taaacagaac ggcaacacgg ccaccgtacc cgggactctg 1080

atcttcacct ctgaggagga gctggcagcc accaacgcca ccgatacgga catgtggggc 1140

aacctacctg gcggtgacca gagcaacagc aacctgccga ccgtggacag actgacagcc 1200

ttgggagccg tgcctggaat ggtctggcaa aacagagaca tttactacca gggtcccatt 1260

tgggccaaga ttcctcatac cgatggacac tttcacccct caccgctgat tggtgggttt 1320

gggctgaaac acccgcctcc tcaaattttt atcaagaaca ccccggtacc tgcgaatcct 1380

gcaacgacct tcagctctac tccggtaaac tccttcatta ctcagtacag cactggccag 1440

gtgtcggtgc agattgactg ggagatccag aaggagcggt ccaaacgctg gaaccccgag 1500

gtccagttta cctccaacta cggacagcaa aactctctgt tgtgggctcc cgatgcggct 1560

gggaaataca ctgagcctag ggctatcggt acccgctacc tcacccacca cctgtaa 1617

<210> 75
<211> 939
<212> DNA
<213> Adeno-associated virus 4

<400> 75
atggagctgg tcgggtggct ggtggaccgc gggatcacgt cagaaaagca atggatccag 60

gaggaccagg cgtcctacat ctccttcaac gccgcctcca actcgcggtc acaaatcaag 120

gccgcgctgg acaatgcctc caaaatcatg agcctgacaa agacggctcc ggactacctg 180

gtgggccaga acccgccgga ggacatttcc agcaaccgca tctaccgaat cctcgagatg 240

aacgggtacg atccgcagta cgcggcctcc gtcttcctgg gctgggcgca aaagaagttc 300

gggaagagga acaccatctg gctctttggg ccggccacga cgggtaaaac caacatcgcg 360

gaagccatcg cccacgccgt gcccttctac ggctgcgtga actggaccaa tgagaacttt 420

ccgttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc 480

aaggtcgtag agagcgccaa ggccatcctg ggcggaagca aggtgcgcgt ggaccaaaag 540

tgcaagtcat cggcccagat cgacccaact cccgtgatcg tcacctccaa caccaacatg 600

tgcgcggtca tcgacggaaa ctcgaccacc ttcgagcacc aacaaccact ccaggaccgg 660

atgttcaagt tcgagctcac caagcgcctg gagcacgact ttggcaaggt caccaagcag 720

gaagtcaaag actttttccg gtgggcgtca gatcacgtga ccgaggtgac tcacgagttt 780

tacgtcagaa agggtggagc tagaaagagg cccgccccca atgacgcaga tataagtgag 840

cccaagcggg cctgtccgtc agttgcgcag ccatcgacgt cagacgcgga agctccggtg 900

gactacgcgg acagattggc tagaggacaa cctctctga 939

<210> 76
<211> 1197
<212> DNA
<213> Adeno-associated virus 4

<400> 76
atggagctgg tcgggtggct ggtggaccgc gggatcacgt cagaaaagca atggatccag 60

gaggaccagg cgtcctacat ctccttcaac gccgcctcca actcgcggtc acaaatcaag 120

gccgcgctgg acaatgcctc caaaatcatg agcctgacaa agacggctcc ggactacctg 180

gtgggccaga acccgccgga ggacatttcc agcaaccgca tctaccgaat cctcgagatg 240

aacgggtacg atccgcagta cgcggcctcc gtcttcctgg gctgggcgca aaagaagttc 300

gggaagagga acaccatctg gctctttggg ccggccacga cgggtaaaac caacatcgcg 360

gaagccatcg cccacgccgt gcccttctac ggctgcgtga actggaccaa tgagaacttt 420

ccgttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc 480

aaggtcgtag agagcgccaa ggccatcctg ggcggaagca aggtgcgcgt ggaccaaaag 540

tgcaagtcat cggcccagat cgacccaact cccgtgatcg tcacctccaa caccaacatg 600

tgcgcggtca tcgacggaaa ctcgaccacc ttcgagcacc aacaaccact ccaggaccgg 660

atgttcaagt tcgagctcac caagcgcctg gagcacgact ttggcaaggt caccaagcag 720

gaagtcaaag actttttccg gtgggcgtca gatcacgtga ccgaggtgac tcacgagttt 780

tacgtcagaa agggtggagc tagaaagagg cccgccccca atgacgcaga tataagtgag 840

cccaagcggg cctgtccgtc agttgcgcag ccatcgacgt cagacgcgga agctccggtg 900

gactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggtatgaa tctgatgctt 960

```
tttccctgcc ggcaatgcga gagaatgaat cagaatgtgg acatttgctt cacgcacggg     1020

gtcatggact gtgccgagtg cttccccgtg tcagaatctc aacccgtgtc tgtcgtcaga     1080

aagcggacgt atcagaaact gtgtccgatt catcacatca tggggagggc gcccgaggtg     1140

gcctgctcgg cctgcgaact ggccaatgtg gacttggatg actgtgacat ggaacaa        1197


<210> 77
<211> 245
<212> DNA
<213> Adeno-associated virus 4

<400> 77
ctccatcatc taggtttgcc cactgacgtc aatgtgacgt cctagggtta gggaggtccc       60

tgtattagca gtcacgtgag tgtcgtattt cgcggagcgt agcggagcgc ataccaagct      120

gccacgtcac agccacgtgg tccgtttgcg acagtttgcg acaccatgtg gtcaggaggg      180

tatataaccg cgagtgagcc agcgaggagc tccattttgc ccgcgaattt tgaacgagca      240

gcagc                                                                  245


<210> 78
<211> 313
<212> PRT
<213> Adeno-associated virus 4


<220>
<221> MOD_RES
<222> (313)..(313)
<223> Any amino acid

<400> 78
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1               5                   10                  15


Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30


Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
        35                  40                  45


Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
    50                  55                  60


Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
65                  70                  75                  80


Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85                  90                  95


Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110


Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
```

```
        115                 120                 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
                245                 250                 255

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
            260                 265                 270

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
    290                 295                 300

Arg Leu Ala Arg Gly Gln Pro Leu Xaa
305                 310


<210> 79
<211> 399
<212> PRT
<213> Adeno-associated virus 4

<400> 79
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1               5                   10                  15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
        35                  40                  45
```

```
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
    50                  55                  60

Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
65                  70                  75                  80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
                245                 250                 255

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
            260                 265                 270

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
    290                 295                 300

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305                 310                 315                 320
```

```
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
                325                 330                 335


Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
            340                 345                 350


Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
        355                 360                 365


Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
    370                 375                 380


Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
385                 390                 395


<210> 80
<211> 623
<212> PRT
<213> Adeno-associated virus 4

<400> 80
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15


Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30


Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60


Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95


Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110


Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125


Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140


Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160


Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
```

```
                165                 170                 175


Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190


Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205


Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220


Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240


Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255


Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270


Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285


Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300


Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320


Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335


Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350


Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365


Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380


Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400


Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415


Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430


Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
```

```
        435                 440                 445

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
                485                 490                 495

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
        515                 520                 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
545                 550                 555                 560

Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
                565                 570                 575

Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
            580                 585                 590

Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
        595                 600                 605

Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
    610                 615                 620


<210> 81
<211> 537
<212> PRT
<213> Adeno-associated virus 4


<220>
<221> MOD_RES
<222> (537)..(537)
<223> Any amino acid

<400> 81
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
```

```
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60


Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95


Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110


Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125


Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140


Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160


Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
                165                 170                 175


Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190


Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205


Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220


Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240


Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255


Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270


Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285


Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300


Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
```

```
305                 310                 315                 320


Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335


Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350


Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365


Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380


Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400


Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415


Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430


Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445


Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460


Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480


Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
                485                 490                 495


Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510


Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
        515                 520                 525


Arg Leu Ala Arg Gly Gln Pro Leu Xaa
    530                 535


<210> 82
<211> 623
<212> PRT
<213> Adeno-associated virus 4

<400> 82
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15
```

```
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30


Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60


Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95


Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110


Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125


Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140


Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160


Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
                165                 170                 175


Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190


Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205


Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220


Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240


Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255


Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270


Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285
```

```
Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300


Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320


Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335


Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350


Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365


Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380


Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400


Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415


Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430


Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445


Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460


Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480


Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
                485                 490                 495


Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510


Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
        515                 520                 525


Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540


Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
545                 550                 555                 560
```

```
Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
                565                 570                 575


Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
            580                 585                 590


Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
        595                 600                 605


Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
    610                 615                 620


<210> 83
<211> 544
<212> PRT
<213> Adeno-associated virus 4

<400> 83
Met Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val
1               5                   10                  15


Glu Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp
            20                  25                  30


His Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr
        35                  40                  45


Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu
    50                  55                  60


Gly Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
65                  70                  75                  80


Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
                85                  90                  95


Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met
            100                 105                 110


Arg Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
        115                 120                 125


Gly Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
    130                 135                 140


Ala Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
145                 150                 155                 160


Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
                165                 170                 175


Gly Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp
```

```
            180                 185                 190

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
        195                 200                 205

Thr Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe
    210                 215                 220

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
225                 230                 235                 240

Leu Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr
                245                 250                 255

Thr Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro
            260                 265                 270

Thr Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile
        275                 280                 285

Lys Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro
    290                 295                 300

Ala Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu
305                 310                 315                 320

Asp Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala
                325                 330                 335

Gly Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly
            340                 345                 350

Pro Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe
        355                 360                 365

Thr Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met
    370                 375                 380

Trp Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr
385                 390                 395                 400

Val Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln
                405                 410                 415

Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
            420                 425                 430

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
        435                 440                 445

Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
```

450 455 460

Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr
465 470 475 480

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln
485 490 495

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
500 505 510

Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys
515 520 525

Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
530 535 540

<210> 84
<211> 734
<212> PRT
<213> Adeno-associated virus 4

<400> 84
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
130 135 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145 150 155 160

```
Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430
```

```
Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700
```

```
Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720


Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 85
<211> 598
<212> PRT
<213> Adeno-associated virus 4

<400> 85
Thr Ala Pro Gly Lys Lys Arg Pro Leu Ile Glu Ser Pro Gln Gln Pro
1               5                   10                  15


Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Lys Gln Pro Ala Lys Lys
            20                  25                  30


Lys Leu Val Phe Glu Asp Glu Thr Gly Ala Gly Asp Gly Pro Pro Glu
        35                  40                  45


Gly Ser Thr Ser Gly Ala Met Ser Asp Asp Ser Glu Met Arg Ala Ala
    50                  55                  60


Ala Gly Gly Ala Ala Val Glu Gly Gly Gln Gly Ala Asp Gly Val Gly
65                  70                  75                  80


Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu Gly His
                85                  90                  95


Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn
            100                 105                 110


His Leu Tyr Lys Arg Leu Gly Glu Ser Leu Gln Ser Asn Thr Tyr Asn
        115                 120                 125


Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
    130                 135                 140


His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
145                 150                 155                 160


Met Arg Pro Lys Ala Met Arg Val Lys Ile Phe Asn Ile Gln Val Lys
                165                 170                 175


Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ala Asn Asn Leu Thr
            180                 185                 190


Ser Thr Val Gln Ile Phe Ala Asp Ser Ser Tyr Glu Leu Pro Tyr Val
        195                 200                 205


Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe Pro Asn Asp Val
```

```
    210                 215                 220


Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val Thr Gly Asn Thr
225                 230                 235                 240


Ser Gln Gln Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe
                245                 250                 255


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Ile Thr Tyr Ser
            260                 265                 270


Phe Glu Lys Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu
        275                 280                 285


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Trp Gly Leu Gln
    290                 295                 300


Ser Thr Thr Thr Gly Thr Thr Leu Asn Ala Gly Thr Ala Thr Thr Asn
305                 310                 315                 320


Phe Thr Lys Leu Arg Pro Thr Asn Phe Ser Asn Phe Lys Lys Asn Trp
                325                 330                 335


Leu Pro Gly Pro Ser Ile Lys Gln Gln Gly Phe Ser Lys Thr Ala Asn
            340                 345                 350


Gln Asn Tyr Lys Ile Pro Ala Thr Gly Ser Asp Ser Leu Ile Lys Tyr
        355                 360                 365


Glu Thr His Ser Thr Leu Asp Gly Arg Trp Ser Ala Leu Thr Pro Gly
    370                 375                 380


Pro Pro Met Ala Thr Ala Gly Pro Ala Asp Ser Lys Phe Ser Asn Ser
385                 390                 395                 400


Gln Leu Ile Phe Ala Gly Pro Lys Gln Asn Gly Asn Thr Ala Thr Val
                405                 410                 415


Pro Gly Thr Leu Ile Phe Thr Ser Glu Glu Glu Leu Ala Ala Thr Asn
            420                 425                 430


Ala Thr Asp Thr Asp Met Trp Gly Asn Leu Pro Gly Gly Asp Gln Ser
        435                 440                 445


Asn Ser Asn Leu Pro Thr Val Asp Arg Leu Thr Ala Leu Gly Ala Val
    450                 455                 460


Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile
465                 470                 475                 480


Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
```

```
                485                 490                 495


Ile Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Phe Ile Lys
            500                 505                 510


Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro
        515                 520                 525


Val Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Gln
    530                 535                 540


Ile Asp Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu
545                 550                 555                 560


Val Gln Phe Thr Ser Asn Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala
                565                 570                 575


Pro Asp Ala Ala Gly Lys Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg
            580                 585                 590


Tyr Leu Thr His His Leu
        595


<210> 86
<211> 129
<212> DNA
<213> Adeno-associated virus 4

<400> 86
ttggccactc cctctatgcg cgctcgctca ctcactcggc cctgcggcca gaggccggca        60

gtctggagac ctttggtgtc cagggcaggg ccgagtgagt gagcgagcgc gcatagaggg       120

agtggccaa                                                               129


<210> 87
<211> 125
<212> DNA
<213> Adeno-associated virus 4

<400> 87
ttggccactc cctctatgcg cgctcgctca ctcactcggc cctggagacc aaaggtctcc        60

agactgccgg cctctggccg gcagggccga gtgagtgagc gagcgcgcat agagggagtg       120

gccaa                                                                   125


<210> 88
<211> 4768
<212> DNA
<213> Adeno-associated virus 4


<220>
<221> modified_base
<222> (3009)..(3009)
<223> a, c, t or g
```

<400> 88

ttggccactc cctctatgcg cgctcgctca ctcactcggc cctggagacc aaaggtctcc 60

agactgccgg cctctggccg gcagggccga gtgagtgagc gagcgcgcat agagggagtg 120

gccaactcca tcatctaggt ttgcccactg acgtcaatgt gacgtcctag ggttagggag 180

gtccctgtat tagcagtcac gtgagtgtcg tatttcgcgg agcgtagcgg agcgcatacc 240

aagctgccac gtcacagcca cgtggtccgt ttgcgacagt ttgcgacacc atgtggtcag 300

gagggtatat aaccgcgagt gagccagcga ggagctccat tttgcccgcg aattttgaac 360

gagcagcagc catgccgggg ttctacgaga tcgtgctgaa ggtgcccagc gacctggacg 420

agcacctgcc cggcatttct gactcttttg tgagctgggt ggccgagaag gaatgggagc 480

tgccgccgga ttctgacatg gacttgaatc tgattgagca ggcacccctg accgtggccg 540

aaaagctgca acgcgagttc ctggtcgagt ggcgccgcgt gagtaaggcc ccggaggccc 600

tcttctttgt ccagttcgag aagggggaca gctacttcca cctgcacatc ctggtggaga 660

ccgtgggcgt caaatccatg gtggtgggcc gctacgtgag ccagattaaa gagaagctgg 720

tgacccgcat ctaccgcggg gtcgagccgc agcttccgaa ctggttcgcg gtgaccaaga 780

cgcgtaatgg cgccggaggc gggaacaagg tggtggacga ctgctacatc cccaactacc 840

tgctccccaa gacccagccc gagctccagt gggcgtggac taacatggac cagtatataa 900

gcgcctgttt gaatctcgcg gagcgtaaac ggctggtggc gcagcatctg acgcacgtgt 960

cgcagacgca ggagcagaac aaggaaaacc agaaccccaa ttctgacgcg ccggtcatca 1020

ggtcaaaaac ctccgccagg tacatggagc tggtcgggtg gctggtggac cgcgggatca 1080

cgtcagaaaa gcaatggatc caggaggacc aggcgtccta catctccttc aacgccgcct 1140

ccaactcgcg gtcacaaatc aaggccgcgc tggacaatgc ctccaaaatc atgagcctga 1200

caaagacggc tccggactac ctggtgggcc agaacccgcc ggaggacatt tccagcaacc 1260

gcatctaccg aatcctcgag atgaacgggt acgatccgca gtacgcggcc tccgtcttcc 1320

tgggctgggc gcaaaagaag ttcgggaaga ggaacaccat ctggctcttt gggccggcca 1380

cgacgggtaa aaccaacatc gcggaagcca tcgcccacgc cgtgcccttc tacggctgcg 1440

tgaactggac caatgagaac tttccgttca acgattgcgt cgacaagatg gtgatctggt 1500

gggaggaggg caagatgacg gccaaggtcg tagagagcgc caaggccatc ctgggcggaa 1560

gcaaggtgcg cgtggaccaa aagtgcaagt catcggccca gatcgaccca actcccgtga 1620

tcgtcacctc caacaccaac atgtgcgcgg tcatcgacgg aaactcgacc accttcgagc 1680

accaacaacc actccaggac cggatgttca agttcgagct caccaagcgc ctggagcacg 1740

actttggcaa ggtcaccaag caggaagtca aagacttttt ccggtgggcg tcagatcacg 1800

tgaccgaggt gactcacgag ttttacgtca gaaagggtgg agctagaaag aggcccgccc 1860

ccaatgacgc agatataagt gagcccaagc gggcctgtcc gtcagttgcg cagccatcga 1920

cgtcagacgc ggaagctccg gtggactacg cggacaggta ccaaaacaaa tgttctcgtc 1980

acgtgggtat gaatctgatg ctttttccct gccggcaatg cgagagaatg aatcagaatg 2040 tggacatttg cttcacgcac ggggtcatgg actgtgccga gtgcttcccc gtgtcagaat 2100

ctcaacccgt gtctgtcgtc agaaagcgga cgtatcagaa actgtgtccg attcatcaca 2160

tcatggggag ggcgcccgag gtggcctgct cggcctgcga actggccaat gtggacttgg 2220

atgactgtga catggaacaa taaatgactc aaaccagata tgactgacgg ttaccttcca 2280

gattggctag aggacaacct ctctgaaggc gttcgagagt ggtgggcgct gcaacctgga 2340

gcccctaaac ccaaggcaaa tcaacaacat caggacaacg ctcggggtct tgtgcttccg 2400

ggttacaaat acctcggacc cggcaacgga ctcgacaagg gggaacccgt caacgcagcg 2460

gacgcggcag ccctcgagca cgacaaggcc tacgaccagc agctcaaggc cggtgacaac 2520

ccctacctca agtacaacca cgccgacgcg gagttccagc agcggcttca gggcgacaca 2580

ccgtttgggg gcaacctcgg cagagcagtc ttccaggcca aaaagagggt tcttgaacct 2640

cttggtctgg ttgagcaagc gggtgagacg gctcctggaa agaagagacc gttgattgaa 2700

tccccccagc agcccgactc ctccacgggt atcggcaaaa aaggcaagca gccggctaaa 2760

aagaagctcg ttttcgaaga cgaaactgga gcaggcgacg gaccccctga gggatcaact 2820

tccggagcca tgtctgatga cagtgagatg cgtgcagcag ctggcggagc tgcagtcgag 2880

ggsggacaag gtgccgatgg agtgggtaat gcctcgggtg attggcattg cgattccacc 2940

tggtctgagg gccacgtcac gaccaccagc accagaacct gggtcttgcc cacctacaac 3000

aaccacctnt acaagcgact cggagagagc ctgcagtcca acacctacaa cggattctcc 3060

accccctggg gatactttga cttcaaccgc ttccactgcc acttctcacc acgtgactgg 3120

cagcgactca tcaacaacaa ctggggcatg cgacccaaag ccatgcgggt caaaatcttc 3180

aacatccagg tcaaggaggt cacgacgtcg aacggcgaga caacggtggc taataacctt 3240

accagcacgg ttcagatctt tgcggactcg tcgtacgaac tgccgtacgt gatggatgcg 3300

ggtcaagagg gcagcctgcc tcctttccc aacgacgtct ttatggtgcc ccagtacggc 3360

tactgtggac tggtgaccgg caacacttcg cagcaacaga ctgacagaaa tgccttctac 3420

tgcctggagt actttccttc gcagatgctg cggactggca acaactttga aattacgtac 3480

agttttgaga aggtgccttt ccactcgatg tacgcgcaca gccagagcct ggaccggctg 3540

atgaaccctc tcatcgacca gtacctgtgg ggactgcaat cgaccaccac cggaaccacc 3600

ctgaatgccg ggactgccac caccaacttt accaagctgc ggcctaccaa cttttccaac 3660

tttaaaaaga actggctgcc cgggccttca atcaagcagc agggcttctc aaagactgcc 3720

aatcaaaact acaagatccc tgccaccggg tcagacagtc tcatcaaata cgagacgcac 3780

agcactctgg acggaagatg gagtgccctg acccccggac ctccaatggc cacggctgga 3840

cctgcggaca gcaagttcag caacagccag ctcatctttg cggggcctaa acagaacggc 3900

aacacggcca ccgtacccgg gactctgatc ttcacctctg aggaggagct ggcagccacc 3960

aacgccaccg atacggacat gtggggcaac ctacctggcg gtgaccagag caacagcaac 4020

ctgccgaccg tggacagact gacagccttg ggagccgtgc ctggaatggt ctggcaaaac 4080 agagacattt actaccaggg tcccatttgg gccaagattc ctcataccga tggacacttt 4140

cacccctcac cgctgattgg tgggtttggg ctgaaacacc cgcctcctca aatttttatc 4200

aagaacaccc cggtacctgc gaatcctgca acgaccttca gctctactcc ggtaaactcc 4260

ttcattactc agtacagcac tggccaggtg tcggtgcaga ttgactggga gatccagaag 4320

gagcggtcca aacgctggaa ccccgaggtc cagtttacct ccaactacgg acagcaaaac 4380

tctctgttgt gggctcccga tgcggctggg aaatacactg agcctagggc tatcggtacc 4440

cgctacctca cccaccacct gtaataacct gttaatcaat aaaccggttt attcgtttca 4500

gttgaacttt ggtctccgtg tccttcttat cttatctcgt ttccatggct actgcgtaca 4560

taagcagcgg cctgcggcgc ttgcgcttcg cggtttacaa ctgccggtta atcagtaact 4620

tctggcaaac catgatgatg gagttggcca ctccctctat gcgcgctcgc tcactcactc 4680

ggccctggag accaaaggtc tccagactgc cggcctctgg ccggcagggc cgagtgagtg 4740

agcgagcgcg catagaggga gtggccaa 4768

<210> 89
<211> 3098
<212> PRT
<213> Adeno-associated virus

<400> 89

```
Gly Ala Ala Thr Thr Cys Gly Cys Cys Cys Thr Thr Thr Cys Thr Ala
1               5                   10                  15


Cys Gly Gly Cys Thr Gly Cys Gly Thr Cys Ala Ala Cys Thr Gly Gly
            20                  25                  30


Ala Cys Cys Ala Ala Thr Gly Ala Gly Ala Ala Cys Thr Thr Thr Cys
        35                  40                  45


Cys Cys Thr Thr Cys Ala Ala Cys Gly Ala Thr Thr Gly Cys Gly Thr
    50                  55                  60


Cys Gly Ala Cys Ala Ala Gly Ala Thr Gly Gly Thr Gly Ala Thr Cys
65                  70                  75                  80


Thr Gly Gly Thr Gly Gly Gly Ala Gly Gly Ala Gly Gly Gly Cys Ala
                85                  90                  95


Ala Gly Ala Thr Gly Ala Cys Gly Gly Cys Cys Ala Ala Gly Gly Thr
            100                 105                 110


Cys Gly Thr Gly Gly Ala Gly Thr Cys Cys Gly Cys Cys Ala Ala Gly
        115                 120                 125


Gly Cys Cys Ala Thr Thr Cys Thr Cys Gly Gly Cys Gly Gly Cys Ala
    130                 135                 140
```

```
Gly Cys Ala Ala Gly Gly Thr Gly Cys Gly Cys Gly Thr Gly Gly Ala
145                 150                 155                 160

Cys Cys Ala Ala Ala Ala Gly Thr Gly Cys Ala Ala Gly Thr Cys Thr
                165                 170                 175

Thr Cys Cys Gly Cys Cys Cys Ala Gly Ala Thr Cys Gly Ala Thr Cys
            180                 185                 190

Cys Cys Ala Cys Cys Cys Cys Cys Gly Thr Gly Ala Thr Cys Gly Thr
        195                 200                 205

Cys Ala Cys Thr Thr Cys Cys Ala Ala Cys Ala Cys Cys Ala Ala Cys
    210                 215                 220

Ala Thr Gly Thr Gly Cys Gly Cys Thr Gly Thr Gly Ala Thr Thr Gly
225                 230                 235                 240

Ala Cys Gly Gly Gly Ala Ala Cys Ala Gly Cys Ala Cys Cys Ala Cys
                245                 250                 255

Cys Thr Thr Cys Gly Ala Gly Cys Ala Cys Cys Ala Gly Cys Ala Gly
            260                 265                 270

Cys Cys Gly Thr Thr Ala Cys Ala Ala Gly Ala Cys Cys Gly Gly Ala
        275                 280                 285

Thr Gly Thr Thr Cys Ala Ala Ala Thr Thr Thr Gly Ala Ala Cys Thr
    290                 295                 300

Cys Ala Cys Cys Cys Gly Cys Cys Gly Thr Cys Thr Gly Gly Ala Gly
305                 310                 315                 320

Cys Ala Cys Gly Ala Cys Thr Thr Thr Gly Gly Cys Ala Ala Gly Gly
                325                 330                 335

Thr Gly Ala Cys Ala Ala Ala Gly Cys Ala Gly Gly Ala Ala Gly Thr
            340                 345                 350

Cys Ala Ala Ala Gly Ala Gly Thr Thr Cys Thr Thr Cys Cys Gly Cys
        355                 360                 365

Thr Gly Gly Gly Cys Gly Cys Ala Gly Gly Ala Thr Cys Ala Cys Gly
    370                 375                 380

Thr Gly Ala Cys Cys Gly Ala Gly Gly Thr Gly Gly Cys Gly Cys Ala
385                 390                 395                 400

Thr Gly Ala Gly Thr Thr Cys Thr Ala Cys Gly Thr Cys Ala Gly Ala
                405                 410                 415
```

```
Ala Ala Gly Gly Gly Thr Gly Gly Ala Gly Cys Cys Ala Ala Cys Ala
            420                 425                 430

Ala Gly Ala Gly Ala Cys Cys Cys Gly Cys Cys Cys Cys Cys Gly Ala
        435                 440                 445

Thr Gly Ala Cys Gly Cys Gly Gly Ala Thr Ala Ala Ala Ala Gly Cys
    450                 455                 460

Gly Ala Gly Cys Cys Cys Ala Ala Gly Cys Gly Gly Gly Cys Cys Thr
465                 470                 475                 480

Gly Cys Cys Cys Cys Thr Cys Ala Gly Thr Cys Gly Cys Gly Gly Ala
                485                 490                 495

Thr Cys Cys Ala Thr Cys Gly Ala Cys Gly Thr Cys Ala Gly Ala Cys
            500                 505                 510

Gly Cys Gly Gly Ala Ala Gly Gly Ala Gly Cys Thr Cys Cys Gly Gly
        515                 520                 525

Thr Gly Gly Ala Cys Thr Thr Thr Gly Cys Cys Gly Ala Cys Ala Gly
    530                 535                 540

Gly Thr Ala Cys Cys Ala Ala Ala Ala Cys Ala Ala Ala Thr Gly Thr
545                 550                 555                 560

Thr Cys Thr Cys Gly Thr Cys Ala Cys Gly Cys Gly Gly Gly Cys Ala
                565                 570                 575

Thr Gly Cys Thr Thr Cys Ala Gly Ala Thr Gly Cys Thr Gly Thr Thr
            580                 585                 590

Thr Cys Cys Cys Thr Gly Cys Ala Ala Gly Ala Cys Ala Thr Gly Cys
        595                 600                 605

Gly Ala Gly Ala Gly Ala Ala Thr Gly Ala Ala Thr Cys Ala Gly Ala
    610                 615                 620

Ala Thr Thr Thr Cys Ala Ala Cys Ala Thr Thr Thr Gly Cys Thr Thr
625                 630                 635                 640

Cys Ala Cys Gly Cys Ala Cys Gly Gly Gly Ala Cys Cys Ala Gly Ala
                645                 650                 655

Gly Ala Cys Thr Gly Thr Thr Cys Ala Gly Ala Ala Thr Gly Thr Thr
            660                 665                 670

Thr Cys Cys Cys Cys Gly Gly Cys Gly Thr Gly Thr Cys Ala Gly Ala
        675                 680                 685
```

```
Ala Thr Cys Thr Cys Ala Ala Cys Cys Gly Gly Thr Cys Gly Thr Cys
    690                 695                 700

Ala Gly Ala Ala Ala Gly Ala Gly Gly Ala Cys Gly Thr Ala Thr Cys
705                 710                 715                 720

Gly Gly Ala Ala Ala Cys Thr Cys Thr Gly Thr Gly Cys Cys Ala Thr
                725                 730                 735

Thr Cys Ala Thr Cys Ala Thr Cys Thr Gly Cys Thr Gly Gly Gly Gly
            740                 745                 750

Cys Gly Gly Gly Cys Thr Cys Cys Cys Gly Ala Gly Ala Thr Thr Gly
        755                 760                 765

Cys Thr Thr Gly Cys Thr Cys Gly Gly Cys Cys Thr Gly Cys Gly Ala
    770                 775                 780

Thr Cys Thr Gly Gly Thr Cys Ala Ala Cys Gly Thr Gly Gly Ala Cys
785                 790                 795                 800

Cys Thr Gly Gly Ala Thr Gly Ala Cys Cys Gly Thr Gly Thr Thr Thr
                805                 810                 815

Cys Thr Gly Ala Gly Cys Ala Ala Thr Ala Ala Ala Thr Gly Ala Cys
            820                 825                 830

Thr Thr Ala Ala Ala Cys Cys Ala Gly Gly Thr Ala Thr Gly Gly Cys
        835                 840                 845

Thr Gly Cys Cys Gly Ala Thr Gly Gly Thr Thr Ala Thr Cys Thr Thr
    850                 855                 860

Cys Cys Ala Gly Ala Thr Thr Gly Gly Cys Thr Cys Gly Ala Gly Gly
865                 870                 875                 880

Ala Cys Ala Ala Cys Cys Thr Cys Thr Cys Thr Gly Ala Gly Gly Gly
                885                 890                 895

Cys Ala Thr Thr Cys Gly Cys Gly Ala Gly Thr Gly Gly Thr Gly Gly
            900                 905                 910

Gly Ala Cys Thr Thr Gly Ala Ala Ala Cys Cys Thr Gly Gly Ala Gly
        915                 920                 925

Cys Cys Cys Cys Gly Ala Ala Ala Cys Cys Cys Ala Ala Ala Gly Cys
    930                 935                 940

Cys Ala Ala Cys Cys Ala Gly Cys Ala Ala Ala Ala Gly Cys Ala Gly
945                 950                 955                 960
```

```
Gly Ala Cys Gly Ala Cys Gly Gly Cys Cys Gly Gly Gly Gly Thr Cys
                965                 970                 975


Thr Gly Gly Thr Gly Cys Thr Thr Cys Cys Thr Gly Gly Cys Thr Ala
            980                 985                 990


Cys Ala Ala Gly Thr Ala Cys Cys  Thr Cys Gly Gly Ala  Cys Cys Cys
        995                 1000                 1005


Thr Thr  Cys Ala Ala Cys Gly  Gly Ala Cys Thr Cys  Gly Ala Cys
    1010                 1015                 1020


Ala Ala  Gly Gly Gly Ala Gly  Ala Gly Cys Cys Gly  Gly Thr Cys
    1025                 1030                 1035


Ala Ala  Cys Gly Ala Gly Gly  Cys Ala Gly Ala Cys  Gly Cys Cys
    1040                 1045                 1050


Gly Cys  Gly Gly Cys Cys Cys  Thr Cys Gly Ala Gly  Cys Ala Cys
    1055                 1060                 1065


Gly Ala  Cys Ala Ala Gly Gly  Cys Cys Thr Ala Cys  Gly Ala Cys
    1070                 1075                 1080


Ala Ala  Gly Cys Ala Gly Cys  Thr Cys Gly Ala Gly  Cys Ala Gly
    1085                 1090                 1095


Gly Gly  Gly Gly Ala Cys Ala  Ala Cys Cys Cys Gly  Thr Ala Cys
    1100                 1105                 1110


Cys Thr  Cys Ala Ala Gly Thr  Ala Cys Ala Ala Cys  Cys Ala Cys
    1115                 1120                 1125


Gly Cys  Cys Gly Ala Cys Gly  Cys Cys Gly Ala Gly  Thr Thr Thr
    1130                 1135                 1140


Cys Ala  Gly Gly Ala Gly Cys  Gly Thr Cys Thr Thr  Cys Ala Ala
    1145                 1150                 1155


Gly Ala  Ala Gly Ala Thr Ala  Cys Gly Thr Cys Thr  Thr Thr Thr
    1160                 1165                 1170


Gly Gly  Gly Gly Gly Cys Ala  Ala Cys Cys Thr Cys  Gly Gly Gly
    1175                 1180                 1185


Cys Gly  Ala Gly Cys Ala Gly  Thr Cys Thr Thr Cys  Cys Ala Gly
    1190                 1195                 1200


Gly Cys  Cys Ala Ala Gly Ala  Ala Gly Cys Gly Gly  Gly Thr Thr
    1205                 1210                 1215
```

```
Cys Thr  Cys Gly Ala Ala Cys  Cys Thr Cys Thr Cys  Gly Gly Thr
    1220                 1225                 1230

Cys Thr  Gly Gly Thr Thr Gly  Ala Gly Gly Ala Ala  Gly Gly Cys
    1235                 1240                 1245

Gly Cys  Thr Ala Ala Gly Ala  Cys Gly Gly Cys Thr  Cys Cys Thr
    1250                 1255                 1260

Gly Gly  Ala Ala Ala Gly Ala  Ala Gly Ala Gly Ala  Cys Cys Cys
    1265                 1270                 1275

Ala Thr  Ala Gly Ala Ala Thr  Cys Cys Cys Cys Cys  Gly Ala Cys
    1280                 1285                 1290

Thr Cys  Cys Thr Cys Cys Ala  Cys Gly Gly Gly Cys  Ala Thr Cys
    1295                 1300                 1305

Gly Gly  Cys Ala Ala Gly Ala  Ala Ala Gly Gly Cys  Cys Ala Gly
    1310                 1315                 1320

Cys Ala  Gly Cys Cys Cys Gly  Cys Thr Ala Ala Ala  Ala Ala Gly
    1325                 1330                 1335

Ala Ala  Gly Cys Thr Cys Ala  Ala Cys Thr Thr Thr  Gly Gly Gly
    1340                 1345                 1350

Cys Ala  Gly Ala Cys Thr Gly  Gly Cys Gly Ala Cys  Thr Cys Ala
    1355                 1360                 1365

Gly Ala  Gly Thr Cys Ala Gly  Thr Gly Cys Cys Cys  Gly Ala Cys
    1370                 1375                 1380

Cys Cys  Cys Cys Ala Ala Cys  Cys Thr Cys Thr Cys  Gly Gly Ala
    1385                 1390                 1395

Gly Ala  Ala Cys Cys Thr Cys  Cys Cys Gly Cys Cys  Gly Cys Gly
    1400                 1405                 1410

Cys Cys  Cys Thr Cys Ala Gly  Gly Thr Cys Thr Gly  Gly Gly Ala
    1415                 1420                 1425

Thr Cys  Thr Gly Gly Thr Ala  Cys Ala Ala Thr Gly  Gly Cys Thr
    1430                 1435                 1440

Gly Cys  Ala Gly Gly Cys Gly  Gly Thr Gly Gly Cys  Gly Cys Ala
    1445                 1450                 1455

Cys Cys  Ala Ala Thr Gly Gly  Cys Ala Gly Ala Cys  Ala Ala Thr
    1460                 1465                 1470
```

Ala Ala Cys Gly Ala Ala Gly Gly Cys Gly Cys Cys Gly Ala Cys
1475 1480 1485

Gly Gly Ala Gly Thr Gly Gly Gly Thr Ala Ala Thr Gly Cys Cys
1490 1495 1500

Thr Cys Cys Gly Gly Ala Ala Ala Thr Thr Gly Gly Cys Ala Thr
1505 1510 1515

Thr Gly Cys Gly Ala Thr Thr Cys Cys Ala Cys Ala Thr Gly Gly
1520 1525 1530

Cys Thr Gly Gly Gly Cys Gly Ala Cys Ala Gly Ala Gly Thr Cys
1535 1540 1545

Ala Thr Cys Ala Cys Cys Ala Cys Cys Ala Gly Cys Ala Cys Cys
1550 1555 1560

Cys Gly Cys Ala Cys Cys Thr Gly Gly Gly Cys Cys Cys Thr Gly
1565 1570 1575

Cys Cys Cys Ala Cys Cys Thr Ala Cys Ala Ala Cys Ala Ala Cys
1580 1585 1590

Cys Ala Cys Cys Thr Cys Thr Ala Cys Ala Ala Gly Cys Ala Gly
1595 1600 1605

Ala Thr Ala Thr Cys Ala Ala Gly Thr Cys Ala Gly Ala Gly Cys
1610 1615 1620

Gly Gly Gly Gly Cys Thr Ala Cys Cys Ala Ala Cys Gly Ala Cys
1625 1630 1635

Ala Ala Cys Cys Ala Cys Thr Thr Cys Thr Thr Cys Gly Gly Cys
1640 1645 1650

Thr Ala Cys Ala Gly Cys Ala Cys Cys Cys Cys Cys Thr Gly Gly
1655 1660 1665

Gly Gly Cys Thr Ala Thr Thr Thr Thr Gly Ala Cys Thr Thr Cys
1670 1675 1680

Ala Ala Cys Ala Gly Ala Thr Thr Cys Cys Ala Cys Thr Gly Cys
1685 1690 1695

Cys Ala Cys Thr Thr Cys Thr Cys Ala Cys Cys Ala Cys Gly Thr
1700 1705 1710

Gly Ala Cys Thr Gly Gly Cys Ala Gly Cys Gly Ala Cys Thr Cys
1715 1720 1725

```
Ala Thr  Cys Ala Ala Cys Ala  Ala Cys Ala Ala Cys  Thr Gly Gly
    1730                 1735                 1740


Gly Gly  Ala Thr Thr Cys Cys  Gly Gly Cys Cys Cys  Ala Gly Ala
    1745                 1750                 1755


Ala Ala  Gly Cys Thr Gly Cys  Gly Gly Thr Thr Cys  Ala Ala Gly
    1760                 1765                 1770


Thr Thr  Gly Thr Thr Cys Ala  Ala Cys Ala Thr Cys  Cys Ala Gly
    1775                 1780                 1785


Gly Thr  Cys Ala Ala Gly Gly  Ala Gly Gly Thr Cys  Ala Cys Gly
    1790                 1795                 1800


Ala Cys  Gly Ala Ala Cys Gly  Ala Cys Gly Gly Cys  Gly Thr Thr
    1805                 1810                 1815


Ala Cys  Gly Ala Cys Cys Ala  Thr Cys Gly Cys Thr  Ala Ala Thr
    1820                 1825                 1830


Ala Ala  Cys Cys Thr Thr Ala  Cys Cys Ala Gly Cys  Ala Cys Gly
    1835                 1840                 1845


Ala Thr  Thr Cys Ala Gly Gly  Thr Cys Thr Thr Cys  Thr Cys Gly
    1850                 1855                 1860


Gly Ala  Cys Thr Cys Gly Gly  Ala Gly Thr Ala Cys  Cys Ala Ala
    1865                 1870                 1875


Cys Thr  Gly Cys Cys Gly Thr  Ala Cys Gly Thr Cys  Cys Thr Cys
    1880                 1885                 1890


Gly Gly  Cys Thr Cys Thr Gly  Cys Gly Cys Ala Cys  Cys Ala Gly
    1895                 1900                 1905


Gly Gly  Cys Thr Gly Cys Cys  Thr Cys Cys Cys Thr  Cys Cys Gly
    1910                 1915                 1920


Thr Thr  Cys Cys Cys Thr Gly  Cys Gly Gly Ala Cys  Gly Thr Gly
    1925                 1930                 1935


Thr Thr  Cys Ala Thr Gly Ala  Thr Thr Cys Cys Thr  Cys Ala Gly
    1940                 1945                 1950


Thr Ala  Cys Gly Gly Ala Thr  Ala Thr Cys Thr Gly  Ala Cys Thr
    1955                 1960                 1965


Cys Thr  Ala Ala Ala Cys Ala  Ala Cys Gly Gly Cys  Ala Gly Thr
    1970                 1975                 1980
```

```
Cys Ala  Gly Thr Cys Thr Gly  Thr Gly Gly Gly Ala  Cys Gly Thr
    1985                 1990                 1995


Thr Cys  Cys Thr Cys Cys Thr  Thr Cys Thr Ala Cys  Thr Gly Cys
    2000                 2005                 2010


Cys Thr  Gly Gly Ala Gly Thr  Ala Cys Thr Thr Thr  Cys Cys Thr
    2015                 2020                 2025


Thr Cys  Thr Cys Ala Gly Ala  Thr Gly Cys Thr Gly  Ala Gly Ala
    2030                 2035                 2040


Ala Cys  Gly Gly Gly Cys Ala  Ala Thr Ala Ala Cys  Thr Thr Thr
    2045                 2050                 2055


Gly Ala  Ala Thr Thr Cys Ala  Gly Cys Thr Ala Cys  Ala Cys Cys
    2060                 2065                 2070


Thr Thr  Thr Gly Ala Gly Gly  Ala Ala Gly Thr Gly  Cys Cys Thr
    2075                 2080                 2085


Thr Thr  Cys Cys Ala Cys Ala  Gly Cys Ala Gly Cys  Thr Ala Thr
    2090                 2095                 2100


Gly Cys  Gly Cys Ala Cys Ala  Gly Cys Cys Ala Gly  Ala Gly Cys
    2105                 2110                 2115


Cys Thr  Gly Gly Ala Cys Cys  Gly Gly Cys Thr Gly  Ala Thr Gly
    2120                 2125                 2130


Ala Ala  Thr Cys Cys Cys Cys  Thr Cys Ala Thr Cys  Gly Ala Cys
    2135                 2140                 2145


Cys Ala  Gly Thr Ala Cys Cys  Thr Gly Thr Ala Cys  Thr Ala Cys
    2150                 2155                 2160


Cys Thr  Gly Gly Cys Cys Cys  Gly Gly Ala Cys Cys  Cys Ala Gly
    2165                 2170                 2175


Ala Gly  Cys Ala Cys Thr Ala  Cys Gly Gly Gly Gly  Thr Cys Cys
    2180                 2185                 2190


Ala Cys  Ala Ala Gly Gly Gly  Ala Gly Cys Thr Gly  Cys Ala Gly
    2195                 2200                 2205


Thr Thr  Cys Cys Ala Thr Cys  Ala Gly Gly Cys Thr  Gly Gly Gly
    2210                 2215                 2220


Cys Cys  Cys Ala Ala Cys Ala  Cys Cys Ala Thr Gly  Gly Cys Cys
    2225                 2230                 2235
```

```
Gly Ala  Gly Cys Ala Ala Thr  Cys Ala Ala Ala Gly  Ala Ala Cys
    2240                 2245                 2250

Thr Gly  Gly Cys Thr Gly Cys  Cys Cys Gly Gly Ala  Cys Cys Cys
    2255                 2260                 2265

Thr Gly  Thr Thr Ala Thr Cys  Gly Gly Cys Ala Gly  Cys Ala Gly
    2270                 2275                 2280

Ala Gly  Ala Cys Thr Gly Thr  Cys Ala Ala Ala Ala  Ala Ala Cys
    2285                 2290                 2295

Ala Thr  Ala Gly Ala Cys Ala  Gly Cys Ala Ala Cys  Ala Ala Cys
    2300                 2305                 2310

Ala Ala  Cys Ala Gly Thr Ala  Ala Cys Thr Thr Thr  Gly Cys Cys
    2315                 2320                 2325

Thr Gly  Gly Ala Cys Cys Gly  Gly Gly Gly Cys Cys  Ala Cys Thr
    2330                 2335                 2340

Ala Ala  Ala Thr Ala Cys Cys  Ala Thr Cys Thr Gly  Ala Ala Thr
    2345                 2350                 2355

Gly Gly  Thr Ala Gly Ala Ala  Ala Thr Thr Cys Ala  Thr Thr Ala
    2360                 2365                 2370

Ala Cys  Cys Ala Ala Cys Cys  Cys Gly Gly Gly Cys  Gly Thr Ala
    2375                 2380                 2385

Gly Cys  Cys Ala Thr Gly Gly  Cys Cys Ala Cys Cys  Ala Ala Cys
    2390                 2395                 2400

Ala Ala  Gly Gly Ala Cys Gly  Ala Cys Gly Ala Gly  Gly Ala Cys
    2405                 2410                 2415

Cys Ala  Gly Thr Thr Cys Thr  Thr Thr Cys Cys Cys  Ala Thr Cys
    2420                 2425                 2430

Ala Ala  Cys Gly Gly Ala Gly  Thr Gly Cys Thr Gly  Gly Thr Thr
    2435                 2440                 2445

Thr Thr  Thr Gly Gly Cys Gly  Ala Ala Ala Cys Gly  Gly Gly Gly
    2450                 2455                 2460

Gly Cys  Thr Gly Cys Cys Ala  Ala Cys Ala Ala Gly  Ala Cys Ala
    2465                 2470                 2475

Ala Cys  Gly Cys Thr Gly Gly  Ala Ala Ala Ala Cys  Gly Thr Gly
    2480                 2485                 2490
```

Cys Thr Ala Ala Thr Gly Ala Cys Cys Ala Gly Cys Gly Ala Gly
2495 2500 2505

Gly Ala Gly Gly Ala Gly Ala Thr Cys Ala Ala Ala Ala Cys Cys
2510 2515 2520

Ala Cys Cys Ala Ala Thr Cys Cys Cys Gly Thr Gly Gly Cys Thr
2525 2530 2535

Ala Cys Ala Gly Ala Ala Gly Ala Ala Thr Ala Cys Gly Gly Thr
2540 2545 2550

Gly Thr Gly Gly Thr Cys Thr Cys Cys Ala Gly Cys Ala Ala Cys
2555 2560 2565

Cys Thr Gly Cys Ala Ala Thr Cys Gly Thr Cys Thr Ala Cys Gly
2570 2575 2580

Gly Cys Cys Gly Gly Ala Cys Cys Cys Cys Ala Gly Ala Cys Ala
2585 2590 2595

Cys Ala Gly Ala Cys Thr Gly Thr Cys Ala Ala Cys Ala Gly Cys
2600 2605 2610

Cys Ala Gly Gly Gly Gly Gly Cys Thr Cys Thr Gly Cys Cys Cys
2615 2620 2625

Gly Gly Cys Ala Thr Gly Gly Thr Cys Thr Gly Gly Cys Ala Gly
2630 2635 2640

Ala Ala Cys Cys Gly Gly Gly Ala Cys Gly Thr Gly Thr Ala Cys
2645 2650 2655

Cys Thr Gly Cys Ala Gly Gly Gly Thr Cys Cys Cys Ala Thr Cys
2660 2665 2670

Thr Gly Gly Gly Cys Cys Ala Ala Ala Ala Thr Thr Cys Cys Thr
2675 2680 2685

Cys Ala Cys Ala Cys Gly Gly Ala Cys Gly Gly Cys Ala Ala Cys
2690 2695 2700

Thr Thr Thr Cys Ala Cys Cys Cys Gly Thr Cys Thr Cys Cys Cys
2705 2710 2715

Cys Thr Gly Ala Thr Gly Gly Gly Cys Gly Gly Ala Thr Thr Thr
2720 2725 2730

Gly Gly Ala Cys Thr Cys Ala Ala Ala Cys Ala Cys Cys Cys Gly
2735 2740 2745

Cys Cys Thr Cys Cys Thr Cys Ala Ala Ala Thr Thr Cys Thr Cys
2750 2755 2760

Ala Thr Cys Ala Ala Ala Ala Ala Cys Ala Cys Cys Cys Cys Gly
2765 2770 2775

Gly Thr Ala Cys Cys Thr Gly Cys Thr Ala Ala Thr Cys Cys Thr
2780 2785 2790

Cys Cys Ala Gly Ala Gly Gly Thr Gly Thr Thr Thr Ala Cys Thr
2795 2800 2805

Cys Cys Thr Gly Cys Cys Ala Ala Gly Thr Thr Thr Gly Cys Cys
2810 2815 2820

Thr Cys Ala Thr Thr Thr Ala Thr Cys Ala Cys Gly Cys Ala Gly
2825 2830 2835

Thr Ala Cys Ala Gly Cys Ala Cys Cys Gly Gly Cys Cys Ala Gly
2840 2845 2850

Gly Thr Cys Ala Gly Cys Gly Thr Gly Gly Ala Gly Ala Thr Cys
2855 2860 2865

Gly Ala Gly Thr Gly Gly Gly Ala Ala Cys Thr Gly Cys Ala Gly
2870 2875 2880

Ala Ala Ala Gly Ala Ala Ala Ala Cys Ala Gly Cys Ala Ala Ala
2885 2890 2895

Cys Gly Cys Thr Gly Gly Ala Ala Thr Cys Cys Ala Gly Ala Gly
2900 2905 2910

Ala Thr Thr Cys Ala Gly Thr Ala Cys Ala Cys Cys Thr Cys Ala
2915 2920 2925

Ala Ala Thr Thr Ala Thr Gly Cys Cys Ala Ala Gly Thr Cys Thr
2930 2935 2940

Ala Ala Thr Ala Ala Thr Gly Thr Gly Gly Ala Ala Thr Thr Thr
2945 2950 2955

Gly Cys Thr Gly Thr Cys Ala Ala Cys Ala Ala Cys Gly Ala Ala
2960 2965 2970

Gly Gly Gly Gly Thr Thr Thr Ala Thr Ala Cys Thr Gly Ala Gly
2975 2980 2985

Cys Cys Thr Cys Gly Cys Cys Cys Cys Ala Thr Thr Gly Gly Cys
2990 2995 3000

Ala Cys Cys Cys Gly Thr Thr Ala Cys Cys Thr Cys Ala Cys Cys
3005 3010 3015

Cys Gly Thr Ala Ala Cys Cys Thr Gly Thr Ala Ala Thr Thr Gly
3020 3025 3030

Cys Cys Thr Gly Thr Thr Ala Ala Thr Cys Ala Ala Thr Ala Ala
3035 3040 3045

Ala Cys Cys Gly Gly Thr Thr Ala Ala Thr Thr Cys Gly Thr Thr
3050 3055 3060

Thr Cys Ala Gly Thr Thr Gly Ala Ala Cys Thr Thr Thr Gly Gly
3065 3070 3075

Thr Cys Thr Cys Thr Gly Cys Gly Ala Ala Gly Gly Gly Cys Gly
3080 3085 3090

Ala Ala Thr Thr Cys
3095

<210> 90
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 90
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415
```

```
His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Glu Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685
```

```
Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 91
<211> 2495
<212> DNA
<213> Adeno-associated virus

<400> 91
gaattcgccc tttctacggc tgcgtcaact agaccaatga gaactttccc ttcaacgatt        60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt       120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg       180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt       240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac       360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac       480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt       540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct       660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag       720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac       780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct       840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc       900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc       960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc      1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc      1080

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg      1140

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg      1200

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg      1260

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg      1320

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt      1380

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga      1440
```

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1500

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1560

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1620

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1680

agactgtcaa aaaacataga cagcaacaac accagtaact ttgcctggac cggggccact 1740

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1800

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

accaatcccg tggctacaga acagtacggt gtggtctcca gcaacctgca atcgtctacg 1980

gccggacccc agacacagac tgtcaacagc cagggggctc tgcccggcat ggtctggcag 2040

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 2100

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 2160

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 2220

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2280

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2340

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2400

acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcgtt 2460

tcagttgaac tttggtctct gcgaagggcg aattc 2495

<210> 92
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 92
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
```

370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Thr Ser Asn Phe Ala Trp
485 490 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
515 520 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
530 535 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545 550 555 560

Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ser Ser Asn Leu
565 570 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro

```
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 93
<211> 2504
<212> DNA
<213> Adeno-associated virus

<400> 93
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt       60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt      120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg      180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt      240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc      300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt      540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag      720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac      780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct      840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc      900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc      960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc     1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc     1080

aacagattcc actgccactt ctcatcacgt gactggcagc gactcatcaa caacaactgg     1140

ggattccggc ccaagagact caacttcaag ctcttcaaca tccaggtcaa ggaggtcacg     1200
```

```
cagaatgaag gcaccaagac catcgccaat aaccttacca gcacgattca ggtctttacg     1260

gactcggaat accggctccc gtacgtcctc ggctctgcgc accagggctg cctgcctccg     1320

ttcccggcgg acgtcttcat gattcctcag tacgggtacc tgactctgaa caacggcagt     1380

caggccgtgg gccgttcctc cttctactgc ctggagtact ttccttctca aatgctgaga     1440

acgggcaaca actttgagtt cagctaccag tttgaggacg tgccttttca cagcagctac     1500

gcgcacagcc aaagcctgga ccggctgatg aacccccctca tcgaccagta cctgtactac    1560

ctgtctcgga ctcagtccac gggaggtacc gcaggaactc agcagttgct attttctcag     1620

gccgggccta ataacatgtc ggctcaggcc aaaaactggc tacccgggcc ctgctaccgg     1680

cagcaacgcg tctccacgac actgtcgcaa aataacaaca gcaactttgc ttggaccggt     1740

gccaccaagt atcatctgaa tggcagagac tctctggtaa atcccggtgt cgctatggca     1800

acgcacaagg acgacgaaga gcgatttttt ccatccagcg gagtcttgat gtttgggaaa     1860

cagggagctg gaaaagacaa cgtggactat agcagcgtta tgctaaccag tgaggaagaa     1920

atcaaaacca ccaacccagt ggccacagaa cagtacggcg tggtggccga taacctgcaa     1980

cagcaaaacg ccgctcctat tgtaggggcc gtcaacagtc aaggagcctt acctggcatg     2040

gtctggcaga accgggacgt gtacctgcag ggtcctatct gggccaagat tcctcacacg     2100

gacggcaact ttcatccttc gccgctgatg ggaggctttg gactgaaaca cccgcctcct     2160

cagatcctga ttaagaatac acctgttccc gcggatcctc caactacctt cagtcaagcc     2220

aagccggcgt cgttcatcac gcagtacagc accggacagg tcagcgtgga aattgaatgg     2280

gagctgcaga aagagaacag caagcgctgg aacccagaga ttcagtatac ttccaactac     2340

tacaaatcta caaatgtgga ctttgctgtc aatactgagg gtacttattc agagcctcgc     2400

cccattggca cccgttacct cacccgtaac ctgtaattgc ctgttaatca ataaaccggt     2460

taattcgttt cagttgaact ttggtctctg cgaagggcga attc                     2504


<210> 94
<211> 731
<212> PRT
<213> Adeno-associated virus

<400> 94
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190


Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205


Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220


His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255


Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270


Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285


Ser Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300


Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320


Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335
```

Gln Val Phe Thr Asp Ser Glu Tyr Arg Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
435 440 445

Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
450 455 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465 470 475 480

Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
485 490 495

Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
500 505 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
515 520 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
530 535 540

Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545 550 555 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
565 570 575

Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
580 585 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
595 600 605

```
Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620


His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640


Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
                645                 650                 655


Phe Ser Gln Ala Lys Pro Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670


Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685


Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
    690                 695                 700


Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705                 710                 715                 720


Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210> 95
<211> 3128
<212> DNA
<213> Adeno-associated virus

<400> 95
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt       60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt      120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg      180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg      240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg      300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt      360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg      420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct      480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg      540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca      600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact      660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc      720

ggaaactctg tgccattcat catctgctag ggcgggctcc cgagattgct tgctcggcct      780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca      840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt      900
```

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

accccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

```
gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact     3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa     3060

ttgcctgtta atcaataaac cggctaattc gtttcagttg aactttggtc tctgcgaagg     3120

gcgaattc                                                              3128


<210> 96
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 96
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
```

210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser

```
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 97
```

<211> 3084
<212> DNA
<213> Adeno-associated virus

<400> 97
gaattcgccc tttctacggc tgcatcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac caagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gcggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacgtgcga gaaaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact 660

gctcagaatg tttccccggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc 720

agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc 1320

atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac 1380

tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca tctctacaag 1620

caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680

accccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtgtt tacggactcg gaataccagc tcccgtacgt ccccggctct 1920

```
gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg     1980

tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa     2040

tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag     2100

gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccggct gatgaaccct     2160

ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt     2220

actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtcggctca ggccaagaac     2280

tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac     2340

aacagcaatt ttgcttggac cggtgccacc aagtatcacc tgaatggcag agactccctg     2400

gttaatcccg gcgttgccat ggctacccac aaggacgacg aggagcgctt cttcccgtca     2460

agcggagttc taatgtttgg caagcagggg gctggaaaag acaatgtgga ctacagcagc     2520

gtgatgctca ccagcgaaga agaaattaaa actactaacc cagtggctac agagcagtat     2580

ggtgtggtgg cagacaacct gcagcagacc aacggagctc ccattgtggg aactgtcaac     2640

agccaggggg ccttacctgg tatggtctgg caaaaccggg acgtgtacct gcagggcccc     2700

atctgggcca aaattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc     2760

tttggactga aacacccgcc tcctcagatc ctggtgaaaa acactcctgt tcctgcggat     2820

cctccgacca ccttcagcca ggccaagctg gcttctttta tcacgcagta cagcaccgga     2880

caggtcagcg tggaaatcga atgggagctg cagaaagaaa acagcaagcg ctggaaccca     2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact     3000

gagggtactt attcagagcc tcgccccatt ggcactcgtt atctcacccg taatctgtaa     3060

ttgcttgtta atcaataaac cggt                                            3084


<210> 98
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 98
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350
```

```
Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590


Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 99
<211> 3123
<212> DNA
<213> Adeno-associated virus

<400> 99
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc        60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc       120

aaggccattc tcggcggcag caaggtgcgc gtggaccaaa agtgcaagtc gtccgcccag       180

atcgacccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg       240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa gttcgaactc       300

acccgccgtc tggagcacga ctttggcaag gtgaccaagc aggaagtcaa agagttcttc       360

cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tctacgtcag aaagggcgga       420

gccagcaaaa gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcctgcccc       480

tcagtcgcgg atccatcgac gtcagacgcg gaaggagctc cggtggactt tgccgacagg       540

taccaaaaca aatgttctcg tcacgcgggc atgctccaga tgctgtttcc ctgcaaaacg       600

tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acggggtcag agactgctca       660

gaatgtttcc ccggtgcatc agaatctcaa ccggtcgtca gaaaaaaaac gtatcagaaa       720

ctgtgtgcca ttcatcatct gctggggcgg gcacccgaga ttgcttgctc ggcctgcgat       780

ctggtcaacg tggacctgga cgactgtgtt tctgagcaat aaatgactta aaccaggtat       840

ggctgccgat ggttatcttc cagattggct tgaggacaac ctctctgagg gcattcgcga       900
```

gtggtgggac ctgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga 960

cggccggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 1020

gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cacgacaagg cctacgacca 1080

gcagctcaaa gcgggtgaca atccgtacct gcggtataac cacgccgacg ccgagtttca 1140

ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc 1200

caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggctcctgg 1260

aaagaagaga ccggtagagc catcacctca gcgttccccc gactcctcca cgggcatcgg 1320

caagaaaggc caccagcccg cgagaaagag actgaacttt gggcagactg gcgactcgga 1380

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 1440

tggtacaatg gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg 1500

agtgggtagt tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 1560

caccaccagc acccgaacct gggccctgcc cacctacaac aaccatctct acaagcaaat 1620

ctccaacggg acatcgggag gaagcactaa cgacaacacc tactttggct acagcacccc 1680

ctgggggtat tttgacttca acagattcca ctgccacttc tcaccacgtg actggcagcg 1740

actcatcaac aataactggg gattccggcc caagagactc aacttcaagc tcttcaacat 1800

ccaggtcaag gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag 1860

cacgattcag gtgtttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca 1920

ccagggctgc ctccctccgt tcccggcgga cgtcttcatg attcctcagt acgggtatct 1980

gaccctaaac aatggcagtc aggctgtggg ccgttcctcc ttctactgcc tggaatactt 2040

cccttctcaa atgctgagga cgggcaacaa ctttgaattc agctacacct tcgaggacgt 2100

gcctttccac agcagctacg cgcacagcca gagcctggac cggctgatga accctctcat 2160

cgaccagtac ctgtattact tatccagaac tcagtccaca ggaggaactc aaggtactca 2220

gcaattgtta ttttctcaag ccgggcccgc aaacatgtcg gctcaggcca agaactggct 2280

acctggaccg tgttaccgtc agcaacgagt ttccacgaca ctgtcgcaaa acaacaacag 2340

caattttgct tggaccggtg ccaccaagta tcacctgaat ggcagagact ccctggttaa 2400

tcccggcgtt gccatggcta cccacaagga cgacgaggag cgcttcttcc cgtcaagcgg 2460

agttctaatg tttggcaagc agggggctgg aaaagacaat gtggactaca gcagcgtgat 2520

gctcaccagc gaagaagaaa ttaaaactac taacccagtg gctacagagc agtatggtgt 2580

ggtggcagac aacctgcagc agaccaacgg agctcccatt gtgggaactg tcaacagcca 2640

gggggcctta cctggtatgg tctggcaaaa ccgggacgtg tacctgcagg gccccatctg 2700

ggccaaaatt cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg 2760

actgaaacac ccgcctcctc agatcctggt gaaaaacact cctgttcctg cggatcctcc 2820

gaccaccttc agccaggcca agctggcttc ttttatcacg cagtacagca ccggacaggt 2880

cagcgtggaa atcgaatggg agctgcagaa agaaaacagc aagcgctgga acccagagat 2940

```
tcagtatact tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg     3000

tacttattca gagcctcgcc ccattggcac tcgttatctc acccgtaatc tgtaattgct     3060

tgttaatcaa taaaccggtt aattcgtttc agttgaactt tggtctctgc gaagggcgaa     3120

ttc                                                                   3123


<210> 100
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 100
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
```

210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser

```
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 101
```

<211> 3122
<212> DNA
<213> Adeno-associated virus

<400> 101
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag cgccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaagcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataatcacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagactggt agagcagtcg ccacaagagc cagactcctc ctcgggcatc 1320

ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 1380

gagtcagtcc ccgacccaca acctctcgga gaacctccag cagccccctc aggtctggga 1440

cctaatacaa tggcttcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 1500

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 1560

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 1620

atctccaacg gcacctcggg aggaagcacc aacgacaaca cctattttgg ctacagcacc 1680

ccctgggggt attttgactt caacagattc cactgtcact tttcaccacg tgactggcaa 1740

cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac 1800

atccaggtca aggaagtcac gacgaacgaa ggcaccaaga ccatcgccaa taatctcacc 1860

agcaccgtgc aggtctttac ggactcggag taccagttac cgtacgtgct aggatccgct 1920 caccagggat gtctgcctcc gttcccggcg gacgtcttca cggttcctca gtacggctat 1980

ttaactttaa acaatggaag ccaagccctg ggacgttcct ccttctactg tctggagtat 2040

ttcccatcgc agatgctgag aaccggcaac aactttcagt tcagctacac cttcgaggac 2100

gtgcctttcc acagcagcta cgcgcacagc cagagcctgg acaggctgat gaatcccctc 2160

atcgaccagt acctgtacta cctggtcaga acgcaaacga ctggaactgg agggacgcag 2220

actctggcat tcagccaagc gggtcctagc tcaatggcca accaggctag aaattgggtg 2280

cccggacctt gctaccggca gcagcgcgtc tccacgacaa ccaaccagaa caacaacagc 2340

aactttgcct ggacgggagc tgccaagttt aagctgaacg gccgagactc tctaatgaat 2400

ccgggcgtgg caatggcttc ccacaaggat gacgacgacc gcttcttccc ttcgagcggg 2460

gtcctgattt ttggcaagca aggagccggg aacgatggag tggattacag ccaagtgctg 2520

attacagatg aggaagaaat caaggctacc aaccccgtgg ccacagaaga atatggagca 2580

gtggccatca acaaccaggc cgccaatacg caggcgcaga ccggactcgt gcacaaccag 2640

ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg 2700

gccaaaattc ctcacacgga cggcaacttt cacccgtctc ccctgatggg cggctttgga 2760

ctgaagcacc cgcctcctca aattctcatc aagaacacac cggttccagc ggacccgccg 2820

cttaccttca accaggccaa gctgaactct ttcatcacgc agtacagcac cggacaggtc 2880

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt 2940

caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggaagga 3000

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 102
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 102
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Leu Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 103
<211> 3117
<212> DNA
<213> Adeno-associated virus

<400> 103
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc        60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc       120

aaggccattc tcggcggcag caaggtgcgt gtggaccaaa agtgcaagtc ttccgcccag       180

atcgatccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg       240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa atttgaactc       300

acccgccgtc tggagcatga ctttggcaag gtgacgaagc aggaagtcaa agagttcttc       360

cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tccacgtcag aaagggtgga       420

gccaacaaga gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcctgcccc       480

tcagtcgcgg atccatcgac gtcagacgcg gaaggagctc cggtggactt tgccgacagg       540

taccaaaaca aatgttctcg tcacgcgggc atgcttcaga tgctgtttcc ctgcaagaca       600

tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acgggaccag agactgttca       660

gaatgtttcc ccggcgtgtc agaatctcaa ccggtcgtca gaaagaggac gtatcggaaa       720

ctctgtgcga ttcatcatct gctggggcgg gctcccgaga ttgcttgctc ggcctgcgat       780

ctggtcaacg tggacctgga tgactgtgtt tctgagcaat aaatgactta aaccaggtat       840

ggctgccgat ggttatcttc cagattggct cgaggacaac ctctctgagg gcattcgcga       900

gtggtgggac ttgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga       960
```

cggccggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 1020

gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cacgacaaag cctacgacca 1080

gcagctcaaa gcgggtgaca atccgtacct gcggtataat cacgccgacg ccgagtttca 1140

ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc 1200

caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggctcctgg 1260

aaagaagaga ccggtagagc agtcgccaca agagccagac tcctcctcgg gcatcggcaa 1320

gacaggccag cagcccgcta aaaagagact caattttggt cagactggcg actcagagtc 1380

agtccccgac ccacaacctc tcggagaacc tccagcagcc ccctcaggtc tgggacctaa 1440

tacaatggct tcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt 1500

gggtaattcc tcgggaaatt ggcattgcga ttccacatgg ctgggggaca gagtcatcac 1560

caccagcacc cgaacctggg ccctgcccac ctacaacaac cacctctaca agcaaatctc 1620

caacggcacc tcgggaggaa gcaccaacga caacacctat tttggctaca gcaccccctg 1680

ggggtatttt gacttcaaca gattccactg tcacttttca ccacgtgact ggcaacgact 1740

catcaacaac aattggggat tccggcccaa aagactcaac ttcaagctgt tcaacatcca 1800

ggtcaaggaa gtcacgacga acgaaggcac caagaccatc gccaataatc tcaccagcac 1860

cgtgcgggtc tttacggact cggagtacca gttaccgtac gtgctaggat ccgctcacca 1920

gggatgtctg cctccgttcc cggcggacgt cttcatggtt cctcagtacg gctatttaac 1980

tttaaacaat ggaagccaag ccctgggacg ttcctccttc tactgtctgg agtatttccc 2040

atcgcagatg ctgagaaccg gcaacaactt tcagttcagc tacaccttcg aggacgtgcc 2100

tttccacagc agctacgcgc acagccagag cctggacagg ctgatgaatc ccctcatcga 2160

ccagtacctg tactacctgg tcagaacgca aacgactgga actggaggga cgcagactct 2220

ggcattcagc caagcgggtc ctagctcaat ggccaaccag gctagaaatt gggtgcccgg 2280

accttgctac cggcagcagc gcgtctccac gacaaccaac cagagcaaca acagcaactt 2340

tgcctggacg ggagctgcca agtttaagct gaacggccga gactctctaa tgaatccggg 2400

cgtggcaatg gcttcccaca aggatgacga cgaccgcttc ttcccttcga gcggggtcct 2460

gatttttggc aagcaaggag ccgggaacga tggagtggat tacagccaag tgctgattac 2520

agatgaggaa gaaatcaagg ctaccaaccc cgtggccaca gaagaatatg gagcagtggc 2580

catcaacaac caggccgcca atacgcaggc gcagaccgga ctcgtgcaca accagggggt 2640

gattcccggc atggtgtggc agaatagaga cgtgtacctg cagggtccca tctgggccaa 2700

aattcctcac acggacggca actttcaccc gtctcccctg atgggcggct ttggactgaa 2760

gcacccgcct cctcaaattc tcatcaagaa cacaccggtt ccagcggacc cgccgcttac 2820

cttcaaccag gccaagctga actctttcat cacgcagtac agcaccggac aggtcagcgt 2880

ggaaatcgag tgggagctgc agaaagaaaa cagcaaacgc tggaatccag agattcaata 2940

cacttccaac tactacaaat ctacaaatgt ggactttgct gtcaacacgg aaggagttta 3000 tagcgagcct cgccccattg gcacccgtta cctcacccgc aacctgtaat tacatgttaa 3060

tcaataaacc ggttaattcg tttcagttga actttggtct ctgcgaaggg cgaattc 3117

<210> 104
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 104
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Arg Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Ser
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
```

```
            500                 505                 510


Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590


Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 105
<211> 3121
<212> DNA
<213> Adeno-associated virus

<400> 105
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgattg       60

cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc      120
```

cgccaaggcc attctcggcg gcagcaaggt gcgtgtggac caaaagtgca agtcttccgc 180

ccagatcgat cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 300

actcacccgc cgtctggagc atgactttgg caaggtgacg aagcaggaag tcaaagagtt 360

cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttccacg tcagaaaggg 420

tggcgccaac aagagacccg cccccgatga cgcggatata agcgagccca agcgggcctg 480

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600

gacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660

ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720

gaaactctgt gcgattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 900

gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 1020

acaaggggga gcccgtcaac gcggcggacg cagcggccct cgagcacgac aaagcctacg 1080

accagcagct caaagcgggt gacaatccgt acctgcggta taatcacgcc gacgccgagt 1140

ttcaggagcg tctgcaagaa gatacgtcct ttgggggcaa cctcgggcga gcagtcttcc 1200

aggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc 1260

ctggaaagaa gagaccggta gagcagtcgc cacaagagcc agactcctcc tcgggcatcg 1320

gcaagacagg ccagcagccc gctaaaaaga gactcaattt tggtcagact ggcgactcag 1380

agtcagtccc cgacccacaa cctctcggag aacctccagc agccccctca ggtctgggac 1440

ctaatacaat ggcttcaggc ggtggcgctc caatggcaga caataacgaa ggcgccgacg 1500

gagtgggtaa ttcctcggga aattggcatt gcgattccac atggctgggg gacagagtca 1560

tcaccaccag cacccgaacc tgggccctgc ccacctacaa caaccacctc tacaagcaaa 1620

tctccaacgg cacctcggga ggaagcacca acgacaacac ctattttggc tacagcaccc 1680

cctgggggta ttttgacttc aacagattcc actgtcactt ttcaccacgt gactggcaac 1740

gactcatcaa caacaattgg ggattccggc ccaaaagact caacttcaag ctgttcaaca 1800

tccaggtcaa ggaagtcacg acgaacgaag gcaccaagac catcgccaat aatctcacca 1860

gcaccgtgca ggtctttacg gacttggagt accagttacc gtacgtgcta ggatccgctc 1920

accagggatg tctgcctccg ttcccggcgg acgtcttcat ggttcctcag tacggctatt 1980

taactttaaa caatggaagc caagccctgg gacgttcctc cttctactgt ctggagtatt 2040

tcccatcgca gatgccgaga accggcaaca actttcagtt cagctacacc ttcgaggacg 2100

tgcctttcca cagcagctac gcgcacagcc agagcctgga caggctgatg aatcccctca 2160

```
tcgaccagta cctgtactac ctggtcagaa cgcaaacgac tggaactgga gggacgcaga     2220

ctctggcatt cagccaagcg ggtcctagct caatggccaa ccaggctaga aattgggtgc     2280

ccggaccttg ctaccggcag cagcgcgtct ccacgacaac caaccagaac aacaacagca     2340

actttgcctg gacgggagct gccaagttta agctgaacgg ccgagactct ctaatgaatc     2400

cgggcgtggc aatggcttcc cacaaggatg acgacgaccg cttcttccct tcgagcgggg     2460

tcctgatttt tggcaagcaa ggagccggga acgatggagt ggattacagc caagtgctga     2520

ttacagatga ggaagaaatc aaggctacca accccgtggc cacagaagaa tatggagcag     2580

tggccatcaa caaccaggcc gccaatacgc aggcgcagac cggactcgtg cacaaccagg     2640

gggtgattcc cggcatggtg tggcagaata gagacgtgta cctgcagggt cccatctggg     2700

ccaaaattcc tcacacggac ggcaactttc acccgtctcc cctgatgggc ggctttggac     2760

tgaagcaccc gcctcctcaa attctcatca agaacacacc ggttccagcg gacccgccgc     2820

ttaccttcaa ccaggccaag ctgaactctt tcatcacgca gtacagcacc ggacaggtca     2880

gcgtggaaat cgagtgggag ctgcagaaag aaaacagcaa acgctggaat ccagagattc     2940

aatacacttc caactactac aaatctacaa atgtggactt tgctgtcaac acggaaggag     3000

tttatagcga gcctcgcccc attggcaccc gttacctcac ccgcaacctg taattacatg     3060

ttaatcaata aaccggttaa ttcgtttcag ttgaactttg gtctctgcga agggcgaatt     3120

c                                                                     3121
```

```
<210> 106
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 106
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Pro Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 107
<211> 3122
<212> DNA
<213> Adeno-associated virus

<400> 107
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagggt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtgcgagccc 420

aagcgggcct gcccctcagt cgcggatcca tcgacgtcag accagaaagg gtggagccaa 480

caagagaccc gcccccgatg acgcggatat aagcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaagcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataatcacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200 caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagcagtcg ccacaagagc cagactcctc ctcgggcatc 1320

ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 1380

gagtcagtcc ccgacccaca acctctcgga gaacctccag cagccccctc aggtctggga 1440

cctaatacaa tggcttcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 1500

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 1560

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 1620

atctccaacg gcacctcggg aggaagcacc aacgacaaca cctattttgg ctacagcacc 1680

ccctgggggt attttgactt caacagattc cactgtcact tttcaccacg tgactggcaa 1740

cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac 1800

atccaggtca aggaagtcac gacgaacgaa ggcaccaaga ccatcgccaa taatctcacc 1860

agcaccgtgc aggtctttac ggactcggag taccagttac cgtacgtgct aggatccgct 1920

caccagggat gtctgcctcc gttcccggcg gacgtcttca tggttcctca gtacggctat 1980

ttaactttaa acaatggaag ccaagccctg ggacgttcct ccttctactg tctggagtat 2040

ttcccatcgc agatgctgag aaccggcaac aactttcagt tcagctacac cttcgaggac 2100

gtgcctttcc acagcagcta cgcgcacagc cagagcctgg acaggctgat gaatcccctc 2160

atcgaccagt acctgtacta cctggtcaga acgcaaacga ctggaactgg agggacgcag 2220

actctggcat tcagccaagc gggtcctagc tcaatggcca accaggctag aaattgggtg 2280

cccggacctt gctaccggca gcagcgcgtc tccacgacaa ccaaccagaa caacaacagc 2340

aactttgcct ggacgggagc tgccaagttt aagctgaacg gccgagactc tctaatgaat 2400

ccgggcgtgg caatggcttc ccacaaggat gacgacgacc gcttcttccc ttcgagcggg 2460

gtcctgattt ttggcaagca aggagccggg aacgatggag tggattacag ccaagtgctg 2520

attacagatg aggaagaaat caaggctacc aaccccgtgg ccacagaaga atatggagca 2580

gtggccatca acaaccaggc cgccaatacg caggcgcaga ccggactcgt gcacaaccag 2640

ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg 2700

gccaaaattc ctcacacgga cggcaacttt cacccgtctc ccctgatggg cggctttgga 2760

ctgaagcacc cgcctcctca aattctcatc aagaacacac cggttccagc ggacccgccg 2820

cttaccttca accaggccaa gctgaactct ttcatcacgc agtacagcac cggacaggtc 2880

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt 2940

caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggagggg 3000

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 108

<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 108

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20              25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590


Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 109
<211> 2370
<212> DNA
<213> Adeno-associated virus

<400> 109
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt        60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt       120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg       180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg       240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg       300
```

aactcacccg ccgtctggag cacgactttg gcaaggtgac caagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gcggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagacgctg tttccctgca 600

aaacgtgcga gagaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact 660

gctcagaatg tttccccggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc 720

agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc 1320

atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac 1380

tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca tctctacaag 1620

caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680

accccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtgtt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa 2040

tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag 2100

gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccggct gatgaaccct 2160

ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt 2220

actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtyggctca ggccaagaac 2280

tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac 2340

```
aacagcaatt ttgctggacc ggtgccacca                                      2370


<210> 110
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 110
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 111
<211> 2205
<212> DNA
<213> Adeno-associated virus

<400> 111
```

atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atcccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg ggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc   2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact   2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa   2205

<210> 112
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 112
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1   5   10   15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20   25   30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50   55   60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65   70   75   80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115   120   125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130   135   140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145   150   155   160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165   170   175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180   185   190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195   200   205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210   215   220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225   230   235   240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245   250   255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260   265   270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275   280   285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290   295   300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305   310   315   320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325   330   335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340   345   350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355   360   365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370   375   380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385   390   395   400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405   410   415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420   425   430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435   440   445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450   455   460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465   470   475   480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485   490   495

```
Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510


Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525


Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540


Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560


Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575


Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590


Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605


Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620


Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640


Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655


Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670


Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685


Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700


Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720


Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 113
<211> 3128
<212> DNA
<213> Adeno-associated virus

<400> 113
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt       60
```

gcgtcgacaa gatgttgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagccgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgcg ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc 1680

accccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100 gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact gtaaatcccg gtgtcgctat ggcaacccac aaggacgacg aagagcgatt 2400

ttgcctggac cggtgccacc aagtatcatc tgaatggcag agactctctg ttttccgtcc 2460

agcggagtct taatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaattaaa accaccaacc cagtggccac ggaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agctaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaaccca 2940

gagattcaat acacttccaa ctactacaaa tctacaaatg tggacttcgc tgttaacaca 3000

gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa 3060

ttgctcgtta atcaataaac cggttgattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 114
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 114
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

```
Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 115
<211> 3128
<212> DNA
<213> Adeno-associated virus

<400> 115
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt tgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

```
gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac      1080
gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag      1140
tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc      1200
caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct      1260
cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc      1320
atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac      1380
tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg      1440
ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc      1500
gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga      1560
gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag      1620
caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc      1680
acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg      1740
cagcgactca tcaacaacaa ctggggattc cggcccaaga gacccaactt caagctcttc      1800
aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt      1860
accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct      1920
gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg      1980
tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag      2040
tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag      2100
gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc      2160
ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga      2220
actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac      2280
tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac      2340
aacagcaact ttgcctggac cggtgccacc aagtatcatc tgaatggcag agactctctg      2400
gtaaatcccg gtgtcgctat ggcaacccac aaggacgacg aagagcgatt ttttccgtcc      2460
agcggagtct taatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc      2520
gttatgctaa ccagtgagga agaaattaaa accaccaacc cagtggccac agaacagtac      2580
ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac      2640
agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct      2700
atctgggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc      2760
tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat      2820
cctccaacta ccttcagtca agctaagctg gcgtcgttca tcacgcagta cagcaccgga      2880
caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaaccca      2940
gagattcaat acacttccaa ctactacaaa tctacaaatg tggactttgc tgttaacaca      3000
gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa      3060
```

ttgcttgtta atcaataaac cggttgattc gtttcagttg aactttggtc tctgcgaagg   3120

gcgaattc   3128

<210> 116
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 116
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195   200   205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210   215   220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val

225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Pro Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His

```
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu


<210> 117
<211> 738
<212> PRT
<213> Adeno-associated virus
```

```
<400> 117
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590


Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 118
<211> 2172
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 118
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag       60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa      120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga      180
```

```
ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag      240
cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag      300
gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc      360
aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc      420
ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc      480
aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc      540
ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca      600
ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc      660
gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc      720
agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc      780
aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc      840
cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg      900
tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc      960
accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag     1020
ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc     1080
tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc     1140
gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac     1200
aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt     1260
cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc     1320
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc     1380
tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg     1440
gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg     1500
agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc     1560
tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc     1620
acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc     1680
gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc     1740
gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac     1800
gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc     1860
tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac     1920
acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc     1980
cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc     2040
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac     2100
tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt     2160
acccgacccc tt                                                         2172
```

<210> 119
<211> 720
<212> PRT
<213> Adeno-associated virus

<400> 119

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240
```

```
Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510
```

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

<210> 120
<211> 724
<212> PRT
<213> Adeno-associated virus 5

<400> 120
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

```
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320
```

```
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595   600   605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610   615   620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625   630   635   640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645   650   655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660   665   670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675   680   685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690   695   700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705   710   715   720

Thr Arg Pro Leu

<210> 121
<211> 2175
<212> PRT
<213> Adeno-associated virus 5

<400> 121
Ala Thr Gly Thr Cys Thr Thr Thr Thr Gly Thr Thr Gly Ala Thr Cys
1   5   10   15

Ala Cys Cys Cys Thr Cys Cys Ala Gly Ala Thr Thr Gly Gly Thr Thr
            20   25   30

Gly Gly Ala Ala Gly Ala Ala Gly Thr Thr Gly Gly Thr Gly Ala Ala
        35   40   45

Gly Gly Thr Cys Thr Thr Cys Gly Cys Gly Ala Gly Thr Thr Thr Thr
    50   55   60

Thr Gly Gly Gly Cys Cys Thr Thr Gly Ala Ala Gly Cys Gly Gly Gly
65   70   75   80

Cys Cys Cys Ala Cys Cys Gly Ala Ala Ala Cys Cys Ala Ala Ala Ala
                85   90   95

```
Cys Cys Cys Ala Ala Thr Cys Ala Gly Cys Ala Gly Cys Ala Thr Cys
            100                 105                 110

Ala Ala Gly Ala Thr Cys Ala Ala Gly Cys Cys Cys Gly Thr Gly Gly
        115                 120                 125

Thr Cys Thr Thr Gly Thr Gly Cys Thr Gly Cys Cys Thr Gly Gly Thr
    130                 135                 140

Thr Ala Thr Ala Ala Cys Thr Ala Thr Cys Thr Cys Gly Gly Ala Cys
145                 150                 155                 160

Cys Cys Gly Gly Ala Ala Ala Cys Gly Gly Thr Cys Thr Cys Gly Ala
                165                 170                 175

Thr Cys Gly Ala Gly Gly Ala Gly Ala Gly Cys Cys Thr Gly Thr Cys
            180                 185                 190

Ala Ala Cys Ala Gly Gly Gly Cys Ala Gly Ala Cys Gly Ala Gly Gly
        195                 200                 205

Thr Cys Gly Cys Gly Cys Gly Ala Gly Ala Gly Cys Ala Cys Gly Ala
    210                 215                 220

Cys Ala Thr Cys Thr Cys Gly Thr Ala Cys Ala Ala Cys Gly Ala Gly
225                 230                 235                 240

Cys Ala Gly Cys Thr Thr Gly Ala Gly Gly Cys Gly Gly Gly Ala Gly
                245                 250                 255

Ala Cys Ala Ala Cys Cys Cys Cys Thr Ala Cys Cys Thr Cys Ala Ala
            260                 265                 270

Gly Thr Ala Cys Ala Ala Cys Cys Ala Cys Gly Cys Gly Gly Ala Cys
        275                 280                 285

Gly Cys Cys Gly Ala Gly Thr Thr Thr Cys Ala Gly Gly Ala Gly Ala
    290                 295                 300

Ala Gly Cys Thr Cys Gly Cys Cys Gly Ala Cys Gly Ala Cys Ala Cys
305                 310                 315                 320

Ala Thr Cys Cys Thr Thr Cys Gly Gly Gly Gly Gly Ala Ala Ala Cys
                325                 330                 335

Cys Thr Cys Gly Gly Ala Ala Ala Gly Gly Cys Ala Gly Thr Cys Thr
            340                 345                 350

Thr Thr Cys Ala Gly Gly Cys Cys Ala Ala Gly Ala Ala Ala Ala Gly
        355                 360                 365
```

```
Gly Gly Thr Thr Cys Thr Cys Gly Ala Ala Cys Cys Thr Thr Thr Thr
    370                 375                 380


Gly Gly Cys Cys Thr Gly Gly Thr Thr Gly Ala Ala Gly Ala Gly Gly
385                 390                 395                 400


Gly Thr Gly Cys Thr Ala Ala Gly Ala Cys Gly Gly Cys Cys Cys Cys
                405                 410                 415


Thr Ala Cys Cys Gly Gly Ala Ala Ala Gly Cys Gly Gly Ala Thr Ala
            420                 425                 430


Gly Ala Cys Gly Ala Cys Cys Ala Cys Thr Thr Thr Cys Cys Ala Ala
        435                 440                 445


Ala Ala Ala Gly Ala Ala Ala Gly Ala Ala Gly Gly Cys Thr Cys Gly
    450                 455                 460


Gly Ala Cys Cys Gly Ala Ala Gly Ala Gly Gly Ala Cys Thr Cys Cys
465                 470                 475                 480


Ala Ala Gly Cys Cys Thr Thr Cys Cys Ala Cys Cys Thr Cys Gly Thr
                485                 490                 495


Cys Ala Gly Ala Cys Gly Cys Cys Gly Ala Ala Gly Cys Thr Gly Gly
            500                 505                 510


Ala Cys Cys Cys Ala Gly Cys Gly Gly Ala Thr Cys Cys Cys Ala Gly
        515                 520                 525


Cys Ala Gly Cys Thr Gly Cys Ala Ala Ala Thr Cys Cys Cys Ala Gly
    530                 535                 540


Cys Cys Cys Ala Ala Cys Cys Ala Gly Cys Cys Thr Cys Ala Ala Gly
545                 550                 555                 560


Thr Thr Thr Gly Gly Gly Ala Gly Cys Thr Gly Ala Thr Ala Cys Ala
                565                 570                 575


Ala Thr Gly Thr Cys Thr Gly Cys Gly Gly Gly Ala Gly Gly Thr Gly
            580                 585                 590


Gly Cys Gly Gly Cys Cys Cys Ala Thr Thr Gly Gly Gly Cys Gly Ala
        595                 600                 605


Cys Ala Ala Thr Ala Ala Cys Cys Ala Ala Gly Gly Thr Gly Cys Cys
    610                 615                 620


Gly Ala Thr Gly Gly Ala Gly Thr Gly Gly Gly Cys Ala Ala Thr Gly
625                 630                 635                 640
```

```
Cys Cys Thr Cys Gly Gly Gly Ala Gly Ala Thr Thr Gly Gly Cys Ala
                645                 650                 655

Thr Thr Gly Cys Gly Ala Thr Thr Cys Cys Ala Cys Gly Thr Gly Gly
            660                 665                 670

Ala Thr Gly Gly Gly Gly Gly Ala Cys Ala Gly Ala Gly Thr Cys Gly
        675                 680                 685

Thr Cys Ala Cys Cys Ala Ala Gly Thr Cys Cys Ala Cys Cys Cys Gly
    690                 695                 700

Ala Ala Cys Cys Thr Gly Gly Gly Thr Gly Cys Thr Gly Cys Cys Cys
705                 710                 715                 720

Ala Gly Cys Thr Ala Cys Ala Ala Cys Ala Ala Cys Cys Ala Cys Cys
                725                 730                 735

Ala Gly Thr Ala Cys Cys Gly Ala Gly Ala Gly Ala Thr Cys Ala Ala
            740                 745                 750

Ala Ala Gly Cys Gly Gly Cys Thr Cys Cys Gly Thr Cys Gly Ala Cys
        755                 760                 765

Gly Gly Ala Ala Gly Cys Ala Ala Cys Gly Cys Cys Ala Ala Cys Gly
    770                 775                 780

Cys Cys Thr Ala Cys Thr Thr Thr Gly Gly Ala Thr Ala Cys Ala Gly
785                 790                 795                 800

Cys Ala Cys Cys Cys Cys Cys Thr Gly Gly Gly Gly Gly Thr Ala Cys
                805                 810                 815

Thr Thr Thr Gly Ala Cys Thr Thr Thr Ala Ala Cys Cys Gly Cys Thr
            820                 825                 830

Thr Cys Cys Ala Cys Ala Gly Cys Cys Ala Cys Thr Gly Gly Ala Gly
        835                 840                 845

Cys Cys Cys Cys Cys Gly Ala Gly Ala Cys Thr Gly Gly Cys Ala Ala
    850                 855                 860

Ala Gly Ala Cys Thr Cys Ala Thr Cys Ala Ala Cys Ala Ala Cys Thr
865                 870                 875                 880

Ala Cys Thr Gly Gly Gly Gly Cys Thr Thr Cys Ala Gly Ala Cys Cys
                885                 890                 895

Cys Cys Gly Gly Thr Cys Cys Cys Thr Cys Ala Gly Ala Gly Thr Cys
            900                 905                 910
```

Ala Ala Ala Ala Thr Cys Thr Thr Cys Ala Ala Cys Ala Thr Thr Cys
915 920 925

Ala Ala Gly Thr Cys Ala Ala Ala Gly Ala Gly Gly Thr Cys Ala Cys
930 935 940

Gly Gly Thr Gly Cys Ala Gly Gly Ala Cys Thr Cys Cys Ala Cys Cys
945 950 955 960

Ala Cys Cys Ala Cys Cys Ala Thr Cys Gly Cys Cys Ala Ala Cys Ala
965 970 975

Ala Cys Cys Thr Cys Ala Cys Cys Thr Cys Cys Ala Cys Cys Gly Thr
980 985 990

Cys Cys Ala Ala Gly Thr Gly Thr Thr Thr Ala Cys Gly Gly Ala Cys
995 1000 1005

Gly Ala Cys Gly Ala Cys Thr Ala Cys Cys Ala Gly Cys Thr Gly
1010 1015 1020

Cys Cys Cys Thr Ala Cys Gly Thr Cys Gly Thr Cys Gly Gly Cys
1025 1030 1035

Ala Ala Cys Gly Gly Gly Ala Cys Cys Gly Ala Gly Gly Gly Ala
1040 1045 1050

Thr Gly Cys Cys Thr Gly Cys Cys Gly Gly Cys Cys Thr Thr Cys
1055 1060 1065

Cys Cys Thr Cys Cys Gly Cys Ala Gly Gly Thr Cys Thr Thr Thr
1070 1075 1080

Ala Cys Gly Cys Thr Gly Cys Cys Gly Cys Ala Gly Thr Ala Cys
1085 1090 1095

Gly Gly Thr Thr Ala Cys Gly Cys Gly Ala Cys Gly Cys Thr Gly
1100 1105 1110

Ala Ala Cys Cys Gly Cys Gly Ala Cys Ala Ala Cys Ala Cys Ala
1115 1120 1125

Gly Ala Ala Ala Ala Thr Cys Cys Cys Ala Cys Cys Gly Ala Gly
1130 1135 1140

Ala Gly Gly Ala Gly Cys Ala Gly Cys Thr Thr Cys Thr Thr Cys
1145 1150 1155

Thr Gly Cys Cys Thr Ala Gly Ala Gly Thr Ala Cys Thr Thr Thr
1160 1165 1170

Cys Cys Cys Ala Gly Cys Ala Ala Gly Ala Thr Gly Cys Thr Gly
1175 1180 1185

Ala Gly Ala Ala Cys Gly Gly Gly Cys Ala Ala Cys Ala Ala Cys
1190 1195 1200

Thr Thr Thr Gly Ala Gly Thr Thr Thr Ala Cys Cys Thr Ala Cys
1205 1210 1215

Ala Ala Cys Thr Thr Thr Gly Ala Gly Gly Ala Gly Gly Thr Gly
1220 1225 1230

Cys Cys Cys Thr Thr Cys Cys Ala Cys Thr Cys Cys Ala Gly Cys
1235 1240 1245

Thr Thr Cys Gly Cys Thr Cys Cys Cys Ala Gly Thr Cys Ala Gly
1250 1255 1260

Ala Ala Cys Cys Thr Gly Thr Thr Cys Ala Ala Gly Cys Thr Gly
1265 1270 1275

Gly Cys Cys Ala Ala Cys Cys Cys Gly Cys Thr Gly Gly Thr Gly
1280 1285 1290

Gly Ala Cys Cys Ala Gly Thr Ala Cys Thr Thr Gly Thr Ala Cys
1295 1300 1305

Cys Gly Cys Thr Thr Cys Gly Thr Gly Ala Gly Cys Ala Cys Ala
1310 1315 1320

Ala Ala Thr Ala Ala Cys Ala Cys Thr Gly Gly Cys Gly Gly Ala
1325 1330 1335

Gly Thr Cys Cys Ala Gly Thr Thr Cys Ala Ala Cys Ala Ala Gly
1340 1345 1350

Ala Ala Cys Cys Thr Gly Gly Cys Cys Gly Gly Gly Ala Gly Ala
1355 1360 1365

Thr Ala Cys Gly Cys Cys Ala Ala Cys Ala Cys Cys Thr Ala Cys
1370 1375 1380

Ala Ala Ala Ala Ala Cys Thr Gly Gly Thr Thr Cys Cys Cys Gly
1385 1390 1395

Gly Gly Gly Cys Cys Cys Ala Thr Gly Gly Gly Cys Cys Gly Ala
1400 1405 1410

Ala Cys Cys Cys Ala Gly Gly Gly Cys Thr Gly Gly Ala Ala Cys
1415 1420 1425

```
Cys Thr  Gly Gly Gly Cys Thr  Cys Cys Gly Gly Gly  Gly Thr Cys
    1430                 1435                 1440


Ala Ala  Cys Cys Gly Cys Gly  Cys Cys Ala Gly Thr  Gly Thr Cys
    1445                 1450                 1455


Ala Gly  Cys Gly Cys Cys Thr  Thr Cys Gly Cys Cys  Ala Cys Gly
    1460                 1465                 1470


Ala Cys  Cys Ala Ala Thr Ala  Gly Gly Ala Thr Gly  Gly Ala Gly
    1475                 1480                 1485


Cys Thr  Cys Gly Ala Gly Gly  Gly Cys Gly Cys Gly  Ala Gly Thr
    1490                 1495                 1500


Thr Ala  Cys Cys Ala Gly Gly  Thr Gly Cys Cys Cys  Cys Cys Gly
    1505                 1510                 1515


Cys Ala  Gly Cys Cys Gly Ala  Ala Cys Gly Gly Cys  Ala Thr Gly
    1520                 1525                 1530


Ala Cys  Cys Ala Ala Cys Ala  Ala Cys Cys Thr Cys  Cys Ala Gly
    1535                 1540                 1545


Gly Gly  Cys Ala Gly Cys Ala  Ala Cys Ala Cys Cys  Thr Ala Thr
    1550                 1555                 1560


Gly Cys  Cys Cys Thr Gly Gly  Ala Gly Ala Ala Cys  Ala Cys Thr
    1565                 1570                 1575


Ala Thr  Gly Ala Thr Cys Thr  Thr Cys Ala Ala Cys  Ala Gly Cys
    1580                 1585                 1590


Cys Ala  Gly Cys Cys Gly Gly  Cys Gly Ala Ala Cys  Cys Cys Gly
    1595                 1600                 1605


Gly Gly  Cys Ala Cys Cys Ala  Cys Cys Gly Cys Cys  Ala Cys Gly
    1610                 1615                 1620


Thr Ala  Cys Cys Thr Cys Gly  Ala Gly Gly Gly Cys  Ala Ala Cys
    1625                 1630                 1635


Ala Thr  Gly Cys Thr Cys Ala  Thr Cys Ala Cys Cys  Ala Gly Cys
    1640                 1645                 1650


Gly Ala  Gly Ala Gly Cys Gly  Ala Gly Ala Cys Gly  Cys Ala Gly
    1655                 1660                 1665


Cys Cys  Gly Gly Thr Gly Ala  Ala Cys Cys Gly Cys  Gly Thr Gly
    1670                 1675                 1680
```

Gly Cys Gly Thr Ala Cys Ala Ala Cys Gly Thr Cys Gly Gly Cys
1685 1690 1695

Gly Gly Gly Cys Ala Gly Ala Thr Gly Gly Cys Cys Ala Cys Cys
1700 1705 1710

Ala Ala Cys Ala Ala Cys Cys Ala Gly Ala Gly Cys Thr Cys Cys
1715 1720 1725

Ala Cys Cys Ala Cys Thr Gly Cys Cys Cys Cys Cys Gly Cys Gly
1730 1735 1740

Ala Cys Cys Gly Gly Cys Ala Cys Gly Thr Ala Cys Ala Ala Cys
1745 1750 1755

Cys Thr Cys Cys Ala Gly Gly Ala Ala Ala Thr Cys Gly Thr Gly
1760 1765 1770

Cys Cys Cys Gly Gly Cys Ala Gly Cys Gly Thr Gly Thr Gly Gly
1775 1780 1785

Ala Thr Gly Gly Ala Gly Ala Gly Gly Gly Ala Cys Gly Thr Gly
1790 1795 1800

Thr Ala Cys Cys Thr Cys Cys Ala Ala Gly Gly Ala Cys Cys Cys
1805 1810 1815

Ala Thr Cys Thr Gly Gly Gly Cys Cys Ala Ala Gly Ala Thr Cys
1820 1825 1830

Cys Cys Ala Gly Ala Gly Ala Cys Gly Gly Gly Gly Gly Cys Gly
1835 1840 1845

Cys Ala Cys Thr Thr Thr Cys Ala Cys Cys Cys Cys Thr Cys Thr
1850 1855 1860

Cys Cys Gly Gly Cys Cys Ala Thr Gly Gly Gly Cys Gly Gly Ala
1865 1870 1875

Thr Thr Cys Gly Gly Ala Cys Thr Cys Ala Ala Ala Cys Ala Cys
1880 1885 1890

Cys Cys Ala Cys Cys Gly Cys Cys Cys Ala Thr Gly Ala Thr Gly
1895 1900 1905

Cys Thr Cys Ala Thr Cys Ala Ala Gly Ala Ala Cys Ala Cys Gly
1910 1915 1920

Cys Cys Thr Gly Thr Gly Cys Cys Cys Gly Gly Ala Ala Ala Thr
1925 1930 1935

```
Ala Thr  Cys Ala Cys Cys Ala  Gly Cys Thr Thr Cys  Thr Cys Gly
    1940                 1945                 1950


Gly Ala  Cys Gly Thr Gly Cys  Cys Cys Gly Thr Cys  Ala Gly Cys
    1955                 1960                 1965


Ala Gly  Cys Thr Thr Cys Ala  Thr Cys Ala Cys Cys  Cys Ala Gly
    1970                 1975                 1980


Thr Ala  Cys Ala Gly Cys Ala  Cys Cys Gly Gly Gly  Cys Ala Gly
    1985                 1990                 1995


Gly Thr  Cys Ala Cys Cys Gly  Thr Gly Gly Ala Gly  Ala Thr Gly
    2000                 2005                 2010


Gly Ala  Gly Thr Gly Gly Gly  Ala Gly Cys Thr Cys  Ala Ala Gly
    2015                 2020                 2025


Ala Ala  Gly Gly Ala Ala Ala  Ala Cys Thr Cys Cys  Ala Ala Gly
    2030                 2035                 2040


Ala Gly  Gly Thr Gly Gly Ala  Ala Cys Cys Cys Ala  Gly Ala Gly
    2045                 2050                 2055


Ala Thr  Cys Cys Ala Gly Thr  Ala Cys Ala Cys Ala  Ala Ala Cys
    2060                 2065                 2070


Ala Ala  Cys Thr Ala Cys Ala  Ala Cys Gly Ala Cys  Cys Cys Cys
    2075                 2080                 2085


Cys Ala  Gly Thr Thr Thr Gly  Thr Gly Gly Ala Cys  Thr Thr Thr
    2090                 2095                 2100


Gly Cys  Cys Cys Cys Gly Gly  Ala Cys Ala Gly Cys  Ala Cys Cys
    2105                 2110                 2115


Gly Gly  Gly Gly Ala Ala Thr  Ala Cys Ala Gly Ala  Ala Cys Cys
    2120                 2125                 2130


Ala Cys  Cys Ala Gly Ala Cys  Cys Thr Ala Thr Cys  Gly Gly Ala
    2135                 2140                 2145


Ala Cys  Cys Cys Gly Ala Thr  Ala Cys Cys Thr Thr  Ala Cys Cys
    2150                 2155                 2160


Cys Gly  Ala Cys Cys Cys Cys  Thr Thr Thr Ala Ala
    2165                 2170                 2175
```

<210> 122
<211> 2208
<212> DNA
<213> Adeno-associated virus 6

<400> 122
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980 gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctg 2208

<210> 123
<211> 736
<212> PRT
<213> Adeno-associated virus 6

<400> 123
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala

```
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
```

485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 124
<211> 623
<212> PRT
<213> Adeno-associated virus 6

<400> 124
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1   5   10   15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20   25   30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35   40   45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50   55   60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65   70   75   80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85   90   95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100   105   110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115   120   125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130   135   140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145   150   155   160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165   170   175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala His Asp
            180   185   190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195   200   205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210   215   220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225   230   235   240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245   250   255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260   265   270

```
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
                485                 490                 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
    530                 535                 540
```

```
Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560


Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
                565                 570                 575


Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
            580                 585                 590


Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
        595                 600                 605


Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620
```

<210> 125
<211> 4683
<212> DNA
<213> Adeno-associated virus 6

<400> 125
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag 180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240

gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga 300

ggtttgaacg cgcagcgcca tgccggggtt ttacgagatt gtgattaagg tccccagcga 360

ccttgacgag catctgcccg gcatttctga cagctttgtg aactgggtgg ccgagaagga 420

atgggagttg ccgccagatt ctgacatgga tctgaatctg attgagcagg cacccctgac 480

cgtggccgag aagctgcagc gcgacttcct ggtccagtgg cgccgcgtga gtaaggcccc 540

ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc tccatattct 600

ggtggagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc agattaggga 660

caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact ggttcgcggt 720

gaccaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt gctacatccc 780

caactacctc ctgcccaaga ctcagcccga gctgcagtgg gcgtggacta acatggagga 840

gtatataagc gcgtgtttaa acctggccga gcgcaaacgg ctcgtggcgc acgacctgac 900

ccacgtcagc cagacccagg agcagaacaa ggagaatctg aaccccaatt ctgacgcgcc 960

tgtcatccgg tcaaaaacct ccgcacgcta catggagctg gtcgggtggc tggtggaccg 1020

gggcatcacc tccgagaagc agtggatcca ggaggaccag gcctcgtaca tctccttcaa 1080

cgccgcctcc aactcgcggt cccagatcaa ggccgctctg gacaatgccg gcaagatcat 1140

ggcgctgacc aaatccgcgc ccgactacct ggtaggcccc gctccgcccg ccgacattaa 1200

aaccaaccgc atttaccgca tcctggagct gaacggctac gaccctgcct acgccggctc 1260 cgtctttctc ggctgggccc agaaaaggtt cggaaaacgc aacaccatct ggctgtttgg 1320

gccggccacc acgggcaaga ccaacatcgc ggaagccatc gcccacgccg tgcccttcta 1380

cggctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg acaagatggt 1440

gatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca aggccattct 1500

cggcggcagc aaggtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga tcgatcccac 1560

ccccgtgatc gtcacctcca acaccaacat gtgcgccgtg attgacggga acagcaccac 1620

cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactca cccgccgtct 1680

ggagcatgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc gctgggcgca 1740

ggatcacgtg accgaggtgg cgcatgagtt ctacgtcaga aagggtggag ccaacaagag 1800

acccgccccc gatgacgcgg ataaaagcga gcccaagcgg gcctgcccct cagtcgcgga 1860

tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt accaaaacaa 1920

atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaaaacat gcgagagaat 1980

gaatcagaat ttcaacattt gcttcacgca cgggaccaga gactgttcag aatgtttccc 2040

cggcgtgtca gaatctcaac cggtcgtcag aaagaggacg tatcggaaac tctgtgccat 2100

tcatcatctg ctggggcggg ctcccgagat tgcttgctcg gcctgcgatc tggtcaacgt 2160

ggatctggat gactgtgttt ctgagcaata aatgacttaa accaggtatg gctgccgatg 2220

gttatcttcc agattggctc gaggacaacc tctctgaggg cattcgcgag tggtgggact 2280

tgaaacctgg agccccgaaa cccaaagcca accagcaaaa gcaggacgac ggccggggtc 2340

tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag ggggagcccg 2400

tcaacgcggc ggatgcagcg gccctcgagc acgacaaggc ctacgaccag cagctcaaag 2460

cgggtgacaa tccgtacctg cggtataacc acgccgacgc cgagtttcag gagcgtctgc 2520

aagaagatac gtcttttggg ggcaacctcg ggcgagcagt cttccaggcc aagaagaggg 2580

ttctcgaacc ttttggtctg gttgaggaag gtgctaagac ggctcctgga aagaaacgtc 2640

cggtagagca gtcgccacaa gagccagact cctcctcggg cattggcaag acaggccagc 2700

agcccgctaa aaagagactc aattttggtc agactggcga ctcagagtca gtccccgacc 2760

cacaacctct cggagaacct ccagcaaccc ccgctgctgt gggacctact acaatggctt 2820

caggcggtgg cgcaccaatg gcagacaata acgaaggcgc cgacggagtg ggtaatgcct 2880

caggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc accagcaccc 2940

gaacatgggc cttgcccacc tataacaacc acctctacaa gcaaatctcc agtgcttcaa 3000

cgggggccag caacgacaac cactacttcg gctacagcac cccctggggg tattttgatt 3060

tcaacagatt ccactgccat ttctcaccac gtgactggca gcgactcatc aacaacaatt 3120

ggggattccg gcccaagaga ctcaacttca agctcttcaa catccaagtc aaggaggtca 3180

cgacgaatga tggcgtcacg accatcgcta ataaccttac cagcacggtt caagtcttct 3240

cggactcgga gtaccagttg ccgtacgtcc tcggctctgc gcaccagggc tgcctccctc 3300

```
cgttcccggc ggacgtgttc atgattccgc agtacggcta cctaacgctc aacaatggca     3360

gccaggcagt gggacggtca tccttttact gcctggaata tttcccatcg cagatgctga     3420

gaacgggcaa taactttacc ttcagctaca ccttcgagga cgtgcctttc cacagcagct     3480

acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag tacctgtatt     3540

acctgaacag aactcagaat cagtccggaa gtgcccaaaa caaggacttg ctgtttagcc     3600

gggggtctcc agctggcatg tctgttcagc ccaaaaactg gctacctgga ccctgttacc     3660

ggcagcagcg cgtttctaaa acaaaaacag acaacaacaa cagcaacttt acctggactg     3720

gtgcttcaaa atataacctt aatgggcgtg aatctataat caaccctggc actgctatgg     3780

cctcacacaa agacgacaaa gacaagttct ttcccatgag cggtgtcatg atttttggaa     3840

aggagagcgc cggagcttca aacactgcat tggacaatgt catgatcaca gacgaagagg     3900

aaatcaaagc cactaacccc gtggccaccg aaagatttgg gactgtggca gtcaatctcc     3960

agagcagcag cacagaccct gcgaccggag atgtgcatgt tatgggagcc ttacctggaa     4020

tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa attcctcaca     4080

cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag cacccgcctc     4140

ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag ttttcggcta     4200

caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg gagattgaat     4260

gggagctgca gaaagaaaac agcaaacgct ggaatcccga agtgcagtat acatctaact     4320

atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat actgagcctc     4380

gccccattgg cacccgttac ctcacccgtc ccctgtaatt gtgtgttaat caataaaccg     4440

gttaattcgt gtcagttgaa ctttggtctc atgtcgttat tatcttatct ggtcaccata     4500

gcaaccggtt acacattaac tgcttagttg cgcttcgcga atacccctag tgatggagtt     4560

gcccactccc tctatgcgcg ctcgctcgct cggtggggcc ggcagagcag agctctgccg     4620

tctgcggacc tttggtccgc aggccccacc gagcgagcga gcgcgcatag agggagtggg     4680

caa                                                                   4683


<210> 126
<211> 2211
<212> DNA
<213> Adeno-associated virus 6

<400> 126
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
```

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 127
<211> 736
<212> PRT
<213> Adeno-associated virus

```
<400> 127
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 128
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 128
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
```

325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 129
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 129
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 130
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 130
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg

```
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
```

705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 131
<211> 2214
<212> DNA
<213> Adeno-associated virus 7

<400> 131
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

gcaaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacag tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

attaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtg aaactgcagg tagtaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctgc ggttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020

acgattcagg tattctcgga ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctcaaca atggcagtca gtctgtggga cgttcctcct tctactgcct ggagtacttc 1200

ccctctcaga tgctgagaac gggcaacaac tttgagttca gctacagctt cgaggacgtg 1260

cctttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcccctcatc 1320

gaccagtact tgtactacct ggccagaaca cagagtaacc caggaggcac agctggcaat 1380

cgggaactgc agttttacca gggcgggcct tcaactatgg ccgaacaagc caagaattgg 1440

ttacctggac cttgcttccg gcaacaaaga gtctccaaaa cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcgttggtt 1560

aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca actaacaaaa ctacattgga aaatgtgtta 1680

```
atgacaaatg aagaagaaat tcgtcctact aatcctgtag ccacggaaga atacgggata     1740

gtcagcagca acttacaagc ggctaatact gcagcccaga cacaagttgt caacaaccag     1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg     1860

gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga     1920

cttaaacatc cgcctcctca gatcctgatc aagaacactc ccgttcccgc taatcctccg     1980

gaggtgttta ctcctgccaa gtttgcttcg ttcatcacac agtacagcac cggacaagtc     2040

agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt     2100

cagtacacct ccaactttga aaagcagact ggtgtggact ttgccgttga cagccagggt     2160

gtttactctg agcctcgccc tattggcact cgttacctca cccgtaatct gtaa           2214


<210> 132
<211> 738
<212> PRT
<213> Adeno-associated virus 7

<400> 132
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
```

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
450 455 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
530 535 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 133
<211> 737
<212> PRT
<213> Adeno-associated virus 7

<400> 133
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
195 200 205

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

```
<210> 134
<211> 623
<212> PRT
<213> Adeno-associated virus 7

<400> 134
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15


Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30


Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60


Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Val Leu Val Glu
                85                  90                  95


Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110


Arg Glu Lys Leu Val Gln Thr Ile Tyr Arg Gly Val Glu Pro Thr Leu
        115                 120                 125


Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140


Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160


Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175


Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190


Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205


Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220


Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240


Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255
```

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260   265   270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
        275   280   285

Leu Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290   295   300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305   310   315   320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325   330   335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340   345   350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355   360   365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370   375   380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385   390   395   400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405   410   415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420   425   430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435   440   445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450   455   460

Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465   470   475   480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
                485   490   495

Pro Asp Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500   505   510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515   520   525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Ile Gln Met
    530   535   540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545   550   555   560

Cys Phe Thr His Gly Val Arg Asp Cys Leu Glu Cys Phe Pro Gly Val
                565   570   575

Ser Glu Ser Gln Pro Val Val Arg Lys Lys Thr Tyr Arg Lys Leu Cys
            580   585   590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
        595   600   605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610   615   620

<210> 135
<211> 4721
<212> DNA
<213> Adeno-associated virus 7

<400> 135
ttggccactc cctctatgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60

agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcat agagggagtg 120

gccaactcca tcactagggg taccgcgaag cgcctcccac gctgccgcgt cagcgctgac 180

gtaaatcacg tcatagggga gtggtcctgt attagctgtc acgtgagtgc ttttgcgaca 240

ttttgcgaca ccacgtggcc atttgaggta tatatggccg agtgagcgag caggatctcc 300

attttgaccg cgaaatttga acgagcagca gccatgccgg gtttctacga gatcgtgatc 360

aaggtgccga gcgacctgga cgagcacctg ccgggcattt ctgactcgtt tgtgaactgg 420

gtggccgaga aggaatggga gctgcccccg gattctgaca tggatctgaa tctgatcgag 480

caggcacccc tgaccgtggc cgagaagctg cagcgcgact tcctggtcca atggcgccgc 540

gtgagtaagg ccccggaggc cctgttcttt gttcagttcg agaagggcga gagctacttc 600

caccttcacg ttctggtgga gaccacgggg gtcaagtcca tggtgctagg ccgcttcctg 660

agtcagattc gggagaagct ggtccagacc atctaccgcg gggtcgagcc cacgctgccc 720

aactggttcg cggtgaccaa gacgcgtaat ggcgccggcg gggggaacaa ggtggtggac 780

gagtgctaca tccccaacta cctcctgccc aagacccagc ccgagctgca gtgggcgtgg 840

actaacatgg aggagtatat aagcgcgtgt ttgaacctgg ccgaacgcaa acggctcgtg 900

gcgcagcacc tgacccacgt cagccagacg caggagcaga acaaggagaa tctgaacccc 960

aattctgacg cgcccgtgat caggtcaaaa acctccgcgc gctacatgga gctggtcggg 1020

tggctggtgg accggggcat cacctccgag aagcagtgga tccaggagga ccaggcctcg 1080 tacatctcct tcaacgccgc ctccaactcg cggtcccaga tcaaggccgc gctggacaat 1140

gccggcaaga tcatggcgct gaccaaatcc gcgcccgact acctggtggg gccctcgctg 1200

cccgcggaca ttaaaaccaa ccgcatctac cgcatcctgg agctgaacgg gtacgatcct 1260

gcctacgccg gctccgtctt tctcggctgg gcccagaaaa agttcgggaa gcgcaacacc 1320

atctggctgt ttgggcccgc caccaccggc aagaccaaca ttgcggaagc catcgcccac 1380

gccgtgccct tctacggctg cgtcaactgg accaatgaga actttccctt caacgattgc 1440

gtcgacaaga tggtgatctg gtgggaggag ggcaagatga cggccaaggt cgtggagtcc 1500

gccaaggcca ttctcggcgg cagcaaggtg cgcgtggacc aaaagtgcaa gtcgtccgcc 1560

cagatcgacc ccacccccgt gatcgtcacc tccaacacca acatgtgcgc cgtgattgac 1620

gggaacagca ccaccttcga gcaccagcag ccgttgcagg accggatgtt caaatttgaa 1680

ctcacccgcc gtctggagca cgactttggc aaggtgacga agcaggaagt caaagagttc 1740

ttccgctggg ccagtgatca cgtgaccgag gtggcgcatg agttctacgt cagaaagggc 1800

ggagccagca aaagacccgc ccccgatgac gcggatataa gcgagcccaa gcgggcctgc 1860

ccctcagtcg cggatccatc gacgtcagac gcggaaggag ctccggtgga ctttgccgac 1920

aggtaccaaa acaaatgttc tcgtcacgcg ggcatgattc agatgctgtt tccctgcaaa 1980

acgtgcgaga gaatgaatca gaatttcaac atttgcttca cacacggggt cagagactgt 2040

ttagagtgtt tccccggcgt gtcagaatct caaccggtcg tcagaaaaaa gacgtatcgg 2100

aaactctgcg cgattcatca tctgctgggg cgggcgcccg agattgcttg ctcggcctgc 2160

gacctggtca acgtggacct ggacgactgc gtttctgagc aataaatgac ttaaaccagg 2220

tatggctgcc gatggttatc ttccagattg gctcgaggac aacctctctg agggcattcg 2280

cgagtggtgg gacctgaaac ctggagcccc gaaacccaaa gccaaccagc aaaagcagga 2340

caacggccgg ggtctggtgc ttcctggcta caagtacctc ggacccttca acggactcga 2400

caagggggag cccgtcaacg cggcggacgc agcggccctc gagcacgaca aggcctacga 2460

ccagcagctc aaagcgggtg acaatccgta cctgcggtat aaccacgccg acgccgagtt 2520

tcaggagcgt ctgcaagaag atacgtcatt tgggggcaac ctcgggcgag cagtcttcca 2580

ggccaagaag cgggttctcg aacctctcgg tctggttgag gaaggcgcta agacggctcc 2640

tgcaaagaag agaccggtag agccgtcacc tcagcgttcc cccgactcct ccacgggcat 2700

cggcaagaaa ggccagcagc ccgccagaaa gagactcaat ttcggtcaga ctggcgactc 2760

agagtcagtc cccgaccctc aacctctcgg agaacctcca gcagcgccct ctagtgtggg 2820

atctggtaca gtggctgcag gcggtggcgc accaatggca gacaataacg aaggtgccga 2880

cggagtgggt aatgcctcag gaaattggca ttgcgattcc acatggctgg gcgacagagt 2940

cattaccacc agcacccgaa cctgggccct gcccacctac aacaaccacc tctacaagca 3000

aatctccagt gaaactgcag gtagtaccaa cgacaacacc tacttcggct acagcacccc 3060

ctgggggtat tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg 3120 actcatcaac aacaactggg gattccggcc caagaagctg cggttcaagc tcttcaacat 3180

ccaggtcaag gaggtcacga cgaatgacgg cgttacgacc atcgctaata accttaccag 3240

cacgattcag gtattctcgg actcggaata ccagctgccg tacgtcctcg gctctgcgca 3300

ccagggctgc ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acggctacct 3360

gactctcaac aatggcagtc agtctgtggg acgttcctcc ttctactgcc tggagtactt 3420

cccctctcag atgctgagaa cgggcaacaa ctttgagttc agctacagct tcgaggacgt 3480

gcctttccac agcagctacg cacacagcca gagcctggac cggctgatga atcccctcat 3540

cgaccagtac ttgtactacc tggccagaac acagagtaac ccaggaggca cagctggcaa 3600

tcgggaactg cagttttacc agggcgggcc ttcaactatg gccgaacaag ccaagaattg 3660

gttacctgga ccttgcttcc ggcaacaaag agtctccaaa acgctggatc aaaacaacaa 3720

cagcaacttt gcttggactg gtgccaccaa atatcacctg aacggcagaa actcgttggt 3780

taatcccggc gtcgccatgg caactcacaa ggacgacgag gaccgctttt tcccatccag 3840

cggagtcctg atttttggaa aaactggagc aactaacaaa actacattgg aaaatgtgtt 3900

aatgacaaat gaagaagaaa ttcgtcctac taatcctgta gccacggaag aatacgggat 3960

agtcagcagc aacttacaag cggctaatac tgcagcccag acacaagttg tcaacaacca 4020

gggagcctta cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcccatctg 4080

ggccaagatt cctcacacgg atggcaactt tcacccgtct cctttgatgg gcggctttgg 4140

acttaaacat ccgcctcctc agatcctgat caagaacact cccgttcccg ctaatcctcc 4200

ggaggtgttt actcctgcca agtttgcttc gttcatcaca cagtacagca ccggacaagt 4260

cagcgtggaa atcgagtggg agctgcagaa ggaaaacagc aagcgctgga acccggagat 4320

tcagtacacc tccaactttg aaaagcagac tggtgtggac tttgccgttg acagccaggg 4380

tgtttactct gagcctcgcc ctattggcac tcgttacctc acccgtaatc tgtaattgca 4440

tgttaatcaa taaaccggtt gattcgtttc agttgaactt tggtctcctg tgcttcttat 4500

cttatcggtt tccatagcaa ctggttacac attaactgct tgggtgcgct tcacgataag 4560

aacactgacg tcaccgcggt acccctagtg atggagttgg ccactccctc tatgcgcgct 4620

cgctcgctcg gtggggcctg cggaccaaag gtccgcagac ggcagagctc tgctctgccg 4680

gccccaccga gcgagcgagc gcgcatagag ggagtggcca a 4721

<210> 136
<211> 2214
<212> DNA
<213> Adeno-associated virus 7

<400> 136
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

```
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300
caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag      360
gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420
gcaaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcatc      480
ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca      540
gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tagtgtggga      600
tctggtacag tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac      660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720
attaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa      780
atctccagtg aaactgcagg tagtaccaac gacaacacct acttcggcta cagcaccccc      840
tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga      900
ctcatcaaca acaactgggg attccggccc aagaagctgc ggttcaagct cttcaacatc      960
caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc     1020
acgattcagg tattctcgga ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac     1080
cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg     1140
actctcaaca atggcagtca gtctgtggga cgttcctcct tctactgcct ggagtacttc     1200
ccctctcaga tgctgagaac gggcaacaac tttgagttca gctacagctt cgaggacgtg     1260
cctttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcccctcatc     1320
gaccagtact tgtactacct ggccagaaca cagagtaacc caggaggcac agctggcaat     1380
cgggaactgc agttttacca gggcgggcct tcaactatgg ccgaacaagc caagaattgg     1440
ttacctggac cttgcttccg gcaacaaaga gtctccaaaa cgctggatca aaacaacaac     1500
agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcgttggtt     1560
aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc     1620
ggagtcctga tttttggaaa aactggagca actaacaaaa ctacattgga aaatgtgtta     1680
atgacaaatg aagaagaaat tcgtcctact aatcctgtag ccacggaaga atacgggata     1740
gtcagcagca acttacaagc ggctaatact gcagcccaga cacaagttgt caacaaccag     1800
ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg     1860
gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga     1920
cttaaacatc cgcctcctca gatcctgatc aagaacactc ccgttcccgc taatcctccg     1980
gaggtgttta ctcctgccaa gtttgcttcg ttcatcacac agtacagcac cggacaagtc     2040
agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt     2100
cagtacacct ccaactttga aaagcagact ggtgtggact ttgccgttga cagccagggt     2160
gtttactctg agcctcgccc tattggcact cgttacctca cccgtaatct gtaa           2214
```

```
<210> 137
<211> 737
<212> PRT
<213> Adeno-associated virus 7

<400> 137
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540


Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560


Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 138
<211> 2217
<212> DNA
<213> Adeno-associated virus 8

<400> 138
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac       120
```

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160 ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 139
<211> 2213
<212> DNA
<213> Adeno-associated virus 8

<400> 139
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

```
caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc     1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt     1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct     1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag     2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag     2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt aatacagaag     2160

gcgtgtactc tgaaccccgc cccattggca cccgttacct cacccgtaat ctg           2213


<210> 140
<211> 4393
<212> DNA
<213> Adeno-associated virus 8

<400> 140
cagagaggga gtggccaact ccatcactag gggtagcgcg aagcgcctcc cacgctgccg       60

cgtcagcgct gacgtaaatt acgtcatagg ggagtggtcc tgtattagct gtcacgtgag      120

tgcttttgcg gcattttgcg acaccacgtg gccatttgag gtatatatgg ccgagtgagc      180

gagcaggatc tccattttga ccgcgaaatt tgaacgagca gcagccatgc cgggcttcta      240

cgagatcgtg atcaaggtgc cgagcgacct ggacgagcac ctgccgggca tttctgactc      300

gtttgtgaac tgggtggccg agaaggaatg ggagctgccc ccggattctg acatggatcg      360

gaatctgatc gagcaggcac ccctgaccgt ggccgagaag ctgcagcgcg acttcctggt      420

ccaatggcgc cgcgtgagta aggccccgga ggccctcttc tttgttcagt tcgagaaggg      480

cgagagctac tttcacctgc acgttctggt cgagaccacg ggggtcaagt ccatggtgct      540

aggccgcttc ctgagtcaga ttcgggaaaa gcttggtcca gaccatctac ccgcggggtc      600

gagccccacc ttgcccaact ggttcgcggt gaccaaagac gcggtaatgg cgccggcggg      660

ggggaacaag gtggtggacg agtgctacat ccccaactac ctcctgccca agactcagcc      720

cgagctgcag tgggcgtgga ctaacatgga ggagtatata agcgcgtgct tgaacctggc      780

cgagcgcaaa cggctcgtgg cgcagcacct gacccacgtc agccagacgc aggagcagaa      840

caaggagaat ctgaacccca attctgacgc gcccgtgatc aggtcaaaaa cctccgcgcg      900

ctatatggag ctggtcgggt ggctggtgga ccggggcatc acctccgaga agcagtggat      960

ccaggaggac caggcctcgt acatctcctt caacgccgcc tccaactcgc ggtcccagat     1020

caaggccgcg ctggacaatg ccggcaagat catggcgctg accaaatccg cgcccgacta     1080

cctggtgggg ccctcgctgc ccgcggacat tacccagaac cgcatctacc gcatcctcgc     1140

tctcaacggc tacgaccctg cctacgccgg ctccgtcttt ctcggctggg ctcagaaaaa     1200

gttcgggaaa cgcaacacca tctggctgtt tggacccgcc accaccggca agaccaacat     1260

tgcggaagcc atcgcccacg ccgtgccctt ctacggctgc gtcaactgga ccaatgagaa     1320

ctttcccttc aatgattgcg tcgacaagat ggtgatctgg tgggaggagg gcaagatgac     1380
```

ggccaaggtc gtggagtccg ccaaggccat tctcggcggc agcaaggtgc gcgtggacca 1440

aaagtgcaag tcgtccgccc agatcgaccc cacccccgtg atcgtcacct ccaacaccaa 1500

catgtgcgcc gtgattgacg ggaacagcac caccttcgag caccagcagc ctctccagga 1560

ccggatgttt aagttcgaac tcacccgccg tctggagcac gactttggca aggtgacaaa 1620

gcaggaagtc aaagagttct tccgctgggc cagtgatcac gtgaccgagg tggcgcatga 1680

gttttacgtc agaaagggcg gagccagcaa aagacccgcc cccgatgacg cggataaaag 1740

cgagcccaag cgggcctgcc cctcagtcgc ggatccatcg acgtcagacg cggaaggagc 1800

tccggtggac tttgccgaca ggtaccaaaa caaatgttct cgtcacgcgg gcatgcttca 1860

gatgctgttt ccctgcaaaa cgtgcgagag aatgaatcag aatttcaaca tttgcttcac 1920

acacggggtc agagactgct cagagtgttt ccccggcgtg tcagaatctc aaccggtcgt 1980

cagaaagagg acgtatcgga aactctgtgc gattcatcat ctgctggggc gggctcccga 2040

gattgcttgc tcggcctgcg atctggtcaa cgtggacctg gatgactgtg tttctgagca 2100

ataaatgact taaaccaggt atggctgccg atggttatct tccagattgg ctcgaggaca 2160

acctctctga gggcattcgc gagtggtggg cgctgaaacc tggagccccg aagcccaaag 2220

ccaaccagca aaagcaggac gacggccggg gtctggtgct tcctggctac aagtacctcg 2280

gacccttcaa cggactcgac aagggggagc ccgtcaacgc ggcggacgca gcggccctcg 2340

agcacgacaa ggcctacgac cagcagctgc aggcgggtga caatccgtac ctgcggtata 2400

accacgccga cgccgagttt caggagcgtc tgcaagaaga tacgtctttt gggggcaacc 2460

tcgggcgagc agtcttccag gccaagaagc gggttctcga acctctcggt ctggttgagg 2520

aaggcgctaa gacggctcct ggaaagaaga gaccggtaga gccatcaccc cagcgttctc 2580

cagactcctc tacgggcatc ggcaagaaag gccaacagcc cgccagaaaa agactcaatt 2640

ttggtcagac tggcgactca gagtcagttc cagaccctca acctctcgga gaacctccag 2700

cagcgccctc tggtgtggga cctaatacaa tggctgcagg cggtggcgca ccaatggcag 2760

acaataacga aggcgccgac ggagtgggta gttcctcggg aaattggcat tgcgattcca 2820

catggctggg cgacagagtc atcaccacca gcacccgaac ctgggccctg cccacctaca 2880

acaaccacct ctacaagcaa atctccaacg ggacatcggg aggagccacc aacgacaaca 2940

cctacttcgg ctacagcacc ccctgggggt attttgactt taacagattc cactgccact 3000

tttcaccacg tgactggcag cgactcatca acaacaactg gggattccgg cccaagagac 3060

tcagcttcaa gctcttcaac atccaggtca aggaggtcac gcagaatgaa ggcaccaaga 3120

ccatcgccaa taacctcacc agcaccatcc aggtgtttac ggactcggag taccagctgc 3180

cgtacgttct cggctctgcc caccagggct gcctgcctcc gttcccggcg gacgtgttca 3240

tgattcccca gtacggctac ctaacactca acaacggtag tcaggccgtg ggacgctcct 3300

ccttctactg cctggaatac tttccttcgc agatgctgag aaccggcaac aacttccagt 3360

ttacttacac cttcgaggac gtgcctttcc acagcagcta cgcccacagc cagagcttgg 3420 accggctgat gaatcctctg attgaccagt acctgtacta cttgtctcgg actcaaacaa 3480

caggaggcac ggcaaatacg cagactctgg gcttcagcca aggtgggcct aatacaatgg 3540

ccaatcaggc aaagaactgg ctgccaggac cctgttaccg ccaacaacgc gtctcaacga 3600

caaccgggca aaacaacaat agcaactttg cctggactgc tgggaccaaa taccatctga 3660

atggaagaaa ttcattggct aatcctggca tcgctatggc aacacacaaa gacgacgagg 3720

agcgtttttt tcccagtaac gggatcctga tttttggcaa acaaaatgct gccagagaca 3780

atgcggatta cagcgatgtc atgctcacca gcgaggaaga aatcaaaacc actaaccctg 3840

tggctacaga ggaatacggt atcgtggcag ataacttgca gcagcaaaac acggctcctc 3900

aaattggaac tgtcaacagc caggggccct tacccggtat ggtctggcag aaccgggacg 3960

tgtacctgca gggtcccatc tgggccaaga ttcctcacac ggacggcaac ttccacccgt 4020

ctccgctgat gggcggcttt ggcctgaaac atcctccgcc tcagatcctg atcaagaaca 4080

cgcctgtacc tgcggatcct ccgaccacct tcaaccagtc aaagctgaac tctttcatca 4140

cgcaatacag caccggacag gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca 4200

gcaagcgctg gaaccccgag atccagtaca cctccaacta ctacaaatct acaagtgtgg 4260

actttgctgt taatacagaa ggcgtgtact ctgaaccccg ccccattggc acccgttacc 4320

tcacccgtaa tctgtaattg cctgttaatc aataaaccgg ttgattcgtt tcagttgaac 4380

tttggtctct gcg 4393

<210> 141
<211> 738
<212> PRT
<213> Adeno-associated virus 8

<400> 141
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

```
Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 142
<211> 737
<212> PRT
<213> Adeno-associated virus 8

<400> 142
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
```

145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser

```
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460


Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540


Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590


Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
```

690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Ile Gln Lys
705 710 715 720

Ala Cys Thr Leu Asn Pro Ala Pro Leu Ala Pro Val Thr Ser Pro Val
725 730 735

Ile

<210> 143
<211> 2217
<212> DNA
<213> Adeno-associated virus 8

<400> 143
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg ggattccggc cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440 ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 144
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 144
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900 cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgcc tgagcggacg gcgatgagtc ttccgggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctg 2214

<210> 145
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 145
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180   185   190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195   200   205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210   215   220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225   230   235   240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245   250   255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260   265   270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275   280   285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290   295   300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305   310   315   320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala

```
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Pro Glu Arg Thr Ala Met
            580                 585                 590

Ser Leu Pro Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
```

```
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 146
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 146
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc      480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca      540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga      600
```

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgag ttttagtcgt gcggttcttt gtgatggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctg 2214

<210> 147
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 147
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290   295   300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305   310   315   320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325   330   335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340   345   350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355   360   365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370   375   380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385   390   395   400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405   410   415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420   425   430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435   440   445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450   455   460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465   470   475   480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485   490   495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500   505   510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515   520   525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530   535   540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545   550   555   560

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Ser Phe Ser Arg Ala Val
            580                 585                 590

Leu Cys Asp Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 148
<211> 4385
<212> DNA
<213> Adeno-associated virus 9

<400> 148
cagagaggga gtggccaact ccatcactag gggtaatcgc gaagcgcctc ccacgctgcc       60

gcgtcagcgc tgacgtagat tacgtcatag gggagtggtc ctgtattagc tgtcacgtga      120

gtgcttttgc gacattttgc gacaccacat ggccatttga ggtatatatg gccgagtgag      180

cgagcaggat ctccattttg accgcgaaat ttgaacgagc agcagccatg ccgggcttct      240

acgagattgt gatcaaggtg ccgagcgacc tggacgagca cctgccgggc atttctgact      300

cttttgtgaa ctgggtggcc gagaaggaat gggagctgcc cccggattct gacatggatc      360
```

ggaatctgat cgagcaggca cccctgaccg tggccgagaa gctgcagcgc gacttcctgg 420

tccaatggcg ccgcgtgagt aaggccccgg aggccctctt ctttgttcag ttcgagaagg 480

gcgagagcta ctttcacctg cacgttctgg tcgagaccac gggggtcaag tccatggtgc 540

taggccgctt cctgagtcag attcgggaga agctggtcca gaccatctac cgcgggatcg 600

agccgaccct gcccaactgg ttcgcggtga ccaagacgcg taatggcgcc ggcgggggga 660

acaaggtggt ggacgagtgc tacatcccca actacctcct gcccaagact cagcccgagc 720

tgcagtgggc gtggactaac atggaggagt atataagcgc gtgcttgaac ctggccgagc 780

gcaaacggct cgtggcgcag cacctgaccc acgtcagcca gacgcaggag cagaacaagg 840

agaatctgaa ccccaattct gacgcgcccg tgatcaggtc aaaaacctcc gcgcgctaca 900

tggagctggt cgggtggctg gtggaccggg gcatcacctc cgagaagcag tggatccagg 960

aggaccaggc ctcgtacatc tccttcaacg ccgcctccaa ctcgcggtcc cagatcaagg 1020

ccgcgctgga caatgccggc aagatcatgg cgctgaccaa atccgcgccc gactacctgg 1080

taggcccttc acttccggtg gacattacgc agaaccgcat ctaccgcatc ctgcagctca 1140

acggctacga ccctgcctac gccggctccg tctttctcgg ctgggcacaa aagaagttcg 1200

ggaaacgcaa caccatctgg ctgtttgggc cggccaccac gggaaagacc aacatcgcag 1260

aagccattgc ccacgccgtg cccttctacg gctgcgtcaa ctggaccaat gagaactttc 1320

ccttcaacga ttgcgtcgac aagatggtga tctggtggga ggagggcaag atgacggcca 1380

aggtcgtgga gtccgccaag gccattctcg gcggcagcaa ggtgcgcgtg gaccaaaagt 1440

gcaagtcgtc cgcccagatc gaccccactc ccgtgatcgt cacctccaac accaacatgt 1500

gcgccgtgat tgacgggaac agcaccacct tcgagcacca gcagcctctc caggaccgga 1560

tgtttaagtt cgaactcacc cgccgtctgg agcacgactt tggcaaggtg acaaagcagg 1620

aagtcaaaga gttcttccgc tgggccagtg atcacgtgac cgaggtggcg catgagtttt 1680

acgtcagaaa gggcggagcc agcaaaagac ccgcccccga tgacgcggat aaaagcgagc 1740

ccaagcgggc ctgcccctca gtcgcggatc catcgacgtc agacgcggaa ggagctccgg 1800

tggactttgc cgacaggtac caaaacaaat gttctcgtca cgcgggcatg cttcagatgc 1860

tgcttccctg caaaacgtgc gagagaatga atcagaattt caacatttgc ttcacacacg 1920

gggtcagaga ctgctcagag tgtttccccg gcgtgtcaga atctcaaccg gtcgtcagaa 1980

agaggacgta tcggaaactc tgtgcgattc atcatctgct ggggcgggct cccgagattg 2040

cttgctcggc ctgcgatctg gtcaacgtgg acctggatga ctgtgtttct gagcaataaa 2100

tgacttaaac caggtatggc tgccgatggt tatcttccag attggctcga ggacaacctc 2160

tctgagggca ttcgcgagtg gtgggcgctg aaacctggag ccccgaagcc caaagccaac 2220

cagcaaaagc aggacgacgg ccggggtctg gtgcttcctg gctacaagta cctcggaccc 2280

ttcaacggac tcgacaaggg ggagcccgtc aacgcggcgg acgcagcggc cctcgagcac 2340

ggcaaggcct acgaccagca gctgcaggcg ggtgacaatc cgtacctgcg gtataaccac 2400 gccgacgccg agtttcagga gcgtctgcaa gaagatacgt cttttggggg caacctcggg 2460

cgagcagtct tccaggccaa gaagcgggtt ctcgaacctc tcggtctggt tgaggaaggc 2520

gctaagacgg ctcctggaaa gaagagaccg gtagagccat caccccagcg ttctccagac 2580

tcctctacgg gcatcggcaa gaaaggccaa cagcccgcca gaaaaagact caattttggt 2640

cagactggcg actcagagtc agttccagac cctcaacctc tcggagaacc tccagcagcg 2700

ccctctggtg tgggacctaa tacaatggct gcaggcggtg gcgcaccaat ggcagacaat 2760

aacgaaggcg ccgacggagt gggtaattcc tcgggaaatt ggcattgcga ttccacatgg 2820

ctgggggaca gagtcatcac caccagcacc cgaacctggg cattgcccac ctacaacaac 2880

cacctctaca agcaaatctc caatggaaca tcgggaggaa gcaccaacga caacacctac 2940

tttggctaca gcacccccctg gggtatttt gacttcaaca gattccactg ccacttctca 3000

ccacgtgact ggcagcgact catcaacaac aactggggat tccggccaaa gagactcaac 3060

ttcaagctgt tcaacatcca ggtcaaggag gttacgacga acgaaggcac caagaccatc 3120

gccaataacc ttaccagcac cgtccaggtc tttacggact cggagtacca gctaccgtac 3180

gtcctaggct ctgcccacca aggatgcctg ccaccgtttc ctgcagacgt cttcatggtt 3240

cctcagtacg gctacctgac gctcaacaat ggaagtcaag cgttaggacg ttcttctttc 3300

tactgtctgg aatacttccc ttctcagatg ctgagaaccg gcaacaactt tcagttcagc 3360

tacactttcg aggacgtgcc tttccacagc agctacgcac acagccagag tctagatcga 3420

ctgatgaacc ccctcatcga ccagtaccta tactacctgg tcagaacaca gacaactgga 3480

actgggggaa ctcaaacttt ggcattcagc caagcaggcc ctagctcaat ggccaatcag 3540

gctagaaact gggtacccgg gccttgctac cgtcagcagc gcgtctccac aaccaccaac 3600

caaaataaca acagcaactt tgcgtggacg ggagctgcta aattcaagct gaacgggaga 3660

gactcgctaa tgaatcctgg cgtggctatg gcatcgcaca aagacgacga ggaccgcttc 3720

tttccatcaa gtggcgttct catatttggc aagcaaggag ccgggaacga tggagtcgac 3780

tacagccagg tgctgattac agatgaggaa gaaattaaag ccaccaaccc tgtagccaca 3840

gaggaatacg gagcagtggc catcaacaac caggccgcta acacgcaggc gcaaactgga 3900

cttgtgcata accagggagt tattcctggt atggtctggc agaaccggga cgtgtacctg 3960

cagggcccta tttgggctaa aatacctcac acagatggca actttcaccc gtctcctctg 4020

atgggtggat ttggactgaa acacccacct ccacagattc taattaaaaa tacaccagtg 4080

ccggcagatc ctcctcttac cttcaatcaa gccaagctga actctttcat cacgcagtac 4140

agcacgggac aagtcagcgt ggaaatcgag tgggagctgc agaaagaaaa cagcaagcgc 4200

tggaatccag agatccagta tacttcaaac tactacaaat ctacaaatgt ggactttgct 4260

gtcaatacca aaggtgttta ctctgagcct cgccccattg gtactcgtta cctcacccgt 4320

aatttgtaat tgcctgttaa tcaataaacc ggttaattcg tttcagttga actttggtct 4380

ctgcg 4385

<210> 149
<211> 4382
<212> DNA
<213> Adeno-associated virus 9

<400> 149
cagagaggga gtggccaact ccatcactag gggtaatcgc gaagcgcctc ccacgctgcc 60

gcgtcagcgc tgacgtagat tacgtcatag gggagtggtc ctgtattagc tgtcacgtga 120

gtgcttttgc gacattttgc gacaccacat ggccatttga ggtatatatg gccgagtgag 180

cgagcaggat ctccattttg accgcgaaat ttgaacgagc agcagccatg ccgggcttct 240

acgagattgt gatcaaggtg ccgagcgacc tggacgagca cctgccgggc atttctgact 300

cttttgtgaa ctgggtggcc gagaaggaat gggagctgcc cccggattct gacatggatc 360

ggaatctgat cgagcaggca cccctgaccg tggccgagaa gctgtagcgc gacttcctgg 420

tccaatggcg ccgcgtgagt aaggccccgg aggccctctt ctttgttcag ttcgagaagg 480

gcgagagcta ctttcacctg cacgttctgg tcgagaccac gggggtcaag tccatggtgc 540

taggccgctt cctgagtcag attcgggaga agctggtcca gaccatctac cgcgggatcg 600

agccgacccct gcccaactgg ttcgcggtga ccaagacgcg taatggcgcc ggcgggggga 660

acaaggtggt ggacgagtgc tacatcccca actacctcct gcccaagact cagcccgagc 720

tgcagtgggc gtggactaac atggaggagt atataagcgc gtgcttgaac ctggccgagc 780

gcaaacggct cgtggcgcag cacctgaccc acgtcagcca gacgcaggag cagaacaagg 840

agaatctgaa ccccaattct gacgcgcccg tgatcaggtc aaaaacctcc gcgcgctaca 900

tggagctggt cgggtggctg gtggaccggg gcatcacctc cgagaagcag tggatccagg 960

aggaccaggc ctcgtacatc tccttcaacg ccgcctccaa ctcgcggtcc cagatcaagg 1020

ccgcgctgga caatgccggc aagatcatgg cgctgaccaa atccgcgccc gactacctgg 1080

taggcccttc acttccggtg gacattacgc agaaccgcat ctaccgcatc ctgcagctca 1140

acggctacga ccctgcctac gccggctccg tctttctcgg ctgggcacaa aagaagttcg 1200

ggaaacgcaa caccatctgg ctgtttgggc cggccaccac gggaaagacc aacatcgcag 1260

aagccattgc ccacgccgtg cccttctacg gctgcgtcaa ctggaccaat gagaactttc 1320

ccttcaacga ttgcgtcgac aagatggtga tctggtggga ggagggcaag atgacggcca 1380

aggtcgtgga gtccgccaag gccattctcg gcggcagcaa ggtgcgcgtg gaccaaaagt 1440

gcaagtcgtc cgcccagatc gaccccactc ccgtgatcgt cacctccaac accaacatgt 1500

gcgccgtgat tgacgggaac agcaccacct tcgagcacca gcagcctctc caggaccgga 1560

tgtttaagtt cgaactcacc cgccgtctgg agcacgactt tggcaaggtg acaaagcagg 1620

aagtcaaaga gttcttccgc tgggccagtg atcacgtgac cgaggtggcg catgagtttt 1680

acgtcagaaa gggcggagcc agcaaaagac ccgcccccga tgacgcggat aaaagcgagc 1740

ccaagcgggc ctgcccctca gtcgcggatc catcgacgtc agacgcggaa ggagctccgg 1800

tggactttgc cgacaggtac caaaacaaat gttctcgtca cgcgggcatg cttcagatgc 1860 tgcttccctg caaaacgtgc gagagaatga atcagaattt caacatttgc ttcacacacg 1920

gggtcagaga ctgctcagag tgtttccccg gcgtgtcaga atctcaaccg gtcgtcagaa 1980

agaggacgta tcggaaactc tgtgcgattc atcatctgct ggggcgggct cccgagattg 2040

cttgctcggc ctgcgatctg gtcaacgtgg acctggatga ctgtgtttct gagcaataaa 2100

tgacttaaac caggtatggc tgccgatggt tatcttccag attggctcga ggacaacctc 2160

tctgagggca ttcgcgagtg gtgggacctg aaacctggag ccccgaaacc caaagccaac 2220

cagcaaaagc aggacgacgg ccggggtctg gtgcttcctg gctacaagta cctcggaccc 2280

ttcaacggac tcgacaaggg ggagcccgtc aacgcggcgg acgcagcggc cctcgagcac 2340

gacaaggcct acgaccagca gctcaaagcg ggtgacaatc cgtacctgcg gtataaccac 2400

gccgacgccg agtttcagga gcgtctgcaa gaagatacgt cttttggggg caacctcggg 2460

cgagcagtct tccaggccaa gaagcgggtt ctcgaacctc tcggtctggt tgaggaaggc 2520

gctaagacgg ctcctggaaa gaagagaccg gtagagcagt caccccaaga accagactca 2580

tcctcgggca tcggcaaatc aggccagcag cccgctaaaa agagactcaa ttttggtcag 2640

actggcgact cagagtcagt ccccgaccca caacctctcg gagaacctcc agaagccccc 2700

tcaggtctgg gacctaatac aatggcttca ggcggtggcg ctccaatggc agacaataac 2760

gaaggcgccg acggagtggg taattcctcg ggaaattggc attgcgattc cacatggctg 2820

ggggacagag tcatcaccac cagcacccga acctgggcat tgcccaccta caacaaccac 2880

ctctacaagc aaatctccaa tggaacatcg ggaggaagca ccaacgacaa cacctacttt 2940

ggctacagca ccccctgggg gtattttgac ttcaacagat tccactgcca cttctcacca 3000

cgtgactggc agcgactcat caacaacaac tggggattcc ggccaaagag actcaacttc 3060

aagctgttca acatccaggt caaggaggtt acgacgaacg aaggcaccaa gaccatcgcc 3120

aataacctta ccagcaccgt ccaggtcttt acggactcgg agtaccagct accgtacgtc 3180

ctaggctctg cccaccaagg atgcctgcca ccgtttcctg cagacgtctt catggttcct 3240

cagtacggct acctgacgct caacaatgga agtcaagcgt taggacgttc ttctttctac 3300

tgtctggaat acttcccttc tcagatgctg agaaccggca acaactttca gttcagctac 3360

actttcgagg acgtgccttt ccacagcagc tacgcacaca gccagagtct agatcgactg 3420

atgaaccccc tcatcgacca gtacctatac tacctggtca gaacacagac aactggaact 3480

gggggaactc aaactttggc attcagccaa gcaggcccta gctcaatggc caatcaggct 3540

agaaactggg tacccgggcc ttgctaccgt cagcagcgcg tctccacaac caccaaccaa 3600

aataacaaca gcaactttgc gtggacggga gctgctaaat tcaagctgaa cgggagagac 3660

tcgctaatga atcctggcgt ggctatggca tcgcacaaag acgacgagga ccgcttcttt 3720

ccatcaagtg gcgttctcat atttggcaag caaggagccg ggaacgatgg agtcgactac 3780

agccaggtgc tgattacaga tgaggaagaa attaaagcca ccaaccctgt agccacagag 3840

gaatacggag cagtggccat caacaaccag gccgctaaca cgcaggcgca aactggactt 3900

```
gtgcataacc agggagttat tcctggtatg gtctggcaga accgggacgt gtacctgcag     3960

ggccctattt gggctaaaat acctcacaca gatggcaact ttcacccgtc tcctctgatg     4020

ggtggatttg gactgaaaca cccacctcca cagattctaa ttaaaaatac accagtgccg     4080

gcagatcctc ctcttacctt caatcaagcc aagctgaact ctttcatcac gcagtacagc     4140

acgggacaag tcagcgtgga aatcgagtgg gagctgcaga aagaaaacag caagcgctgg     4200

aatccagaga tccagtatac ttcaaactac tacaaatcta caaatgtgga ctttgctgtc     4260

aataccgaag gtgtttactc tgagcctcgc cccattggta ctcgttacct cacccgtaat     4320

ttgtaattgc ctgttaatca ataaaccggt taattcgttt cagttgaact ttggtctctg     4380

cg                                                                    4382


<210> 150
<211> 736
<212> PRT
<213> Adeno-associated virus 9

<400> 150
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 151
<211> 736
<212> PRT
<213> Adeno-associated virus 9

<400> 151
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Glu Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495
```

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500   505   510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530   535   540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565   570   575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580   585   590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595   600   605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 152
<211> 623
<212> PRT
<213> Adeno-associated virus 9

<400> 152
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1   5   10   15

```
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Arg Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Val Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Glu Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
        275                 280                 285
```

```
Leu Pro Val Asp Ile Thr Gln Asn Arg Ile Tyr Arg Ile Leu Gln Leu
    290                 295                 300


Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320


Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335


Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350


Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365


Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380


Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400


Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415


Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430


Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445


Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460


Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480


Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
                485                 490                 495


Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510


Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525


Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
    530                 535                 540


Leu Leu Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560
```

Cys Phe Thr His Gly Val Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
                565   570   575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
            580   585   590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
        595   600   605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610   615   620

<210> 153
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 153
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

```
gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg     1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct     1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata     1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a              2211

<210> 154
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 154
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 155
<211> 2460
<212> DNA
<213> Adeno-associated virus

<400> 155
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgaccg agtcattacc        60

accagcaccc ggacttgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc       120

agccaatcgg gtgccaccaa cgacaaccac tacttcggct acagcacccc ttgggggtat       180

tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac       240

aacaactggg gattcatggc tgccgatggt tatcttccag attggctcga ggacactctc       300

tctgaaggaa tcagacagtg gtggaagctc aaacctggcc caccaccgcc gaaacctaac       360

caacaacacc gggacgacag taggggtctt gtgcttcctg ggtacaagta cctcggaccc       420

ttcaacggac tcgacaaagg agagccggtc aacgaggcag acgccgcggc cctcgagcac       480

gacaaagcct acgaccacca gctcaagcaa ggggacaacc cgtacctcaa atacaaccac       540

gcggacgctg aatttcagga gcgtcttcaa gaagatacgt ctttcggggg caacctcggg       600

cgagcagtct tccaggccaa aaagagggta ctcgagcctc ttggtctggt tgaggaagct       660

gttaagacgg ctcctggaaa aaagagacct atagagcagt ctcctgcaga accggactct       720

tcctcgggca tcggcaaatc aggccagcag cccgctaaga aaagactcaa ttttggtcag       780

actggcgaca cagagtcagt cccagaccct caaccaatcg gagaaccccc cgcagccccc       840

tctggtgtgg gatctaatac aatggcttca ggcggtgggg caccaatggc agacaataac       900

gaaggcgccg acggagtggg taattcctcg ggaaattggc attgcgattc cacatggatg       960

ggcgacagag ttatcaccac cagcacaaga acctgggccc tccccaccta caataatcac      1020

ctctacaagc aaatctccag cgaatcggga gccaccaacg acaaccacta cttcggctac      1080

agcaccccct gggggtattt tgactttaac agattccact gtcacttctc accacgtgac      1140

tggcagcgac tcatcaacaa caactgggga tttagaccca agaaactcaa tttcaagctc      1200

ttcaacatcc aagtcaagga ggtcacgcag aatgatggaa ccacgaccat cgccaataac      1260

cttaccagca cggtgcaggt cttcacagac tctgagtacc agctgcccta cgtcctcggt      1320

tcggctcacc agggctgcct tccgccgttc ccagcagacg tcttcatgat tcctcagtac      1380
```

```
ggctacttga ctctgaacaa tggcagccaa gcggtaggac gttcttcatt ctactgtcta     1440

gagtattttc cctctcagat gctgaggacg ggaaacaact tcaccttcag ctacactttt     1500

gaagacgtgc ctttccacag cagctacgcg cacagccaga gtctggatcg gctgatgaat     1560

cctctcattg accagtacct gtattacctg agcaaaactc agggtacaag tggaacaacg     1620

cagcaatcga gactgcagtt cagccaagct gggcctagct ccatggctca gcaggccaaa     1680

aactggctac cgggacccag ctaccgacag cagcgaatgt ctaagacggc taatgacaac     1740

aacaacagtg aatttgcttg gactgcagcc accaaatatt acctgaatgg aagaaattct     1800

ctggtcaatc ccgggccccc aatggccagt cacaaggacg atgaggaaaa gtatttcccc     1860

atgcacggaa atctcatctt tggaaaacaa ggcacaggaa ctaccaatgt ggacattgaa     1920

tcagtgctta ttacagacga agaagaaatc agaacaacta atcctgtggc tacagaacaa     1980

tacggacagg ttgccaccaa ccatcagagt cagaacacca cagcttccta tggaagtgtg     2040

gacagccagg gaatcttacc tggaatggtg tggcaggacc gcgatgtcta tcttcaaggt     2100

cccatttggg ccaaaactcc tcacacggac ggacactttc atccttctcc gctcatggga     2160

ggctttggac tgaaacaccc tcctccccag atcctgatca aaaacacacc tgtgccagcg     2220

aatcccgcga ccactttcac tcctggaaag tttgcttcgt tcattaccca gtattccacc     2280

ggacaggtca gcgtggaaat agagtgggag ctgcagaaag aaaacagcaa acgctggaac     2340

ccagaaattc agtacacctc caactacaac aagtcggtga atgtggagtt taccgtggac     2400

gcaaacggtg tttattctga accccgccct attggcactc gttaccttac ccggaacttg     2460


<210> 156
<211> 3123
<212> DNA
<213> Adeno-associated virus

<400> 156
gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt       60

gcgtcgacaa gatggtgatc tggtgggagg agggaaagat gaccgccaag gtcgtggaat      120

ctgccaaagc cattctgggt ggaggcaagg ttcgtgtgga ccagaaatgc aagtcttcgg      180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg      240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg      300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact      360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg      420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc      480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcggaca      540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac      600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt      660

tggaatgctt tcccgtgtca gaatctcaac ccgtttctgt cgtcagaaaa acgtatcaga      720
```

aactttgtta cattcatcat atcatgggaa aagtaccaga cgcctgcact gcctgcgacc 780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg 840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag 900

tggtggaagc tcaaacctgg cccaccaccg ccgaaaccta accaacaaca ccgggacgac 960

agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ccttcaacgg actcgacaaa 1020

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaagc ctacgaccac 1080

cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag 1140

gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc 1200

aaaaagaggg tactcgagcc tcttggtctg gttgaggaag ctgttaagac ggctcctgga 1260

aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcaaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccaggcc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cgcggtgcag 1860

gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag 2040

atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160

ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

ttcagccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280

agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacctgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccagtggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccatcaga gtcagaacac cacagcttcc tatggaagtg tggacagcca gggaatctta 2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

cctcacacgg acggacactt tcatccttct ccgctcatgg gaggctttgg actgaaacac 2760 cctcctcccc agatcctgat caaaaacaca cctgtgccag cgaatcccgc gaccactttc 2820

actcctggaa agtttgcttc gttcattacc cagtattcca cctgacaggt cagcgtggaa 2880

atagagtggg agctgcagaa agaaaacagc aaacgctgga acccagaaat tcagtacacc 2940

tccaactaca acaagtcggt gaatgtggag tttaccgtgg acgcaaacgg tgtttattct 3000

gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

taagccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttcgtttaaa 3120

cct 3123

<210> 157
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 157
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Gly Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Ala Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
435 440 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

```
Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Val Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 158
<211> 3123
<212> DNA
<213> Adeno-associated virus

<400> 158
gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggaaagat gaccgccaag gtcgtggaat 120

ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg 180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg 240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg 300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact 360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg 420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc 480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcgggca 540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac 600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt 660

tggaatgctt tcccgtgtca gaatctcaac ccgtttctgt cgtcagaaaa acgtatcaga 720

aactttgtta cattcatcat atcatgggaa aagaaccaga cgcctgcact gcctgcgacc 780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg 840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag 900

tggtggaagc tcaaacctgg cccaccaccg ccgaaaccta accaacaaca ccgggacgac 960

agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ccttcaacgg actcgacaaa 1020

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaagc ctacgaccac 1080

cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag 1140

gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc 1200

aaaaagaggg tactcgagcc tcttggtctg gttgaggaag ctgttaagac ggctcctgga 1260

aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcgaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccagacc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacgata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cacggtgcag 1860 gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag 2040

atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160

ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

ttcagccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280

agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacctgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccaatggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccatcaga gtcaggacac cacagcttcc tatggaagtg tggacagcca gggaatctta 2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

cctcacacgg acggacactt tcatccttct ccgctcatgg gaggctttgg actgaaacac 2760

cctcctcccc agatcctgat caaaaacaca cctgtgccag cgaatcccgc gaccactttc 2820

actcctggaa agtttgcttc gttcattacc cagtattcca ccggacaggt cagcgtggaa 2880

atagagtggg agctgcagaa agaaaacagc aaacgctgga acccagaaat tcagtacacc 2940

tccaactaca acaagtcggt gaatgtggag tttaccgtgg acgcaaacgg tgtttattct 3000

gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

taaaccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttcgcggccg 3120

cta 3123

<210> 159
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 159
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Glu Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asp Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asp Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
```

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 160
<211> 3113
<212> DNA
<213> Adeno-associated virus

<400> 160
gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt       60

gcgtcgacaa gatggtgatc tggtgggagg agggaaagat gaccgccaag gtcgtggaat      120

ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg      180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg      240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg      300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact      360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg      420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc      480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcggaca      540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac      600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt      660

tggaatgctt tcccgtgtca gaatctcaac ccgttcctgt cgtcagaaaa acgtatcaga      720

aactttgtta cattcatcat atcatgggaa aagtaccaga cgcctgcact gcctgcgacc      780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg      840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag      900
```

tggtggaagc tcaaacctgg cccaccaccg ccgaaaccta accaacaaca ccgggacgac 960

agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ccttcaacgg actcgacaaa 1020

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaagc ctacgaccac 1080

cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag 1140

gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc 1200

aaaaagaggg tactcgagcc tcttggtctg gttgaggaag ctgttaagac ggctcctgga 1260

aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcaaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccagacc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaat 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cacggtgcag 1860

gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag 2040

atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160

ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

ttcaaccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280

agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacccgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccaatggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacgac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccgtcaga gtcagaacac cacagcttcc tatggaagtg tggacagcca gggaatctta 2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

cctcacacgg acggacactt tcatccttct ccgctcatgg gaggctttgg actgaaacac 2760

cctcctcccc agatcctgat caaaaacaca cctgtgccag cgaatcccgc gaccactttc 2820

actcctggaa agtttgcttc gttcattacc cagtattcca ccggacaggt cagcgtggaa 2880

atagagtggg agctgcagaa agaaaacagc aaacgctgga acccggaaat tcagtacacc 2940

```
tccaactaca acaagtcggt gaatgtggag tttaccgtgg acgcaaacgg tgtttattct     3000

gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa     3060

taaaccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttc            3113


<210> 161
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 161
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445


Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Asn Gln
    450                 455                 460


Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Pro Asn Gly
            500                 505                 510


Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Gln Val Ala Thr Asn Arg Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590


Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 162
<211> 3122
<212> DNA
<213> Adeno-associated virus

<400> 162
agcggccgcg aattcgccct ttctacggct gcgtcaactg gaccaatgaa aactttccct       60
```

tcaacgattg cgtcgacaag atggtgatct ggtgggagga gggaaagatg accgccaagg 120

tcgtggaatc tgccaaagcc attctgggtg gaagcaaggt tcgtgtggac cagaaatgca 180

ggtcttcggc ccagatcgac ccgactccgg tgattgtcac ctctaacacc aacatgtgcg 240

ccgtgattga cggaaactcg accaccttcg agcaccagca gccgttgcaa gaccggatgt 300

tcaaatttga acttacccgc cgtttggatc atgactttgg gaaggtcacc aagcaggaag 360

tcaaagactt tttccggtgg gctcaagatc acgtgactga ggtggagcat gagttctacg 420

tcaaaaaggg tggagccaag aaaaggcccg cccccgatga tgtatatata aatgagccca 480

agcgggcgcg cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgataaact 540

acgcggacag gtaccaaaac aaatgttctc gtcacgtggg catgaatctg atgctgtttc 600

cctgtcgaca atgcgaaaga atgaatcaga attcaaatat ctgcttcaca cacgggcaaa 660

aagactgttt ggaatgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcagaaaaa 720

cgtatcagaa actttgttac attcatcata tcatgggaaa agtaccagac gcctgcactg 780

cctgcgacct ggtaaatgtg gacttggatg actgtatttc tgagcaataa atgacttaaa 840

tcaggtatgg ctgctgacgg ttatcttcca gattggctcg aggacactct ctctgaagga 900

atcagacagt ggtggaagct caaacctggc ccaccaccgc cgaaacctaa ccaacaacac 960

cgggacgaca gtaggggtct tgtgcttcct gggtacaagt acctcggacc cttcaacgga 1020

ctcgacaaag gagagccggt caacgaggca gacgccgcgg ccctcgagca cgacaaagcc 1080

tacgaccacc agctcaagca aggggacaac ccgtacctca aatacaacca cgcggacgct 1140

gaatttcagg agcgtcttca agaagatacg tctttcgggg gcaacctcgg gcgagcagtc 1200

ttccaggcca aaaagagggt actcgagcct cttggtctgg ttgaggaagc tgttaagacg 1260

gctcctggaa aaaagagacc tatagagcag tctcctgcag aaccggactc ttcctcgggc 1320

atcggcaaat caggccagca gcccgctaag aaaagactca attttggtca gactggcgac 1380

acagagtcag tcccagaccc tcaaccaatc ggagaacccc ccgcagcccc ctctggtgtg 1440

ggatctaata caatggcttc aggcggtggg gcaccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtaattcctc gggaaattgg cattgcgatt ccacatggat gggcgacaga 1560

gttatcacca ccagcacaag aacctgggcc ctccccacct acaataatcg cctctacaag 1620

caaatctcca gcgaatcggg agccaccaac gacaaccact acttcggcta cagcaccccc 1680

tgggggtatt ttgactttaa cagattccac tgtcacttct caccacgtga ctggcagcga 1740

ctcatcaaca acaactgggg atttagaccc aagaaactca atttcaagct cttcaacatc 1800

caagtcaagg aggtcacgca gaatgatgga accacgacca tcgccaataa ccttaccagc 1860

acggtgcagg tcttcacaga ctctgagtac cagctgccct acgtcctcgg ttcggctcac 1920

cagggctgcc ttccgccgtt cccagcagac gtcttcatga ttcctcagta cggctacttg 1980

actctgaaca atggcagcca agcggtagga cgttcttcat tctactgtct agagtatttt 2040

ccctctcaga tgctgaggac gggaaacaac ttcaccttca gctacacttt tgaagacgtg 2100 cctttccaca gcagctacgc gcacagccag agtctggatc ggctgatgaa tcctctcatt 2160

gaccagtacc tgtattacct gagcaaaact cagggtacaa gtggaacaac gcagcaatcg 2220

agactgcagt tcagccaagc tgggcctagc tccatggctc agcaggccaa aaactggcta 2280

ccgggaccca gctaccgaca gcagcgaatg tctaagacgg ctaatgacaa caacaacagt 2340

gaatttgctt ggactgcagc caccaaatat tacctgaatg gaagaaattc tctggtcaat 2400

cccgggcccc caatggccag tcacaaggac gatgaggaaa agtatttccc catgcacgga 2460

aatctcatct ttggaaaaca aggcacagga actaccaatg tggacattga atcagtgctt 2520

attacagacg aagaagaaat cagaacaact aatcctgtgg ctacagaaca atacggacag 2580

gttgccacca accatcagag tcagaacacc acagcttcct atggaagtgt ggacagccag 2640

ggaatcttac ctggaatggt gtggcaggac cgcgatgtct atcttcaagg tcccatttgg 2700

gccaaaactc ctcacacgga cggacacttt catccttctc cgctcatggg aggctttgga 2760

ctgaaacacc ctcctcccca gatcctgatc aaaaacacac ctgtgccagc gaatcccgcg 2820

accactttca ctcctggaaa gtttgcttcg ttcattaccc agtattccac cggacaggtc 2880

agcgtggaaa tagagtggga gctgcagaaa gaaaacagca aacgctggaa cccagaaatt 2940

cagtacacct ccaactacaa caagtcggtg aatgtggagt ttaccgtgga cgcaaacggt 3000

gtttattctg aaccccgccc tattggcact cgttacctta cccggaactt gtaatttcct 3060

gttaatgaat aaaccgattt atgcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 163
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 163
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn Arg Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445


Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510


Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590


Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 164
<211> 3121
<212> DNA
<213> Adeno-associated virus

<400> 164
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagcaatt acagattacg ggtgaggtaa cgggtgccga tggggcgagg ctcagaataa 120

gtgccatctg tgttaacagc aaagtccaca tttgtagatt tgtagtagtt ggaagtgtat 180

tgaatctctg ggttccagcg tttgctgttt tctttctgca gctcccattc aatttccacg 240

ctgacctgtc cggtgctgta ctgcgtgatg aacgacgcca gcttagcttg actgaaggta 300

gttggaggat ccgcgggaac aggtgtattc ttaatcagga tctgaggagg cgggtgtttc 360

agtccaaagc cccccatcag cggcgaggga tgaaagtttc cgtccgtgtg aggaatcttg 420

gcccagatag gaccctgcag gtacacgtcc cggttctgcc agaccatgcc aggtaaggct 480

ccttgactgt tgacggcccc tacaatagga gcggcgtttt gctgttgcag gttatcggcc 540

accacgccgt actgttctgt ggccactggg ttggtggttt taatttcttc ctcactggtt 600

agcataacgc tgctatagtc cacgttgcct tttccagctc cctgtttccc aaacattaag 660

actccgctgg acggaaaaaa tcgctcttcg tcgtccttgt gggttgccat agcgacaccg 720

ggatttacca gagagtctct gccattcaga tgatacttgg tggcaccggt ccaggcaaag 780

ttgctgttgt tattttgcga cagtgtcgtg gagacgcgtt gctgccggta gcagggcccg 840

ggtagccagt ttttggcctg agccgacatg ttattaggcc cggcctgaga aaatagcaac 900

tgctgagttc ctgcggtacc tcccgtggac tgagtccgag acaggtagta caggtactgg 960

tcgatgaggg ggttcatcag ccggtccagg ctttggctgt gcgcgtagct gctgtgaaaa 1020

ggcacgtcct caaactggta gctgaactca aagttgttgc ccgttctcag catttgagaa 1080

ggaaagtact ccaggcagta gaaggaggaa cggcccacgg cctgactgcc attgttcaga 1140 gtcaggtacc cgtactgagg aatcatgaag acgtccgccg ggaacggagg caggcagccc 1200

tggcgcgcag agccgaggac gtacgggagc tggtattccg agtccgtaaa gacctgaatc 1260

gtgctggtaa ggttattggc gatggtcttg gtgccttcat tctgcgtgac ctccttgacc 1320

tggatgttga agagcttgaa gttgagtctc ttgggccgga atccccagtt gttgttgatg 1380

agtcgctgcc agtcacgtgg tgagaagtgg cagtggaatc tgttaaagtc aaaatacccc 1440

cagggggtgc tgtagccgaa gtaggtgttg tcgttggtgc ttcctcccga agtcccgttg 1500

gagatttgct tgtagaggtg gttgttgtag gtggggaggg cccaggttcg ggtgctggtg 1560

gtgatgactc tgtcgcccag ccatgtggaa tcgcaatgcc aatttcctga ggaactaccc 1620

actccgtcgg cgccttcgtt attgtctgcc attggagcgc caccgcctgc agccattgta 1680

ccagatccca gaccagaggg gcctgcgggg ggttctccga ttggttgagg gtcgggcact 1740

gactctgagt cgccagtctg cccaaagttg agtctctttt tcgcgggctg ctggcctttc 1800

ttgccgatgc ccgtagtgga gtctggagaa cgctggggtg atggctctac cggtctcttc 1860

tttccaggag ccgtcttagc gccttcctca accagaccga gaggttcgag aacccgcttc 1920

ttggcctgga agactgctcg tccgaggttg cccccaaaag acgtatcttc ttgcagacgc 1980

tcctgaaact cggcgtcggc gtggttatac cgcaggtacg gattgtcacc cgctttgagc 2040

tgctggtcgt aggccttgtc gtgctcgagg gccgctgcgt ccgccgcgtt gacgggctcc 2100

cccttgtcga gtccgttgaa gggtccgagg tacttgtagc caggaagcac cagaccccgg 2160

ccgtcgtcct gcttttgctg gttggctttg ggcttcgggg ctccaggttt cagcgcccac 2220

cactcgcgaa tgccctcaga gaggttgtcc tcgagccaat ctggaagata accatcggca 2280

gccatacctg atctaaatca tttattgttc aaagatgcag tcatccaaat ccacattgac 2340

cagatcgcag gcagtgcaag cgtctggcac ctttcccatg atatgatgaa tgtagcacag 2400

tttctgatac gcctttttga cgacagaaac gggttgagat tctgacacgg gaaagcactc 2460

taaacagtct ttctgtccgt gagtgaagca gatatttgaa ttctgattca ttctctcgca 2520

ttgtctgcag ggaaacagca tcagattcat gcccacgtga cgagaacatt tgttttggta 2580

cctgtccgcg tagttgatcg aagcttccgc gtctgacgtc gatggctgcg caactgactc 2640

gcgcacccgt ttgggctcac ttatatctgc gtcactgggg gcgggtcttt tcttggctcc 2700

acccttttg acgtagaatt catgctccac ctcaaccacg tgatcctttg cccaccggaa 2760

aaagtctttg acttcctgct tggtgacctt cccaaagtca tgatccagac ggcgggtgag 2820

ttcaaatttg aacatccggt cttgcaacgg ctgctggtgt tcgaaggtcg ttgagttccc 2880

gtcaatcacg gcgcacatgt tggtgttgga ggtgacgatc acgggagtcg ggtctatctg 2940

ggccgaggac ttgcatttct ggtccacgcg caccttgctt cctccgagaa tggctttggc 3000

cgactccacg accttggcgg tcatcttccc ctcctcccac cagatcacca tcttgtcgac 3060

acagtcgttg aagggaaagt tctcattggt ccagttgacg cagccgtaga agggcgaatt 3120

c 3121

```
<210> 165
<211> 733
<212> PRT
<213> Adeno-associated virus

<400> 165
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Leu
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe His Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160


Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175


Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190


Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205


Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220


Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240


Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
```

245 250 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305 310 315 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
325 330 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
340 345 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
355 360 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
420 425 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
435 440 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
450 455 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465 470 475 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
485 490 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
500 505 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser

515 520 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
530 535 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545 550 555 560

Gly Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
565 570 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
580 585 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
610 615 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
645 650 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
675 680 685

Ser Lys Arg Arg Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 166
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 166
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445


Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510


Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
```

```
Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590


Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 167
<211> 3127
<212> DNA
<213> Adeno-associated virus

<400> 167
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt        60

attgattaac atgcaattac agattacggg tgaggtaacg agtgccaata gggcgaggct       120

cagagtaaac accctggctg tcaacggcaa agtccacacc agtctgcttt tcaaagttgg       180

aggtgtactg aatctccggg tcccagcgct tgctgttttc cttctgcagc tcccactcga       240

tttccacgct gacttgtccg gtgctgtact gtgtgatgaa cgaagcaaac ttggcaggag       300

taaacacctc cggaggatta gcgggaacgg gagtgttctt gatcaggatc tgaggaggcg       360

gatgtttaag tccaaagccg cccatcaaag gagacgggtg aaagttgcca tccgtgtgag       420

gaatcttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccag       480

gtaaggctcc ctggttgttg acaacttgtg tctgggctgc agtattagcc gcttgtaagt       540

tgctgctgac tatcccgtat tcttccgtgg ctacaggatt agtaggacga atttcttctt       600

catttgtcat taacacattt tccaatgtag ttttgttagt tgctccagtt tttccaaaaa       660
```

tcaggactcc gctggatggg aaaaagcggt cctcgtcgtc cttgtgagtt gccatggcga 720

cgccgggatt aaccaacgag tttctgccgt tcaggtgata tttggtggca ccagtccaag 780

caaagttgct gttgttgttt tgatccagcg ttttggagac cctttgttgc cggaagcagg 840

gtccaggtaa ccaattcttg gcttgttcgg ccatagttga aggcccgccc tggtaaaact 900

gcagttcccg attgccagct gtgcctcctg ggtcactctg tgttctggcc aggtagtaca 960

agtactggtc gatgagggga ttcatcagcc ggtccaggct ctggctgtgt gcgtagctgc 1020

tgtggaaagg cacgtcctcg aagctgtagc tgaactcaaa gttgttgccc gttctcagca 1080

tctgagaggg gaagtactcc aggcagtaga aggaggaacg tcccacagac tgactgccat 1140

tgttgagagt caggtagccg tactgaggaa tcatgaagac gtccgccggg aacggaggca 1200

ggcagccctg gtgcgcagag ccgaggacgt acggcagctg gtattccgag tccgagaata 1260

cctgaatcgt gctggtaagg ttattagcga tggtcgtaac gccgtcattc gtcgtgacct 1320

ccttgacctg gatgttgaag agcttgaacc gcagcttctt gggccggaat ccccagttgt 1380

tgttgatgag tcgctgccag tcacgtggtg agaagtggca gtggaatctg ttaaagtcaa 1440

aataccccca gggggtgctg tagccgaagt aggtgttgtc gttggtacta cctgcagttt 1500

cactggagat ttgctcgtag aggtggttgt tgtaggtggg cagggcccag gttcgggtgc 1560

tggtggtaat gactctgtcg cccagccatg tggaatcgca atgccaattt cctgaggcat 1620

tacccactcc gtcggcacct tcgttattgt ctgccattgg tgcgccaccg cctgcagcca 1680

ctgtaccaga tcccacacta gagggcgctg ctggaggttc tccgagaggt tgagggtcgg 1740

ggactgactc tgagtcgcca gtctgaccga aattgagtct ctttctggcg ggctgctggc 1800

ccttcttgcc gatgcccgtg gaggagtcgg gggaacgctg aggtgacggc tctaccggtc 1860

tcttctttgc aggagccgtc ttagcgcctt cctcaaccag accgagaggt tcgagaaccc 1920

gcttcttggc ctggaagact gctcgcccga ggttgccccc aaatgacgta tcttcttgca 1980

gacgctcctg aaactcggcg tcggcgtggt tataccgcag gtacgggttg tcacccgcat 2040

tgagctgctg gtcgtaggcc ttgtcgtgct cgagggccgc tgcgtccgcc gcgttgacgg 2100

gctcccccctt gtcgagtccg ttgaagggtc cgaggtactt gtagccagga agcaccagac 2160

cccggccgtt gtcctgcttt tgctggttgg ctttgggttt cggggctcca ggtttcaggt 2220

cccaccactc gcgaatgccc tcagagaggt tgtcctcgag ccaatctgga agataaccat 2280

cggcagccat acctgattta aatcatttat tgttcaaaga tgcagtcatc caaatccaca 2340

ttgaccagat cgcaggcagt gcaagcgtct ggcacctttc ccatgatatg atgaatgtag 2400

cacagtttct gatacgcctt tttgacgaca gaaacgggtt tagattctga cacgggaaag 2460

cactctaaac agtctttctg tccgtgagtg aagcagatat ttgaattctg attcattctc 2520

tcgcattgtc tgcagggaaa cagcatcaga ttcatgccca cgtgacgaga acatttgttt 2580

tggtacctgt ctgcgtagtt gatcgaagct tccgcgtctg acgtcgatgg ctgcgcaact 2640

gactcgcgca cccgtttggg ctcacttata tctgcgtcac tgggggcggg tcttttcttg 2700

```
gctccaccct ttttgacgta gaattcatgc tccacctcaa ccacgtaatc ctttgcccac     2760

cggaaaaagt ctttgacttc ctgcttggtg accttcccaa agtcatgatc cagacggcgg     2820

gtgagttcaa atttgaacat ccggtcttgc aacggctgct ggtgttcgaa ggtcgttgag     2880

ttcccgtcga tcacggcgca catgttggtg ttggagatga cgatcgcggg agtcgggtct     2940

atctgggccg aggacttgca tttctggtcc acgcgcacct tgcttcctcc gagaatggct     3000

ttggccgact ccacgacctt ggcggtcatc ttcccctcct cccaccagat caccatcttg     3060

tcgacacagt cgttgaaggg aaagttctca ttggtccagt tgacgcagcc gtagaaaggg     3120

cgaattc                                                               3127
```

<210> 168
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 168

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Arg Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Val Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175
```

```
Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Ser Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Val His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445
```

```
Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Cys Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720
```

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 169
<211> 3106
<212> DNA
<213> Adeno-associated virus

<400> 169
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg ggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaattttggc ccagatggga ccctgcaggc acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aagaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtctaggc tctggctgtg cacatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagtag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagctgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740 agtcgccagt ctgcccaaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcga 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccct gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtctgaggta cttgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgtcctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttgacca gatcgcaggc cgagcaagca 2340

atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt 2400

ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460

tgcgtgaagc aaatgttgaa attctgattc actctctcgc atgtcttgca gggaaacagc 2520

atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc 2580

ggagctcctt ccgcgtctga cgtcgatgga ttcgcgactg aggggcaggc ccgcttgggc 2640

tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ccccacccctt tctgacgtag 2700

aacccatgcg ccacctcggt cacgtgatcc tgcgcccagc ggaagaacct tttgacttcc 2760

tgctttgtca ccttgccaaa gttatgctcc agacggcggg tgggttcaaa tttgaacatc 2820

cggtcctgca acggctgctg gtgctcgaag gtggcgctgt tcccgtcaat cacggcgcac 2880

atgttggtgt tggaggtgac ggtcacgggg gtggggtcga tctgggcgga cgacttgcac 2940

ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatct tgccctcctc ccaccagatc accatcttgt cggcgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg tagaaagggc gaattc 3106

<210> 170
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 170
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Ser Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335
```

```
Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Cys Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Val
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Leu
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Arg Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605
```

```
Pro Ile Trp Ala Glu Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 171
<211> 3102
<212> DNA
<213> Adeno-associated virus

<400> 171
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt        60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct       120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg       180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga       240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag       300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg       360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag       420

gaatttcggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg       480

gcagagcccc ctggctgttg acagtctgtg tccggggtcc ggccgtagac gattgcaggt       540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct       600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa       660

ccagcactcc gttgatggga aggaactggt cctcgtcgtc cttgttggtg gccatggcta       720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg       780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg       840

gtccgggcag ccagttcttt gattgctcgg ccacggtgtt gggcccagcc tgatggaact       900
```

```
gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt      960
cgatgagggg attcatcagc cggtccaggc tctggctgtg cgcatagctg ctgtggaaag     1020
gcacttcctc aaaggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag     1080
gaaagtactc caggcagcag aaggaggaac gtcccacaga ctgactgccg ttgtttagag     1140
tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct     1200
ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg     1260
tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct     1320
ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga     1380
gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc     1440
agggggtgct gtagccgaag aagtggttgt cgttggtagc cccgctctga cttgatatct     1500
gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga     1560
ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt     1620
cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc     1680
ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg     1740
agtcgccagt ctgcccaaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga     1800
tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccggaagcc gtcttagcgc     1860
cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc     1920
cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt     1980
ggttgtactt gaggtacggg ttgtccccct gctcgagctg cttgtcgtag gccttgtcgt     2040
gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg     2100
gtccgaggta cttgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt     2160
tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga     2220
ggttgtcctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt     2280
tattgctcag aaacacagtc atccaggtcc acgttgacca gatcgcaggc cgagcaagca     2340
atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt     2400
ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg     2460
tgcgtgaagc aaatgttgaa attctgattc attctctcgc atgtcttgca gggaaacagc     2520
atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc     2580
ggagctcctt ccgcgtctga cgtcgatgga tccgcgactg aggggcaagc ccgcttgggc     2640
tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag     2700
aactcatgcg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc     2760
tgctttgtca ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc     2820
cggtcttgta acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac     2880
atgttggtgt tggaagtgac gatcacgggg gtgggatcga tctgggcgga cgacttgcac     2940
```

```
ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg     3000

gccgtcatct tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga     3060

aagttctcat tggtccagtt gacgcagccg aagggcgaat tc                        3102


<210> 172
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 172
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160


Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190


Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205


Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220
```

```
His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495
```

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
515 520 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
530 535 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545 550 555 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
565 570 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 173
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 173

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Gly Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270
```

```
Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540
```

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545   550   555   560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565   570   575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580   585   590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595   600   605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610   615   620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625   630   635   640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645   650   655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660   665   670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675   680   685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690   695   700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705   710   715   720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725

<210> 174
<211> 3106
<212> DNA
<213> Adeno-associated virus

<400> 174
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat cagccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420 gaattttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aagaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtccaggc tctggctgtg cgcatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttatcgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagtag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagccgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg cggctggccg ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcgc 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtccccct gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtccgaggta cctgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgccctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttggcca gatcgcaggc cgagcaagca 2340

atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt 2400

ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460

```
tgcgtgaagc aaatgttgaa attctgattc attctctcgc atgtcttgca ggggaacagc     2520

atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc     2580

ggagctcctt ccgcgtctga cgtcgatgga tccgcgactg aggggcaggc ccgcttgggc     2640

tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ctccacccctt tctgacgtag     2700

aactcatacg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc     2760

tgctttgtca ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc     2820

cggtcttgta acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac     2880

atgttggtgt tggaagtgac gatcacgggg gtgggatcga tctgggcgga cgacttgcac     2940

ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg     3000

gccgtcatcc tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga     3060

aagttctcat tggtccagtt gacgcagccg tagaaagggc gaattc                    3106
```

```
<210> 175
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 175
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160
```

```
Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Met Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430
```

```
Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Gly Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Gly Val Phe Thr Pro
                645                 650                 655

Ala Leu Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700
```

```
Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 176
<211> 3098
<212> DNA
<213> Adeno-associated virus

<400> 176
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta        60

acaagtaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa       120

accccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgaggtgtac       180

tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg       240

ctgacctggc cggtgctgta ctgcgtgata aatgaggcaa actaggcagg agtaaacacc       300

cctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg       360

agtccaaatc cgcccatcag gggagacggg tgaaagttgc cgtccgtgtg aggaattttg       420

gcccagatgg gaccctgcag gtacacgtcc cggttctgcc agaccatgcc gggcagagcc       480

ccctggctgt tgacagtctg tgtctggggt ccggccgtag acgattgcag gttgctggag       540

accacaccgt attcttctgt agccacggga ttggtggttt tgatctcctc ctcgctggtc       600

attagcacgt tttccagcgt tgtcttgttg gcagcccccg ttttgccaaa aaccagcact       660

ccgttgatgg gaaagaactg gccctcgtcg tccttgttgg tggccatggc tacgcccggg       720

ttggttaatg aatttctacc attcagatgg tatttagtgg ccccggtcca ggcaaagtta       780

ctgttgttgt tgctgtctat gtttttgac agtctctgct gccgataaca gggtccgggc       840

agccagttct ttgattgctc ggccatggtg ttgggcccag cctgatggaa ctgcagctcc       900

cttgtggacc ccgtagtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgagg       960

ggattcatca gccggtccag gctctggctg tgcgcatagc tgctgtggaa aggcacttcc      1020

tcaaaggtgt agctgaattc aaagttattg cccgttctca gcatctgaga aggaaagtac      1080

tccaggcagt agaaggagga acgtcccata gactgactgc cgttgtttag agtcagatat      1140

ccgtactgag gaatcatgaa cacgtccgca gggaacggag ggaggcagcc ctggtgcgca      1200

gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta      1260

aggttattag cgatggtcgt aacgccgtcg ttcgtcgtga cctccttgac ctggatgttg      1320

aacaacttga accgcagctt tctgggccgg aatccccagt tgttgttgat gagtcgctgc      1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttgaagt caaaatagcc ccagggggtg      1440

ctgtagccga agaagtggtt gtcgttggta gccccgctct gacttgatat ctgcttgtag      1500

aggtggttgt tgtaggtggg cagggcccag gtgcgggtgc tggtggtgat gactctgtcg      1560

cccagccatg tggaatcgca atgccaattt ccggaggcat tacccactcc gtcggcgcct      1620
```

tcgttattgt ctgccattgg tgcgccaccg cctgcagcca ttgtaccaga tcccagacct 1680

gagggcgcgg cgggaggttc tccgagaggt tgggggtcgg gcactgactc tgagtcgcca 1740

gtctgcccaa agttgagctt ctttttagcg ggctgctggc ctttcttgcc gatgcccgtg 1800

gaggagtcgg gggattctat gggtctcttc tttccaggag ccgtcttagc gccttcctca 1860

accagaccga gaggttcgag aacccgcttc ttggcctgga agactgctcg cccgaggttg 1920

cccccaaaag acgtatcttc ttgaagacgc tcctgaaact cagcgtcggc gtggttgtac 1980

ttgaggtacg ggttgtcccc ctgctcgagc tgcttgtcgt aggccttgtc gtgctcgagg 2040

gccgcggcgt ctgcctcgtt gaccggctct cccttgtcga gtccgttgaa gggtccgagg 2100

tacttgtagc caggaagcac cagaccccgg ccgtcgtcct gcttttgctg gttggctttg 2160

ggtttcgggg ctccaggttt caagtcccac cactcgcgaa tgccctcaga gaggttgtcc 2220

tcgagccaat ctggaagata accatcggca gccatacctg gtttaagtca tttattgctc 2280

agaaacacag tcatccaggt ccacgttgac cagatcgcag gccgagcaag caatctcggg 2340

agcccgcccc agcagatgat gaatggcaca gagtttccga tacgtcctct ttctgacgac 2400

cggttgagat tctgacacgc cggggaaaca ttctgaacag tctctggtcc cgtgcgtgaa 2460

gcaaatgttg aaattctgat tcattctctc gcatgtcttg cagggaaaca gcatctgaag 2520

catgcccgcg tgacgagaac atttgttttg gtacctgtcg gcaaagtcca ccggagctcc 2580

ttccgcgtct gacgtcgatg gatccgcgac tgaggggcag gcccgcttgg gctcgctttt 2640

atccgcgtca tcgggggcgg gcctcttgtt ggctccaccc tttctgacgt agaactcatg 2700

cgccacctcg gtcacgtgat cctgcgccca gcggaagaac tctttgactt cctgctttgt 2760

caccttgcca aagtcctgct ccagacggcg ggtgagttca aatttgaaca tccggtcttg 2820

taacggctgc tggtgctcga aggtggtgct gttcccgtca atcacggcgc acatgttggt 2880

gttggaagtg acgatcacgg gggtgggatc gatctgggcg gacgacttgc acttttggtc 2940

cacgcgcacc ttgctgccgc cgagaatggc cttggcggac tccacgacct tggccgtcat 3000

cttgccctcc tcccaccaga tcaccatctt gtcgacgcaa tcgttgaagg gaaagttctc 3060

attggtccag ttgacgcagc cgtagaaagg gcgaattc 3098

<210> 177
<211> 2187
<212> DNA
<213> Adeno-associated virus

<400> 177
atggctgccg atggttatct tccagattgg ctcgagggca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 300 caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaacggccag 480

ccgcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct 600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 840

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1140

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1200

acgggcgata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1260

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1320

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

gccggacccc agacacagac tgtcaacagc caggggggctc tgcccggcat ggtctggcag 1800

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 1860

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 1920

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 1980

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2040

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2100

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2160

acccgttacc tcacccgtaa cctgtaa 2187

<210> 178
<211> 728
<212> PRT

<213> Adeno-associated virus

<400> 178
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Gly Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145   150   155   160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165   170   175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180   185   190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195   200   205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210   215   220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225   230   235   240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245   250   255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser

```
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
```

530 535 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545 550 555 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
565 570 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 179
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 179
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145 150 155 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

```
Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590
```

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595   600   605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610   615   620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625   630   635   640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645   650   655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660   665   670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675   680   685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690   695   700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705   710   715   720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725

<210> 180
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 180
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145 150 155 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly

```
    370                 375                 380


Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400


Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415


His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430


Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445


Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460


Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480


Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495


Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510


Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525


Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540


Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560


Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575


Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590


Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
```

```
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 181
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 181
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160
```

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

```
Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700
```

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 182
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 182
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp

210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp

```
                485                 490                 495


Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510


Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525


Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540


Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560


Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575


Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590


Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 183
<211> 2215
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 183
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacgac aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca gcagcgagta tcaaagacat ctgcggataa caacaacagt 1500

gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agtttttttc ctcagagcgg 1620

ggttctcatc tttgggaagc aaggctcaga gaaaacaaat gtggacattg aaaaggtcat 1680

gattacagac gaagaggaaa tcaggacaac caatcccgtg gctacggagc agtatggttc 1740

tgtatctacc aacctccaga gaggcaacag acaagcagct accgcagatg tcaacacaca 1800

aggcgttctt ccaggcatgg tctggcagga cagagatgtg taccttcagg ggcccatctg 1860

ggcaaagatt ccacacacgg acggacattt tcacccctct cccctcatgg gtggattcgg 1920

```
acttaaacac cctccgcctc agatcctgat caagaacacg cctgtacctg cggatcctcc     1980

gaccaccttc aaccagtcaa agctgaactc tttcatcacc cagtattcta ctggccaagt     2040

cagcgtggag atcgagtggg agctgcagaa ggaaaacagc aagcgctgga accccgagat     2100

ccagtacacc tccaactact acaaatctac aagtgtggac tttgctgtta atacagaagg     2160

cgtgtactct gaaccccgcc ccattggcac ccgttacctc acccgtaatc tgtaa          2215


<210> 184
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 184
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Lys Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460
```

```
Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735
```

Leu

<210> 185
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 185
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Lys Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480
```

```
Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Gln Gly Asn Thr Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 186
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 186
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510
```

```
Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Gln Gly Asn Thr Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu


<210> 187
<211> 729
<212> PRT
<213> Adeno-associated virus

<400> 187
```

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
                20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190


Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205


Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220


His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255


Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270
```

```
Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540
```

```
Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560


Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575


Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590


Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605


Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620


Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625                 630                 635                 640


Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655


Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670


Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685


Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700


Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720


Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 188
<211> 3075
<212> DNA
<213> Adeno-associated virus

<400> 188
tgagaacttt cctttcaacg attgcgtcgg acaagatggt gatctggtgg gaggagggga       60

agatgaccgc caaggtcgtg gagtcggcca aagccattct tggaggaagc aaggtgcgtg      120

tggaccagaa atgcaagtcc tcggcccaga tagacccgac tcccgtgatc gtcacctcca      180

acaccaacat gtgcgccgtg attgacggga actcaacgac cttcgagcac cagcagccgt      240

tgcaagaccg gatgttcaaa tttgaactta cccgccgtct ggatcatgac tttggaaagg      300

tcaccaagca ggaagtgaaa gactttttcc ggtgggcaaa ggatcacgtg gttgaggtgg      360

agcatgaatt ctacgtcaaa aagggtggag ctaagaaaag acccgccccc agtgacgcag      420
```

atataagtga gcccaaacgg gcgcgcgagt cagttgcgca gccatcaacg tcagacgcgg 480

aagcttcgat caactacgcg gacaggtacc aaaaacaaat gttctcgtca cgtgggcatg 540

aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 600

ttcactcacg gacagaaaga ctgtttagag tgctttcccg tgtcagaatc tcaacccgtt 660

tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg 720

ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctctgaa 780

caataaatga tttaaatcag gtatggctgc cgatggttat cctccagatt ggctcgagga 840

cactctctct gaagggataa gacagtggtg gaagctcaaa cctggcccac caccaccaaa 900

gcccgcagag cggcataagg acgacagcag gggtcttgtg cttcctgggt acaagtacct 960

cggacccttc aacggactcg acaaggggga gccggtcaac gaggcagacg ccgcggccct 1020

cgagcacgac aaggcctacg accggcagct cgacagcgga gacaacccgt acctcaagta 1080

caaccacgcc gacgcagagt ttcaggagcg ccttaaagaa gatacgtctt ttgggggcaa 1140

cctcggacga gcagtcttcc aggcgaaaaa gagggttctt gaacctctgg gcctggttga 1200

ggaacctgtt aagacggctc cgggaaaaaa gaggccggta gagcactctc ctgtggagcc 1260

agactcctcc tcgggaaccg gaaaagcggg ccagcggcct gcaagaaaaa gattaaattt 1320

tggtcagact ggagacgcag actccgtacc tgacccccag cctctcggac agccaccagc 1380

agccccctct ggtctgggat ctactacaat ggctacaggc agtggcgcac caatggcaga 1440

caataacgag ggtgccgatg gagtgggtaa ttcctcagga aattggcatt gcgattccca 1500

atggctgggc gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacatacaa 1560

caaccacctc tacaagcaaa tctccagcca atcaggagcc agcaacgaca accactactt 1620

tggctacagc accccctggg ggtattttga cttcaacaga ttccactgcc acttttcacc 1680

acgtgactgg caaagactca tcaacaacaa ctggggattc cggcccaaaa gactcaactt 1740

caagctcttt aatattcaag tcaaagaggt cacgcagaat gacggtacga cgacgattgc 1800

caataacctt accagcacgg ttcaggtgtt tactgactcg gagtaccagc tcccgtacgt 1860

cctgggctcg gcgcatcaag gatgcctccc gccgtttcca gcggacgtct tcatggtccc 1920

acagtatgga tacctcaccc tgaacaacgg gagtcaggcg gtaggacgct cttcctttta 1980

ctgcctggag tactttcctt ctcagatgct gcgtactgga aacaactttc agttcagcta 2040

cacttttgaa gacgtgcctt tccacagcag ctacgctcac agccagagtc tggatcggct 2100

gatgaatcct ctgatcgacc agtacctgta ttatctgaac aagacacaaa caaatagtgg 2160

aactcttcag cagtctcggc tactgtttag ccaagctgga ccaaccaaca tgtctcttca 2220

agctaaaaac tggctgcctg gaccttgcta cagacagcag cgtctgtcaa aacaggcaaa 2280

cgacaacaac aacagcaact ttccctggac tgcagctaca aagtatcatc taaatggccg 2340

ggactcgttg gttaatccag gaccagctat ggccagtcac aaggatgacg aagaaaagtt 2400

tttccccatg catggaaccc tgatatttgg taaacaagga acaaatgcca acgacgcgga 2460 tttggaaaat gtcatgatta cagatgaaga agaaatcagg gccaccaatc ccgtggctac 2520

ggagcagtac gggactgtgt caaataattt gcaaaactca aacactggtc caactactgg 2580

aactgtcaat cgccaaggag cgttacctgg tatggtgtgg caggatcgag acgtgtacct 2640

gcagggaccc atttgggcca agattcctca caccgatgga cactttcatc cttctccact 2700

gatgggaggt tttggactca aacacccgcc tcctcagatc atgatcaaaa acactcccgt 2760

tccagccaat cctcccacaa acttcagttc tgccaagttt gcttctttca tcacacagta 2820

ttccacggga caggtcagcg tggagatcga gtgggagctg cagaaggaga acagcaaacg 2880

ctggaatccc gaaattcagt acacttccaa ctacaacaag tctgttaatg tggactttac 2940

tgtggacact aatggtgtgt attcagagcc tcgccccatt ggcaccagat acctgactcg 3000

taatctgtaa ttgcttgtta atcaataaac cgtttaattc gtttcagttg aactttggtc 3060

tctgcgaagg gcgaa 3075

<210> 189
<211> 3142
<212> DNA
<213> Adeno-associated virus

<400> 189
aaaacgacgg gccagtgatt gtaatacgac tcactatagg gcgaaattga aattagcggc 60

cgcgaattcg cctttcgcag agaccaaagt tcaactgaaa cgaattaaac ggtttattga 120

ttaacaagca attacagatt acgagtcagg tatctggtgc caatggggcg aggctctgaa 180

tacacaccat tagtgtccac agtaaagtcc acattaacag acttgttgta gttggaagtg 240

tactgaattt cgggattcca gcgtttgctg ttctccttct gcagctccca ctcgatctcc 300

acgctgacct gtcccgtgga atactgtgtg atgaaagaag caaacttggc agaactgaag 360

tttgtgggag gattggctgg aacgggagtg tttttgatca tgatctgagg aggcgggtgt 420

ttgagtccaa aacctcccat cagtggagaa ggatgaaagt gtccatcggt gtgaggaatc 480

ttggcccaaa tgggtccctg caggtacacg tctcgatcct gccacaccat accaggtaac 540

gctccttggt gattgacagt tccagtagtt ggaccagtgt ttgagttttg caaattattt 600

gacacagtcc cgtactgctc cgtagccacg ggattggtgg ccctgatttc ttcttcatct 660

gtaatcatga cattttccaa atccgcgtcg ttggcatttg ttccttgttt accaaatatc 720

agggttccat gcatggggaa aaacttttct tcgtcatcct tgtgactggc catagctggt 780

cctggattaa ccaacgagtc ccggccattt agatgatact ttgtagctgc agtccaggga 840

aagttgctgt tgttgttgtc gtttgcctgt tttgacagac gctgctgtct gtagcaaggt 900

ccaggcagcc agtttttagc ttgaagagac atgttggttg gtccagcttg gctaaacagt 960

agccgagact gctgaagagt tccactattt gtttgtgtct tgttcagata atacaggtac 1020

tggtcgatca gaggattcat cagccgatcc agactctggc tgtgagcgta gctgctgtgg 1080

aaaggcacgt cttcaaaagt gtagctgaac tgaaagttgt ttccagtacg cagcatctga 1140

gaaggaaagt actccaggca gtaaaaggaa gagcgtccta ccgcctgact cccgttgttc 1200 agggtgaggt atccatactg tgggaccatg aagacgtccg ctggaaacgg cgggaggcat 1260

ccttgatgcg ccgagcccag gacgtacggg agctggtact ccgagtcagt aaacacctga 1320

accgtgctgg taaggttatt ggcaatcgtc gtcgtaccgt cattctgcgt gacctctttg 1380

acttgaatat taaagagctt gaagttgagt cttttgggcc ggaatccccg gttgttgttg 1440

acgagtcttt gccagtcacg tggtgaaaag tggcagtgga atctgttgaa gtcaaaatac 1500

ccccaggggg tgctgtagcc aaagtagtgg ttgtcgttgc tggctcctga ttggctggag 1560

atttgcttgt agaggtggtt gttgtatgtg ggcagggccc aggttcgggt gctggtggtg 1620

atgactctgt cgcccagcca ttgggaatcg caatgccaat ttcctgagga attacccact 1680

ccatcggcac cctcgttatt gtctgccatt ggtgcgccac tgcctgtagc cattgtagta 1740

gatcccagac cagagggggc tgctggtggc tgtccgagag gctgggggtc aggtacggag 1800

tctgcgtctc cagtctgacc aaaatttaat ctttttcttg caggctgctg gcccgctttt 1860

ccggttcccg aggaggagtc tggctccaca ggagagtgct ctaccggcct ctttttttccc 1920

ggagccgtct taacaggctc ctcaaccagg cccagaggtt caagaaccct ctttttcgcc 1980

tggaagactg ctcgtccgag gttgcccccca aaagacgtat cttctttaag gcgctcctga 2040

aactctgcgt cggcgtggtt gtacttgagg tacgggttgt ctccgctgtc gagctgccgg 2100

tcgtaggcct tgtcgtgctc gagggccgcg gcgtctgcct cgttgaccgg ctcccccttg 2160

tcgagtccgt tgaagggtcc gaggtacttg tacccaggaa gcacaagacc cctgctgtcg 2220

tccttatgcc gctctgcggg ctttggtggt ggtgggccag gtttgagctt ccaccactgt 2280

cttattcctt cagagagagt gtcctcgagc caatctggaa gataaccatc ggcagccata 2340

cctgatttaa atcatttatt gttcagagat gcagtcatcc aaatccacat tgaccagatc 2400

gcaggcagtg caagcgtctg gcacctttcc catgatatga tgaatgtagc acagtttctg 2460

atacgccttt ttgacgacag aaacgggttg agattctgac acgggaaagc actctaaaca 2520

gtctttctgt ccgtgagtga agcagatatt tgaattctga ttcattctct cgcattgtct 2580

gcagggaaac agcatcagat tcatgcccac gtgacgagaa catttgtttt ggtacctgtc 2640

cgcgtagttg atcgaagctt ccgcgtctga cgtcgatggc tgcgcaactg actcgcgcgc 2700

ccgtttgggc tcacttatat ctgcgtcact gggggcgggt cttttcttag ctccaccctt 2760

tttgacgtag aattcatgct ccacctcaac cacgtgatcc tttgcccacc ggaaaaagtc 2820

tttcacttcc tgcttggtga cctttccaaa gtcatgatcc agacggcggg taagttcaaa 2880

tttgaacatc cggtcttgca acggctgctg gtgctcgaag gtcgttgagt tcccgtcaat 2940

cacggcgcac atgttggtgt tggaggtgac gatcacggga gtcgggtcta tctgggccga 3000

ggacttgcat ttctggtcca cacgcacctt gcttcctcca agaatggctt tggccgactc 3060

cacgaccttg gcggtcatct tcccctcctc ccaccagatc accatcttgt cgacgcaatg 3120

gtaaaaggaa agttctcatt gg 3142

```
<210> 190
<211> 735
<212> PRT
<213> Adeno-associated virus 2

<400> 190
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asp Lys Ala Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725   730   735

<210> 191
<211> 740
<212> PRT
<213> Adeno-associated virus 2

<400> 191
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
```

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580   585   590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595   600   605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
                725   730   735

Leu Ala Ala Ala
            740

<210> 192
<211> 734
<212> PRT
<213> Adeno-associated virus 2

<400> 192
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445


Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Met Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

```
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Ile Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730


<210> 193
<211> 734
<212> PRT
<213> Adeno-associated virus 2

<400> 193
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Glu Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730

<210> 194
<211> 739
<212> PRT
<213> Adeno-associated virus 2

<400> 194
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
                725                 730                 735
```

```
Leu Ala Ala



<210> 195
<211> 725
<212> PRT
<213> Adeno-associated virus 2

<400> 195
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro
                725


<210> 196
<211> 707
<212> PRT
<213> Adeno-associated virus 2

<400> 196
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
```

```
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Cys Ile Tyr Gln Pro Pro Glu Arg Gln Gln Thr Ser Ser Tyr
            580                 585                 590


Arg Arg Cys Gln His Thr Arg Arg Ser Ser Arg His Gly Leu Ala Gly
        595                 600                 605


Gln Arg Cys Val Pro Ser Gly Ala His Leu Gly Lys Asp Ser Thr His
    610                 615                 620


Gly Arg Thr Phe Ser Pro Leu Ser Pro His Gly Trp Ile Arg Thr Thr
625                 630                 635                 640


Pro Ser Ser Thr Asp Ser His Gln Glu His Pro Gly Thr Cys Glu Ser
                645                 650                 655


Phe Asp His Leu Gln Cys Gly Lys Val Cys Phe Leu His His Thr Val
            660                 665                 670


Leu His Gly Thr Gly Gln Arg Gly Asp Arg Val Arg Ala Ala Glu Gly
        675                 680                 685


Lys Gln Gln Thr Leu Glu Ser Arg Asn Ser Val His Phe Gln Leu Gln
    690                 695                 700


Gln Val Cys
705


<210> 197
<211> 739
<212> PRT
<213> Adeno-associated virus 2

<400> 197
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
725 730 735

Leu Ala Ala

<210> 198
<211> 737
<212> PRT
<213> Adeno-associated virus 2

<400> 198
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn
                485                 490                 495

Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala
            580                 585                 590

Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


Leu



<210> 199
<211> 741
<212> PRT
<213> Adeno-associated virus 2

<400> 199
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160
```

```
Lys Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Leu Ala Asn His Asn
            580                 585                 590

Asn Thr Thr Asn Ala Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
        595                 600                 605

Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
    610                 615                 620

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro
625                 630                 635                 640

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
                645                 650                 655

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser
            660                 665                 670

Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
        675                 680                 685

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
    690                 695                 700
```

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Ile Asn Val
705   710   715   720

Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile
                725   730   735

Gly Thr Arg Tyr Leu
            740

<210> 200
<211> 730
<212> PRT
<213> Adeno-associated virus 2

<400> 200
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg
                725                 730
```

<210> 201
<211> 735

```
<212> PRT
<213> Adeno-associated virus 2


<220>
<221> MOD_RES
<222> (239)..(239)
<223> Any amino acid

<400> 201
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Xaa Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510
```

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725   730   735

<210> 202
<211> 733
<212> PRT
<213> Adeno-associated virus 2

<400> 202
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Leu Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560
```

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr
725 730

<210> 203
<211> 734
<212> PRT
<213> Adeno-associated virus 2

<400> 203
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Asn Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser Arg
    450                 455                 460

Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn Gly
            500                 505                 510

Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys
    530                 535                 540

Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg Phe
                565                 570                 575

Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala Thr
            580                 585                 590

Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

```
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr
705                 710                 715                 720


Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730


<210> 204
<211> 734
<212> PRT
<213> Adeno-associated virus 2

<400> 204
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Ser Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Ile Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725   730

<210> 205
<211> 738
<212> PRT
<213> Adeno-associated virus 2

<400> 205
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180   185   190

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
                725                 730                 735
```

Arg Pro

<210> 206
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 206
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatgg cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg gcaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680 gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga cgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 207
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 207
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Gly Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445
```

```
Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Gly Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Thr Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

```
Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 208
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 208
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc tcgcagagcg gcatcaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc acggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caaccttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740 aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

tacagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgcg gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 209
<211> 735
<212> PRT
<213> Adeno-associated virus

```
<400> 209
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Leu Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Leu Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445
```

```
Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Tyr Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Arg Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

```
Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 210
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 210

```
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac      540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct      600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga      660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc      780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg      840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc      900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc      960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg     1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct     1200

cagatgctgc gtactggaaa caactttacc ttcagctaca cctttgagga cgttcctttc     1260

cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag     1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta     1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga     1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt     1500

ccctggactg cggctacaaa gtatcgtcta aatggccggg actcgttggt taatccagga     1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg     1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca     1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca     1740
```

```
aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg     1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag     1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa     1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac     1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg     2040

gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat     2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 211
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 211
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
```

```
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
```

```
    450                 455                 460


Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr Arg Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590


Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 212
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 212
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgccct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tgggaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

```
ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag     1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa     1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac     1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg     2040

gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat     2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 213
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 213
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Pro Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 214
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 214
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacttg ggccctgccc acctacaaca accatctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctgc agggcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800 cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg ttgacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 215
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 215
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Gly Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 216
<211> 3161
<212> DNA
<213> Adeno-associated virus

<400> 216
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60

ccattcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc 120

aaggtcatgg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa 180

tgtaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccaacatg 240

tgcgccgtga ttgacgggaa ctcaacgacc ttcgagcacc agcagccgtt gcaagaccgg 300

atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag 360

gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 420

tacgtcaaaa agggtggagc caagaaaaga cccgcccccca gtgacgcaga tataagtgag 480

cccaaacggg cgcgcgggtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 540

aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600

tttccctgca gacaatgcga gagaatgaat caaaattcaa atatctgctt cactcacgga 660

cagaaggact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780

actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

taaatcaggt atggctgccg atggttatct tccagattgg ctcaaggaca ctctctctga 900

aggaataaga cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg 960

gcataaggac gacagcgggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa 1020

cggactcgac aagggagagc cggtcaacga ggcagacgcc gcggccctcg agtacgacaa 1080

ggcctacgac cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga 1140

cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc 1200

agtcttccag gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa 1260

gacggctccg ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc 1320

gggaacagga aaagcgggcc agcagcctgc gagaaagaga ttgaattttg gtcagactgg 1380

agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg 1440

tctgggaact aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg 1500

cgccgacgga gtgggtaatt cctcgggaag ttggcattgc gattccacat ggatgggcga 1560

cagagtcatc accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta 1620

caagcagatc tccagccaat caggagccag caacgacaac cactactttg gctacagcac 1680

cccttggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca 1740

aagactcatc aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa 1800

cattcaagtc aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac 1860 cagcacggtt caggtgttta ctgactcgga gtaccagctc ccgtacgtcc ccggctcggc 1920

gcatcaagga tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata 1980

cctcaccctg aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta 2040

ctttccttct cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgagga 2100

tgttcctttc cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct 2160

catcgaccag tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca 2220

gtccaggctt cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg 2280

gcttcctgga ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa 2340

cagtgaatac tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt 2400

gaatccgggc ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag 2460

cggggttctc atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt 2520

catgattaca gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg 2580

ttctgtatct accaacctcc agagcggcaa cacacaagca gctactgcag atgtcaacac 2640

acaaggcgtt cttccaggca tggtctggca ggacagagac gtgcacctgc aggggcctat 2700

ctgggcaaag attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt 2760

tggacttaaa caccctcctc cacagattct catcaagaac accccggtac ctgcaaatcc 2820

ttcgaccacc ttcagtgcgg caaagtttgc ttccttcatc acacagtatt ccacagggca 2880

ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga 2940

gatccagtac acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa 3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt 3060

gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc tgcgaagggc 3120

gaattcgttt aaaccctgca ggactagtcc ctttagtgag g 3161

<210> 217
<211> 3162
<212> DNA
<213> Adeno-associated virus

<400> 217
gaattgaatt tagcggccgc gaattcgccc ttcgcagaga ccaaagttca actgaaacga 60

attaaacggt ttattgatta acaagcaatt acagattacg agtcaggtat ctggtgccaa 120

tggggcgagg ctctgaatac acgccattag tgtccacagt aaagtccaca ttaacagact 180

tgttgtagtt ggaagtgtac tgaatttcgg gattccagcg tttgctgttt tccttctgca 240

gctcccactc gatctccacg ctgacctgtc ccgtggagta ctgtgtgatg aaggaagcaa 300

actttgccgc actgaaggtg gtcgaaggat tcgcaggtac cggggtgttc ttgatgagaa 360

tctgtggagg agggtgttta agtccgaatc cacccatgag gggagagggg tgaaaatgtc 420

cgtccgtgtg tggaatcttt gcccagatgg gcccctgaag gtacacatct ctgtcctgcc 480 agaccatgcc tggaagaacg ccttgtgtgt tgacatctgc ggtagctgct tgtctgttgc 540

ctctctggag gttggtagat acagaaccgt actgctccgt agccacggga ttggttgtcc 600

tgatttcctc ttcgtctgta atcatgacct tttcaatgtc cacatttgtt ttctctgagc 660

cttgcttccc aaagatgaga accccgctct gaggaaaaaa cttttcttca ttgtccttgt 720

ggcttgccat ggccgggccc ggattcacca gagagtctct gccattgagg tggtacttgg 780

tagctccagt ccacgagtat tcactgttgt tgttatccgc agatgtcttt gatactcgct 840

gctggcggta acagggtcca ggaagccagt tcctagactg gtcccgaatg tcactcgctc 900

cggcctgaga aaactgaagc cttgactgcg tggtggttcc acttggagtg tttgttgtgc 960

tcaagtaata caggtactgg tcgatgagag gattcatgag acggtccaga ctctggctgt 1020

gagcgtagcc gctgtggaaa ggaacgtcct caaaagtgta gctgaaggta aagttgtttc 1080

cggtacgcag catctgagaa ggaaagtact ccaggcagta aaatgaagag cgtcctactg 1140

cctgactccc gttgttcagg gtgaggtatc catactgtgg caccatgaag acgtctgctg 1200

ggaacggcgg gaggcatcct tgatgcgccg agccgaggac gtacgggagc tggtactccg 1260

agtcagtaaa cacctgaacc gtgctggtaa ggttattggc aatcgtcgtc gtaccgtcat 1320

tctgcgtgac ctctttgact tgaatgttaa agagcttgaa gttgagtctc ttgggtcgga 1380

atccccagtt gttgttgatg agtctttgcc agtcacgtgg tgaaaagtgg cagtggaatc 1440

tgttgaagtc aaaatacccc caaggggtgc tgtagccaaa gtagtgattg tcgttcgagg 1500

ctcctgattg gctggaaatt tgtttgtaga ggtggttgtt gtaggtgggc agggcccagg 1560

ttcgggtgct ggtggtgatg actctgtcgc ccatccatgt ggaatcgcaa tgccaatttc 1620

ccgaggaatt acccactccg tcggcgccct cgttattgtc tgccattggt gcgccactgc 1680

ctgtagccat cgtattagtt cccagaccag agggggctgc tggtggctgt ccgagaggct 1740

gggggtcagg tactgagtct gcgtctccag tctgaccaaa attcaatctt tttcttgcag 1800

gctgctggcc cgcctttccg gttcccgagg aggagtctgg ctccacagga gagtgctcta 1860

ccggcctctt ttttcctgga gccgtcttga caggttcccc aaccaggccc agaggttcaa 1920

gaaccctctt tttcgcctgg aagactgctc gtccgaggtt gcccccaaaa gacgtatctt 1980

ctttaaggcg ctcctgaaac tccgcgtcgg cgtggttgta cttgaggtac gggttgtctc 2040

cgctgtcgag ctgccggtcg taggctttgt cgtgctcgag ggccgcggcg tctgcctcgt 2100

tgaccggctc tcccttgtcg agtccgttga agggtccgag gtacttgtac ccaggaagca 2160

caagacccct gctgtcgtcc ttatgccgct ctgcgggctt tggtggtggt gggccaggtt 2220

tgagcttcca ccactgtctt attccttcag agagagtgtc ctcgagccaa tctggaagat 2280

aaccatcggc agccatacct gatttaaatc atttattgtt caaagatgca gtcatccaaa 2340

tccacattga ccagatcgca ggcagtgcaa gcgtctggca cctttcccat gatatgatga 2400

atgtagcaca gtttctgata cgccttttttg acgacagaaa cgggttgaga ttctgacacg 2460

ggaaagcact ctaaacagtc tttctgtccg tgagtgaagc agatatttga attctgattc 2520 attctctcgc attgtctgca gggaaacagc atcagattca tgcccacgtg acgagaacat 2580

ttgttttggt acctgtctgc gtagttgatc gaagcttccg cgtctgacgt cgatggctgc 2640

gcaactgact cgcgcacccg tttgggctca cttatatctg cgtcactggg ggcgggtctt 2700

ttcttggctc caccctttt gacgtagaat tcatgctcca cctcaaccac gtgatccttt 2760

gcccaccgga aaaagtcttt gacttcctgc ttggtgacct tcccaaagtc atgatccaga 2820

cggcgggtga gttcaaattt gaacatccgg tcttgcaacg gctgctggtg ttcgaaggtc 2880

gttgagttcc cgtcaatcac ggcgcacatg ttggtgttgg aggtgacgat cacgggagtc 2940

gggtctatct gggccgagga cttgcatttc tggtccacgc gcaccttgct tcctccgaga 3000

atggctttgg ccgactccac gaccttggcg gtcatcttcc cctcctccca ccagatcacc 3060

atcttgtcga cacagtcgtt gaagggaaag ttctcattgg tccagttgac gcagcaaggg 3120

cgaattcgtt taaacctgca ggactagtcc ctttagtgag gg 3162

<210> 218
<211> 3164
<212> DNA
<213> Adeno-associated virus

<400> 218
gcgaattgaa tttagcggcc gcgaattcgc ccttcgcaga gaccaaagtt caactgaaac 60

gaattaaacg gtttattgat taacaagcaa ttacaaatta cgagtcaggt atctggtgcc 120

aatggggcga ggctctgaat acacgccatt agtgtccaca gtaaagtcca cattaacaga 180

cttgttgtag ttggaagtgt actgaatttc gggattccag cgtttgctgt tttccttctg 240

cagctcccac tcgatctcca cgctgacctg tcccgtggag tactgtgtga tgaaggaagc 300

aaactttgcc gcactgaagg tggtcgaagg attcgcaggt accggggtgt tcttgatgag 360

aatctgtgga ggagggtgtt taggtccgaa tccacccatg aggggagagg ggtgaaaatg 420

tccgtccgtg tgtggaatct ttgcccagat gggcccctga aggtacacat ctctgtcctg 480

ccagaccatg cctggaagaa cgccttgtgt gttgacatct gcggtagctg cttgtctgtt 540

gcctctctgg aggttggtag atacagaacc atactgctcc gtagccacgg gattggttgt 600

cctgatttcc tcttcgtctg taatcatgac cttttcaatg tccacatttg ttttctctga 660

gccttgcttc ccaaagatga gaaccccgct ctgaggaaaa aacttttctt cattgtcctt 720

gtggcttgcc atggccgggc ccggattcac cagagagtct ctgccattga ggtggtactt 780

ggtagctcca gtccacgagt attcactgtt gttgttatcc gcagatgtct ttgatactcg 840

ctgctggcgg taacagggtc caggaagcca gttcctagac tggtcccgaa tgtcactcgc 900

tccggcctga gaaaactgaa gccttgactg cgtggtggtt ccacttggag tgtttgttgt 960

gctcaagtaa tacaggtact ggtcgatgag aggattcatg agacggtcca gactctggct 1020

gtgagcgtag ctgctgtgga aaggaacgtc ctcaaaagtg tagctgaagg taaagttgtt 1080

tccggtacgc agcatctgag aaggaaagta ctccgggcag taaaatgaag agcgtcctac 1140

tgcctgactc ccgttgctca gggtgaggta tccatactgt ggcaccatga agacgtctgc 1200 tgggaacggc gggaggcatc cttgatgcgc cgagccgagg acgtacggga gctggtactc 1260

cgagtcagta aacacctgaa ccgtgctggt aaggttattg gcaatcgtcg tcgtaccgtc 1320

attctgcgtg acctctttga cttgaatgtt aaagagcttg aagttgagtc tcttgggtcg 1380

gaatccccag ttgttgttga tgagtctttg ccagtcacgt ggtgaaaagt ggcagtggaa 1440

tctgttgaag tcaaaatacc cccaaggggt gctgtagcca aagtagtgat tgtcgttcga 1500

ggctcctgat tggctggaaa tttgtctgta gaggtggttg ttgtaggtgg gcagggccca 1560

ggttcgggtg ctggtggtga tgactctgtc gcccatccat gtggaatcgc aatgccgatt 1620

tcccgaggaa ttacccactc cgtcggcgcc ctcgttattg tctgccattg gtgcgccact 1680

gcctgtagcc atcgtattag ttcccagacc agagggggct gctggtggct gtccgagagg 1740

ctgggggtca ggtactgagt ctgcgtctcc agtctgacca aaattcaatc tttttcttgc 1800

aggctgctgg cccgcctttc cggttcccga ggaggagtct ggctccacag gagagtgctc 1860

taccggcctc ttttttcccg gagccgtctt aacaggttcc ccaaccaggc ccagaggttc 1920

aagaaccctc tttttcgcct ggaagactgc tcgtccgagg ttgcccccaa aagacgtatc 1980

ttctttaagg cgctcctgaa actccgcgtc ggcgtggttg tacttgaggt acgggttgtc 2040

tccgctgtcg agctgccggt cgtaggcttt gtcgtgctcg agggccgcgg cgtctgcctc 2100

gttgaccggc tctcccttgt cgagtccgtt gaagggtccg aggtacttgt acccaggaag 2160

cacaagaccc ctgctgtcgt ccttatgccg ctctgcgggc tttggtggtg gtgggccagg 2220

tttgagcttc caccactgtc ttattccttc agagagagtg tcctcgagcc aatctggaag 2280

ataaccatcg gcagccatac ctgatttaaa tcatttattg ttcaaagatg cagtcatcca 2340

aatccacatt gaccagatcg caggcagtgc aagcgtctgg cacctttccc atgatatgat 2400

gaatgtagca cagtttctga tacgcctttt tgacgacaga aacgggttga gattctgaca 2460

cgggaaagca ctctaaacag tctttctgtc cgtgagtgaa gcagatattt gaattctgat 2520

tcattctctc gcattgtctg cagggaaaca gcatcagatt catgcccacg tgacgagaac 2580

atttgttttg gtacctgtct gcgtagttga tcgaagcttc cgcgtctgac gtcgatggct 2640

gcgcaactga ctcgcgcacc cgtttgggcc cacttatatc tgcgtcactg ggggcgggtc 2700

ttttcttggc tccacccttt ttgacgtaga attcatgctc cacctcaacc acgtgatcct 2760

ttgcccaccg gaaaaagtct ttgacttcct gcttggtgac cttcccaaag tcatgatcca 2820

gacggcgggt gagttcaaat ttgaacatcc ggtcttgcaa cggctgctgg tgttcgaagg 2880

tcgttgagtt cccgtcaatc acggcgcaca tgttggtgtt ggaggtgacg atcacgggag 2940

tcgggtctat ctgggccgag gacttgcatt tctggtccac gcgcaccttg cttcctccga 3000

gaatggcttt ggccgactcc acgaccttgg cggtcatctt cccctcctcc caccagatca 3060

ccatcttgtc gacacagtcg ttgaagggaa agttctcatt ggtccagttg acgcagcaag 3120

ggcgaattcg tttaaacctg caggactagt ccctttagtg aggg 3164

<210> 219
<211> 3163
<212> DNA
<213> Adeno-associated virus

<400> 219
accctcacta aagggactag tcctgcaggt ttaaacgaat tcgcccttgc tgcgtcaact 60

ggagcaatga gaactttccc ttcaacgact gtgtcgacaa gatggtgatt tggtgggagg 120

aggggaagat gaccgccaag gtcgtggagt cggccaaagc cattctcgga ggaagcaagg 180

tgcgcgtgga ccagaaatgc aagtcctcgg cccagataga tccgactccc gtgatcgtca 240

cctccaacac caacatgtgc gccgtgattg acgggaactc aacgaccttc gaacaccagc 300

agccgttgca agaccggatg ttcaaatttg aactcacccg ccgtctggat catgactttg 360

ggaaggtcac caagcaggaa gtcaaagact ttttccggtg ggcaaaggat cacgtggttg 420

aggtggagca tggattctac gtcaaaaagg gtggagccaa gaaaagaccc gcccctagtg 480

acgcagatat aagtgagccc aaacgggtgc gcgagtcagt tgcgcagcca tcgacgtcgg 540

acgcggaagc ttcgatcaac tacgcggaca ggtaccaaaa caaatgttct cgtcacgtgg 600

gcatgaatct gatgctgttt ccctgcagac aatgcgagag aatgaatcaa aattcaaata 660

tctgcttcac tcacggacag aaagactgtt tagagtgctt tcccgtgtca gaatctcaac 720

ctgtttctgt cgtcaaaaag gcgtatcaga aactgcgcta cattcatcat atcatgggaa 780

aggtgccaga cgcttgcact gcctgcgatc tggtcaatgt ggatttggat gactgcatct 840

ctgaacaata aatgatttaa atcaggtatg gctgccgatg gttatcttcc agattggctc 900

gaggacactc tctctgaagg aataagacag tggtggaagc tcaaacctgg cccaccacca 960

ccaaagcccg cagagcggca taaggacgac agcaggggtc ttgtgcttcc tgggtacaag 1020

tacctcggac ccttcaacgg actcgacaag ggagagccgg tcaacgaggc agacgccgcg 1080

gccctcgagc acgacaaggc ctacgaccgg cagctcgaca gcggagacaa cccgtacctc 1140

aagtacaacc acgccgacgc ggagtttcag gagcgtctta aagaagatac gtcttttggg 1200

ggcaacctcg gacgagcagt cttccaggcg aaaaagaggg ttcttgaacc tctgggcctg 1260

gttgaggaac ctgttaagac ggctccggga aaaaagaggc cggtagagca ctctcctgcg 1320

gagccagact cctcctcggg aaccggaaaa gcgggccagc agcctgcaag aaaaagactg 1380

aatttcggtc agactggaga cgcagactcc gtacctgacc cccagcctct cggacagcca 1440

ccagcagccc ccacaagttt gggatctact acaatggcta caggcagtgg cgcaccaatg 1500

gcagacaata acgagggtgc cgatggagtg ggtaattcct caggaaattg gcattgcgat 1560

tcccaatggc tgggcgacag agtcatcacc accagcaccc gaacctgggc cctgcccacc 1620

tacaacaacc acctttacaa gcaaatctcc agccaatcag gagcctcaaa cgacaaccac 1680

tactttggct acagcacccc ctgggggtat tttgacttca acagattcca ctgccacttt 1740

tcaccacgtg actggcaaag actcatcaac aacaactggg gattccgacc caagagactc 1800

aacttcaagc tctttaacat tcaagtcaaa gaggtcacgc agaatgacgg tacgacgacg 1860

```
attgccaata accttaccag cacggttcag gtgtttactg actcggagta ccagctcccg     1920

tacgtcctcg gctcggcgca tcaaggatgc ctcccgccgt ttccagcgga cgtcttcatg     1980

gtcccacagt atggatacct caccctgaac aacgggagtc aggcggtagg acgctcttcc     2040

ttttactgcc tggagtgctt tccttctcag atgctgcgta ctggaaacaa ctttcagttc     2100

agctacactt ttgaagacgt gcctttccac agcagctacg ctcacagcca gagtttggat     2160

cggctgatga atcctctgat cgaccagtac ctgtattatc taaacagaac acaaacagct     2220

agtggaactc agcagtctcg gctactgttt agccaagctg gacccacaag catgtctctt     2280

caagctaaaa actggctgcc tggaccgtgt tatcgccagc agcgtttgtc aaagcaggca     2340

aacgacaaca acaacagcaa ctttccctgg actggagcta ccaagtacca cctcaatggc     2400

agagactctt tggtgaaccc gggcccggcc atggccagcc acaaggacga tgaagaaaag     2460

tttttcccca tgcatggaac cctaatattt ggtaaagaag gaacaaatgc taccaacgcg     2520

gaattggaaa atgtcatgat tacagatgaa gaggaaatca ggaccaccaa tcccgtggct     2580

acagagcagt acggatatgt gtcaaataat ttgcaaaact caaatactgc tgcaagtact     2640

gaaactgtga atcaccaagg agcattacct ggtatggtgt ggcaggatcg agacgtgtac     2700

ctgcagggac ccatttgggc caagattcct cacaccgatg gacactttca tccttctcca     2760

ctgatgggag gttttggact caaacacccg cctcctcaga ttatgatcaa aaacactccc     2820

gttccagcca atcctcccac aaacttcagt tctgccaagt ttgcttcctt catcacacag     2880

tattccacgg gacaggtcag cgtggagatc gagtgggagc tgcagaagga gaacagcaaa     2940

cgctggaatc ccgaaattca gtacacttcc aactacaaca aatctgttaa tgtggacttt     3000

actgtggaca ctaatggtgt gtattcagag cctcgcccca ttggcaccag atacctgact     3060

cgtaatctgt aattgcttgt taatcaataa accgtttaat tcgtttcagt tgaactttgg     3120

tctctgcgaa gggcgaattc gcggccgcta aattcaattc gcc                       3163

<210> 220
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 220
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro
    50                  55                  60


Val Asp Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
```

```
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
```

```
            340                 345                 350


Val Leu Gly Leu Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445


Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460


Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590


Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
```

610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asp Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Pro Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 221
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 221
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactctac 180

aagggagagc cggtcgacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga gggttcttga acctctgggc ttggttgggg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggca accagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaata accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgaccggca aagactcatc 900

aacaacaact ggggattccg accaaaaaga ctcaacttca agctctttaa cattcaagtc 960 aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggcttggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaatca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactta tgggaggttt tggactcaaa 1920

cacccacctc ctcagatcat gattaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca agtcagcgtg 2040

gagatcgagt gggagctgca gaaggaggac agcaaacgct ggaaccccga gatccagtac 2100

acttccaact ataacaaacc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 222
<211> 3161
<212> DNA
<213> Adeno-associated virus

<400> 222
cgaattgatt tagcggccgc gaattcgccc ttcgcagaga ccaaagttca actgaaacga 60

attaaacggt ttattgatta acaagcaatt acagattacg agtcaggtat ctggtgccaa 120

tggggcgagg ctctgaatac acaccattag tgtccacagt aaagtccaca ttaacagatt 180

tgttgtagtt ggaagtgtac tggatctcgg gattccagcg tttgctgttc tccttctgta 240

gctcccactc gatctccacg ctgacccgcc ccgtggaata ctgtgtgatg aaggaagcaa 300

actttgccgc actgaaggtg gtcgaaggat tcgcaggtac cggggtgttt ttgatgagaa 360

tctgtggagg agggtgttta agtccgaatc cgcccatgag gggagagggg tgaaaatgtc 420

cgtccgtgtg cggaatcttt gcccagatag gcccctgcag gtacacgtct ctgtcctgcc 480

agaccatgcc tggaagaacg ccttgtgtgt tgacatctgc agtagatgct tgtgtgttgc 540

```
cgctctggag gttggtagat acagaaccat actgctccgt ggccacggga ttggtggttc      600
tgatttcctc ttcgtctgta atcatgacct tttcaatgtc cacatttgtt ttctctgatc      660
cttgttttcc aaagatgaga accccgctct gaggaaaaaa cttttcttca tcgtccttgt      720
ggctggccat tgccgggccc ggattcacca gagagtctct gccattgagg tggtacttgg      780
tagctccaat ccacgagtat tcactgttgt tgttgtccgc agatgtcttt gatactcgct      840
gctggcggta acagggtcca ggaagccagt tcctagactg atcccgaatg tcactcgctc      900
cggcctgaga aaactgaagc ctggactgcg tggtggttcc gcttggagtg tttgttctgc      960
tcaagtaata caggtactgg tcgatgagag gattcatgag acggtccaaa ctctggctgt     1020
gagcgtagct gctgtggaaa ggaacatcct caaaggtgta gctgaaggta aagttgtttc     1080
cggtacgcag catctgagaa gggaagtact ccaggcagta aaatgaagag cgtcctactg     1140
cctgactccc gttgttcagg gtgaggtatc catactgtgg caccatgaag acgtctgctg     1200
ggaacggcgg gaggcatcct tgatgcgccg agccgaggac gtacgggagc tggtactccg     1260
agtcagtaaa cacctgaacc gtgctggtaa ggttattggc aatcgtcgtc gtaccatcat     1320
tctgcgtgac ctctctgact tgaatgttaa agagcttgaa gttgagtctc ttgggccgga     1380
atccccagtt gttgttgatg agtctttgcc agtcacgtgg tgaaaagtgg cagtggaatc     1440
tgttgaagtc aaaatacccc caaggggtgc tgtagccaaa gtagtggttg tcgttgctgg     1500
ctcctgattg gctggaaatc tgcttgtaca gatggttgtt gtaggtgggc agagcccagg     1560
ttcgggtgct ggtggtgatg actctgtcgc ccatccatgt ggaatcgcaa tgccaatttc     1620
ccgaggaatt acccactccg tcggcgccat cgttattgtc tgccattggt gcgccactgc     1680
ctgtagccat cgtattagtt cccagaccag agggggctgc tggtggctgt ccgagaggct     1740
gggggtcagg tacggagtct gcgtctccag tctgaccgaa attcaatctc tttcttgcag     1800
gctggttgcc cgcttttccg gttcccgagg aggagtctgg ctccacagga gagtgctcta     1860
ccggcctctt ttttcccgga gccgtcttaa caggctcctc aaccaggccc agaggttcaa     1920
gaaccctctt ttttgcctgg aagactgctc gtccgaggtt gcccccaaaa gacgtatctt     1980
ctttaaggcg ctcctgaaac tccgcgtcgg cgtggtcgta cttgaggtac gggttgtctc     2040
cgctgtcgag ctgccggtcg taggccttgt cgtgctcgag ggccgcggcg tctgcctcgt     2100
tgaccggctc tcccttgtcg agtccgttga agggtccgag gtacttgtac ccaggaagca     2160
caagacccct gctgtcgtcc ttatgccgct ctgcgggctt tggtggtggt gggccaggtt     2220
tgagcttcca ccactgtctt attccttcag agagagtgtc ctcgagccaa tctggaagat     2280
aaccatcggc agccatacct gatttaaatc atttattgtt cagagatgca gtcatccaaa     2340
tccacattga ccagatcgca ggcagtgcaa gcgtctggca cctttcccat gatatgatga     2400
atgtagcaaa gtttctgata cgccttttttg acgacagaaa cgggttgaga ttctgacacg     2460
ggaaagcact ctaaacagtc tttctgtccg tgagtgaagc agatatttga attctgattc     2520
attctctcgc attgtctgca gggaaacagc atcagattca tgcccacgtg acgagaacat     2580
```

```
ttgttttggt acctgtccgc gtagttgatc gaagcttccg cgtctgacgt cgatggctgc     2640

gcaactgact cgcgcgcccg tttgggctca cttatatctg cgtcactggg ggcgggtctt     2700

ttcttggctc caccctttt gacgtagaat tcatgctcca cctcaaccac gtgatccttt      2760

gcccaccgga aaaagtcttt cacttcctgc ttggtgacct tcccaaagtc atgatccaga     2820

cggcgggtta gttcaaattt gaacatccgg tcttgcaacg gctgctggtg ttcgaaggtc     2880

gttgagttcc cgtcaatcac ggcgcacatg ttggtgttgg aggtggcgat cacgggagtc     2940

gggtctatct gggccgagga cttgcacttt tggtccacgc gcaccttgct tcctccgaga     3000

atggcttcgg ccgattccac gaccttggcg gtcatctttc cctcctccca ccagatcacc     3060

atcttgtcga cacagtcgtt gaagggaaag ttctcattgg tccagttgac gcagcaaggg     3120

cgaattcgtt taaacctgca ggaactagtc ccttagtgag g                         3161
```

<210> 223
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 223

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
```

```
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
```

```
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asp Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
```

705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 224
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 224
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccgccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactctac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccgg cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga gggttcttga acctctgggc ttggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggca accagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg accaaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaatca aatagtggaa cccttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

```
gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca     1740

aataatttgc aagactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg     1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag     1860

attcctcaca ccgatggaca ctttcatcct tctccactta tgggaggttt tggactcaaa     1920

cacccacctc ctcagatcat gattaaaaac actcccgttc cagccaatcc tcccacaaac     1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca agtcagcgta     2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtac     2100

acttccaact ataacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 225
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 225
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
```

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn
705                 710                 715                 720
```

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 226
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 226
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctgc aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagacag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080

caccagggct gcccgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaacggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgcggag aacgggcaac aactttgagt tcagctacca gtttgaggac 1260

gtgccttttc acagcagcta cgcgcatagc caaagcctgg accggctgat gaacccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aataacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cttggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560 aatcccggtg tcgctatggc aacgcacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttga tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aatcaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcatcctt cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc caagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta taacaaatct gttaatgtgg actttactgt ggacactaat 2160

ggtgtgtatt cagagcctcg ccccattggc accagatacc tgactcgtaa tctgtaa 2217

<210> 227
<211> 3167
<212> DNA
<213> Adeno-associated virus

<400> 227
attgaattta gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat 60

taaacggttt attgattaac aagcaattac agattacgag tcaggtacct ggtgccaatg 120

gggcgaggct ctgaatacac accattagtg tccacagtaa agtccacatt aacagatttg 180

ttgtagttgg aagtgtactg aatctcggga ttccagcgtt tgctgttctc cttctgcagc 240

tcccactcga tctccacgct gacctgcccc gtggagtact gtgtaatgaa ggaagcaaac 300

tttgccgcac tgaaggtagt cgaaggattc gcaggtaccg ggtgttcttt gatgagaatc 360

tgcgggggag ggtgtttaag tccgaatccg cccatgaggg gagaggggtg aaaatgtccg 420

tccgtgtgtg gaatctttgc ccagatgggc ccctgcaggt acacgtctct gtcctgccac 480

accatgcctg gaagaacgcc ttgtgtgttg acatctgagg tagctgcttg tgtgttgccg 540

ctctggaggt tggtagatac agaaccatac tgctccgtag ccacgggatt ggtggtcctg 600

atttcctctt cgtctgtaat catgaccttt tcaatgtcca cattagtttt tcccgagtct 660

tgttttccaa agatgagaac ccgctctga ggaaaaaact tttcttcatc gtccttgtgg 720

ctggccatgg ccgggcccgg attcaccaga gagtctcttc cattaaggtg gtacttggta 780

gctccagtcc acgagtattc actgttgttg ttatccgcag atgtctttga tactcgctgc 840

tggcggtaac agggtccagg aagccagttc ctagactggt cccgaatgtc acttgctccg 900

gcctgagaaa actgaagcct tgactgcgtg gtggttccgc ttggagtgtt tgttctgctc 960

aagtaataca ggtactggtc gatgagagga ttcatgagac ggtccaaact ctggctgtgg 1020

gcgtagctgc tgtggaaagg aacgtcctca aaggtgtagc tgaaggtaaa gttgtttccg 1080

gtacgcagca tctgagaagg aaagtactcc aggcagtaaa atgaagagcg tcctactgcc 1140

tgactcccgt tgttcagggt gaggtatcca tactgtggca ccatgaagac gtctgctggg 1200

aacggcggga ggcatccttg atgcgccgag ccgaggacgt acgggagctg gtactccgag 1260
tcagtaaaca cctgaaccgt gctggtaagg ttattggcaa tcgtcgtcgt accgtcattc 1320
tgcgtgacct ccttgacttg aatgttaaag agcttgaagt tgagtctttt gggccggaat 1380
ccccaattgt tgttgatgag tctttgccag tcacgtggcg aaaagtggca gtggaatctg 1440
ttgaagtcaa aatacccccca aggggtgctg tagccaaagt agtggttgtc gtttgaggct 1500
cctgattggc tggaaatctg cttgtagagg tggttgttgt aggtgggcag agcccaggtg 1560
cgggtgctgg tggtgatgac tctgtcgccc atccatgtgg aatcgcaatg ccaatttccc 1620
gaggaattac ccactccgtc ggcgccctcg ttattgtctg ccattggtgc gccactgcct 1680
gtagccatcg tattagttcc cagaccagag gggctgctg gtggctgtcc gagaggctgg 1740
gggtcaggta cggagtctgc gtctccagtc tgaccgaaat tcaatctctt tcttgcaggc 1800
tgctggcccg cttttccggt tcccgaggag gagtctggct ccgcaggaga gtgctctacc 1860
ggcctctttt ttcccggagc cgtcttaaca ggttcctcaa ccaggcccag aggttcaaga 1920
accctctttt tcgcctggaa gactgctcgt ccgaggttgc ccccaaaaga cgtatcttct 1980
ttaagacgct cctggaactc cgcgtcggcg tggttgtact tggggtacgg gttgtctccg 2040
ctgtcgagct gccggtcgta ggccttgtcg tgctcgaggg ccgcggcgtc tgcctcgttg 2100
accggctctc ccttgtcgag tccgttgaag ggtccaaggt acttgtaccc aggaagcaca 2160
agacccctgc tgtcgtcctt atgccgctct gcgggctttg gtggtggtgg gccaggtttg 2220
agcttccacc actgtcttat tccttcagag agagtgtcct cgagccaatc tggaagataa 2280
ccatcggcag ccatacctga tttaaatcat ttattgttca gagatgcagt catccaaatc 2340
cacattgacc agatcgcaag cagtgcaagc gtctggcacc tttcccatga tatgatgaat 2400
gtagcacagt ttctgatacg cctttttgac gacagaaacg ggttgagatt ctgacacggg 2460
aaagcactct aaacagtctt tctgtccgtg agtgaagcag atatttgaat tctgattcat 2520
tctctcgcat tgtctgcagg gaaacagcat cagattcatg cccacgtgac gagaacattt 2580
gttttggtac ctgtccgcgt agttgattga agcttccgcg tctgacgtcg atggctgcgc 2640
aactgactcg cgcgcccgtt tgggctcact tatatctgcg tcactggggg cgggtctttt 2700
tttggctcca cccttttga cgtagaattc atgctctacc tcaaccacgt gatcctttgc 2760
ccaccggaaa aagtctttga cttcctgctt ggtgaccttc ccaaagtcat gatccagacg 2820
gcgggtgagt tcaaatttga acatccggtc ttgcaacggc tgctggtgtt cgaaggtcgt 2880
tgagttcccg tcaatcactg cgcacatgtt ggtgttggag gtgacaatca cgggagtcgg 2940
gtctatctgg gccgaggact tgcatttctg gtccacgcgc accttgcttc ctccgagaat 3000
ggctttggcc gactccacga ccttggcggt catcttcccc tcctcccacc agatcaccat 3060
cttgtcgacg caatcattga aaggaaagtt ctcattggtc cagttgacgc agccgtagaa 3120
agggcgaatt cgtttaaacc tgcaggacta gtccctttag tgagggt 3167

<210> 228
<211> 3161
<212> DNA
<213> Adeno-associated virus

<400> 228
aattgaattt agcggccgcg aattcgccct tcgcagagac caaagttcaa ctgaaacgaa 60

ttaaacggtt tattgattaa caagcaatta cagattacga gtcaggtatc tggtgccaat 120

ggggcgaggc tctgaataca caccattagt gtccacagta aagtccacat taacagattt 180

gttgtagttg gaagtgtact gaatctcggg attccagcgt ttgctgttct ccttctgcag 240

ctcccactcg atctccacgc tgacctgccc cgtggagtac tgtgtaatga aggaagcaaa 300

ctttgccgca ctgaaggtag tcgaaggatt cgcaggtacc ggggtgttct tgatgagaat 360

ctgcggggga gggtgtttaa gtccgaatcc gcccatgagg ggagaggggt gaaaatgtcc 420

gtccgtgtgt ggaatctttg cccagatggg cccctgcagg tacacgtctc tgtcctgcca 480

caccatgcct ggaagaacgc cttgtgtgtt gacatctgag gtagctgctt gtgtgttgcc 540

gctctggagg ttggtagata cagaaccata ctgctccgta gccacgggat tggtggtcct 600

gatttcctct tcgtctgtaa tcatgacctt ttcaatgtcc acattagttt ttcccgagtc 660

ttgttttcca aagatgagaa ccccgctctg aggaaaaaac ttttcttcat cgtccttgtg 720

gctggccatg gccgggcccg gattcaccag agagtctctt ccattaaggt ggtacttggt 780

agctccagtc cacgagtatt cactgttgtt gttatccgca gatgtctttg atactcgctg 840

ctggcggtaa cagggtccag gaagccagtt cctagactgg tcccgaatgt cacttgctcc 900

ggcctgagaa aactgaagcc ttgactgcgt ggtggttccg cttggagtgt ttgttctgct 960

caagtaatac aggtactggt cgacgagagg attcatgaga cggtccaaac tctggctgtg 1020

ggcgtagctg ctgtggaaag gaacgtcctc aaaggtgtag ctgaaggtaa agttgtttcc 1080

ggtacgcagc atctgagaag gaaagtactc caggcagtaa aatgaagagc gtcctactgc 1140

ctgactcccg ttgttcaggg tgaggtatcc atactgtggc accatgaaga cgtctgctgg 1200

gaacggcggg aggcatcctt gatgcgccga gccgaggacg tacgggagct ggtactccga 1260

gtcagtaaac acctgaaccg tgctggtaag gttattggca atcgtcgtcg taccgtcatt 1320

ctgcgtgacc tccttgactt gaatgttaaa gagcttgaag ttgagtcttt tgggccggga 1380

tccccaattg ttgttgatga gtctttgcca gtcacgtggc gaaaagtggc agtggaatct 1440

gttgaagtca aaatacccc aaggggtgct gtagccaaag tagtggttgt cgtttgaggc 1500

tcctgattgg ctggaaatct gcctgtagag gtggttgttg taggtgggca gagcccaggt 1560

gcgggtgctg gtggtgatga ctctgtcgcc catccatgtg gaatcgcaat gccaatttcc 1620

cgaggaatta cccactccgt cggcgccctc gttattgtct gccattggtg cgccactgcc 1680

tgtagccatc gtattagttc ccagaccaga gggggctgct ggtggctgtc cgagaggctg 1740

ggggtcaggt acggagtctg cgtctccagt ctgaccgaaa ttcaatctcc ttcttgcagg 1800

ctgctggccc gcttttccgg ttcccgagga ggagtctggc tccgcaagag agtgctctac 1860 cggcctcttt tttcccggag ccgtcttaac aggttcctca accaggccca gaggttcaag 1920

aaccctcttt ttcgcctgga agactgctcg tccgaggttg cccccaaaag acgtatcttc 1980

tttaagacgc tcctggaact ccgcgtcggc gtggttgtac ttgaggtacg ggttgtctcc 2040

gccgtcgagc tgccggtcgt aggccttgtc gtgctcgagg gccgcggcgt ctgcctcgtt 2100

gaccggctct cccttgtcga gtccgttgaa gggtccaagg tacttgtacc caggaagcac 2160

aagacccctg ctgtcgtcct tatgccgctc tgcgggcttt ggtggtggtg ggccaggttt 2220

gagcttccac cactgtctta ttccttcaga gagagtgtcc tcgagccaat ctggaagata 2280

accatcggca gccatacctg atttaaatca tttattgttc agagatgcag tcatccaaat 2340

ccacattgac cagatcgcaa gcagtgcaag cgtctggcac ctttcccatg atatgatgaa 2400

tgtagcacag tttctgatac gcctttttga cgacagaaac gggttgagat tctgacacgg 2460

gaaagcactc taaacagtct ttctgtccgt gagtgaagca gatatttgaa ttctgattca 2520

ttctctcgca ttgtctgcag ggaaacagca tcagattcat gcccacgtga cgagaacatt 2580

tgttttggta cctgtccgcg tagttgattg aagcttccgc gtctgacgtc gatggctgcg 2640

caactgactc gcgcgcccgt ttgggctcac ttatatctgc gtcactgggg gcgggtcttt 2700

ttttggctcc accctttttg acgtagaatt catgctctac ctcaaccacg tgatcctttg 2760

cccaccggaa aaagtctttg acttcctgct tggtgacctt cccaaagtca tgatccagac 2820

ggcgggtgag ttcaaatttg aacatccggt cttgcaacgg ctgctggtgt tcgaaggtcg 2880

ttgagttccc gtcaatcact gcgcacatgt tggtgttgga ggtgacaatc acgggagtcg 2940

ggtctatctg ggccgaggac ttgcatttct ggtccacgcg caccttgctt cctccgagaa 3000

tggctttggc cgactccacg accttggcgg tcatcttccc ctcctcccac cagatcacca 3060

tcttgtcgac gcaatcattg aaaggaaagt tctcattggt ccagttgacg cagcaagggc 3120

gaattcgttt aaacctgcag gactagtccc tttagtgagg g 3161

<210> 229
<211> 3172
<212> DNA
<213> Adeno-associated virus

<400> 229
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60

cccttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgaccgcc 120

aaggtcgtgg agtccgccaa ggccattctg ggtggaagca aggtgcgcgt ggaccaaaag 180

tgcaagtcat cggcccagat cgaccccacg cccgtgatcg tcacctccaa caccaacatg 240

tgcgccgtga tcgacgggaa cagcaccacc ttcgagcacc agcagcccct gcaggaccgc 300

atgttcaagt tcgagctcac ccgccgtctg gagcacgact ttggcaaggt gaccaagcag 360

gaagtcaaag agttcttccg ctgggctcag gatcacgtga ctgaggtggc gcatgagttc 420

tacgtcagaa agggcggagc caccaaaaga cccgccccca gtgacgcgga tataagcgag 480

cccaagcggg cctgcccctc agttgcggag ccatcgacgt cagacgcgga agcaccggtg 540

gactttgcgg acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg 600
tttccctgca agacatgcga gagaatgaat cagaatttca acgtctgctt cacgcacggg 660
gtcagagact gctcagagtg cttccccggc gcgtcggaat ctcaacccgt cgtcagaaaa 720
aagacgtatc agaaactgtg cgcgattcat catctgctgg ggcgggcacc cgagattgcg 780
tgttcggcct gcgatctcgt caacgtggac ttggatgact gtgtttctga gcaataaatg 840
acttaaacca ggtatggctg ctgacggtta tcttccagat tggctcgagg acaacctctc 900
tgagggcatt cgcgagtggt gggacctgaa acctggagcc cccaagccca aggccaacca 960
gcagaagcag gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt 1020
caacggactc gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga 1080
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 1140
cgacgccgag tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg 1200
agcagtcttc caggccaaga agcgggttct cgaacctctc ggtctggttg aggaagctgc 1260
taagacggct cctggaaaga agagaccggt agaaccgtca cctcagcgtt cccccgactc 1320
ctccgcgggc atcggcaaga aaggccagca gcccgctaaa aagagactga actttggtca 1380
gactggcgac tcagagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc 1440
ctctggtctg ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa 1500
cgaaggcgcc gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct 1560
gggcgacaga gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca 1620
cctctacaag caaatatcca atgggacatc gggaggaagc accaacgaca acacctactt 1680
cggctacagc accccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc 1740
acgtgactgg cagcgactca tcaacaacaa ctggggattc cggccaaaaa gactcagctt 1800
caagctcttc aacatccagg tcaaggaggt cacgcagaat gaaggcaccg agaccatcgc 1860
caataacctt accagcacga ttcaggtatt tacggactcg gaataccagc tgccgtacgt 1920
cctcggctcc gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc 1980
ccagtacggc taccttacac tgaacaatgg aagtcaagcc gtaggccgtt cctccttcta 2040
ctgcctggaa tattttccat ctcaaatgct gcgaactgga aacaattttg aattcagcta 2100
caccttcgag gacgtgcctt tccacagcag ctgcgcacac agccagagct cggaccgact 2160
gatgaatcct ctcatcgacc agtacctgta ctacttatcc agaactcggt ccacaggagg 2220
aactcaaggt acccagcaat tgttattttc tcaagctggg cctgcaaaca tgtcggctca 2280
ggctaagaac tggctacctg gaccttgcta ccggcagcag cgagtctcta cgacactgtc 2340
gcaaaacaac aacagcaact ttgcttggac tggtgccacc aaatatcacc tgaacggaag 2400
agactctttg gtaaatcccg gtgtcgccat ggcaacccac aaggacgacg aggaacgctt 2460
cttcccgtcg agtggagtcc tgatgtttgg aaaacagggt gctggaagag acaatgtgga 2520
ctacagcagc gttatgctaa ccagcgaaga agaaattaaa accactaacc ctgtagccac 2580

agaacaatac ggtgtggtgg ctgacaactt gcagcaaacc aatacagggc ctattgtggg 2640

aaatgtcaac agccaaggag ccttacctgg catggtctgg cagaaccgag acgtgtacct 2700

gcagggtccc atctgggcca agattcctca cacggacggc aacttccacc cttcaccgct 2760

aatgggagga tttggactga agcacccacc tcctcagatc ctgatcaaga acacgccggt 2820

acctgcggat cctccaacaa cgttcagcca ggcgaaattg gcttccttca ttacgcagta 2880

cagcaccgga caggtcagcg tggaaatcga gtgggagctg cagaaggaga acagcaaacg 2940

ctggaaccca gagattcagt acacttcaaa ctactacaaa tctacaaatg tggactttgc 3000

tgtcaataca gagggaactt attctgagcc tcgccccatt ggtactcgtt acctcacccg 3060

taatctgtaa ttgctggtta atcaataaac cgtttgattc gtttcagttg aactttggtc 3120

tctgcgaagg gcgaattcgt ttaaacctgc aggactagtc cctttagtga gg 3172

<210> 230
<211> 3172
<212> DNA
<213> Adeno-associated virus

<400> 230
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60

cccttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgaccgcc 120

aaggtcgtgg agtccgccaa ggccattctg ggtggaagca aggtgcgcgt ggaccaaaag 180

tgcaagtcat cggcccagat cgaccccacg cccgtgatcg tcacctccaa caccaacatg 240

tgcgccgtga tcggcgggaa cagcaccacc ttcgagcacc agcagcccct gcaggaccgc 300

atgttcaagt tcgagctcac ccgccgtctg gagcacgact ttggcaaggt gaccaagcag 360

gaagtcaaag agttcttccg ctgggctcag gatcacgtga ctgaggtggc gcatgagttc 420

tacgtcagaa agggcggagc caccaaaaga cccgcccccca gtgacgcgga tataagcgag 480

cccaagcggg cctgcccctc agttgcggag ccatcgacgt cagacgcgga agcaccggtg 540

gactttgcgg acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg 600

tttccctgca agacatgcga gagaatgaat cagaatttca acgtctgctt cacgcacggg 660

gtcagagact gctcagagtg cctccccggc gcgtcagaat ctcaacccgt cgtcagaaaa 720

aagacgtatc agaaactgtg cgcgattcat catctgctgg ggcgggcacc cgagattgcg 780

tgttcggcct gcgatctcgt caacgtggac ttggatgact gtgtttctga gcaataaatg 840

acttaaacca ggtatggctg ctgacggtta tcttccagat tggctcgagg acaacctctc 900

tgagggcatt cgcgagtggt gggacctgaa acctggagcc cccaagccca aggccaacca 960

gcagaagcag gacgacggcc ggggtctggt gcttcttggc tacaagtacc tcggaccctt 1020

caacggactc gacaaggggg agcccgtcaa tgcggcggac gcagcggccc tcgagcacga 1080

caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 1140

cgacgccgag tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg 1200 agcagtcttc caggccaaga agcgggttct cgaacctctc ggtctggttg aggaagctgc 1260

taagacggct cctggaaaga agagaccggt agaaccgtca cctcagcgtt cccccgactc 1320

ctccacgggc atcggcaaga aaggccagca gcccgctaaa aagagactga actttggtca 1380

gactggcgac tcagagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc 1440

ctctggtctg ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa 1500

cgaaggcgcc gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct 1560

gggcgacaga gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca 1620

cctctacaag caaatatcca atgggacatc gggaggaagc accaacgaca acacctactt 1680

cggctacagc accccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc 1740

acgtgactgg cagcgactca tcaacaacaa ctggggattc cggccaaaaa gactcagctt 1800

caagctcttc aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc 1860

caataacctt accagcacga ttcaggtatt tacggactcg gaataccagc tgccgtacgt 1920

cctcggctcc gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc 1980

ccagtacggc taccttacac tgaacaatgg aagtcaagcc gtaggccgtt cctccttcta 2040

ctgcctggaa tattttccat ctcaaatgct gcgaactgga aacaattttg aattcagcta 2100

caccttcgag gacgtgcctt tccacagcgg ctacgcacac agccagagct tggaccgact 2160

gatgaatcct ctcatcgacc agtacctgta ctacttatcc agaactcagt ccacaggagg 2220

aactcaaggt acccagcaat tgttattttc tcaagctggg cctgcaaaca tgtcggctca 2280

ggctaagaac tggctacctg gaccttgcta ccggcagcag cgagtctcta cgacactgtc 2340

gcaaaacaac aacagcaact ttgcttggac tggtgccacc aaatatcacc tgaacggaag 2400

agactctttg gtaaatcccg gtgtcgccat ggcaacccac aaggacgacg aggaacgctt 2460

cttcccgtcg agtggagtcc tgatgtttgg aaaacagggt gctggaagag acaatgtgga 2520

ctacagcagc gttatgctaa ccagcgaaga agaaattaaa accactaacc ctgtagccac 2580

agaacaatac ggtgtggtgg ctgacaactt gcagcaaacc aatacagggc ctattgtggg 2640

aaatgtcaac agccaaggag ccttacctgg catggtctgg cagaaccgag acgtgtacct 2700

gcagggtccc atctgggcca agattcctca cacggacggc aacttccacc cttcaccgct 2760

aatgggagga tttggactga agcacccacc tcctcagatc ctgatcaaga acacgccggt 2820

acctgcggat cctccaacga cgttcagcca ggcgaaattg gcttccttca ttacgcagta 2880

cagcaccgga caggtcagcg tggaaatcga gtgggagctg cagaaggaga acagcaaacg 2940

ctggaaccca gagattcagt acacttcaaa ctactacaaa tctacaaatg tggactttgc 3000

tgtcaataca gagggaactt attctgagcc tcgccccatt ggtactcgtt acctcacccg 3060

taatctgtaa ttgctggtta atcaataaac cgtttgattc gtttcagttg aactttggtc 3120

tctgcgaagg gcgaattcgt ttaaacctgc aggactagtc cctttagtga gg 3172

<210> 231

<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 231
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg aaagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc gagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg cttcaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacagct ggggattccg acccaaaaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caagtgttta ccgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttt atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcccttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctgc tgaatcctct gatcgaccag 1320

tacctatatt atctgaacaa gacacaatca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca cggacggcca ctttcatcct tctccactaa tgggaggttt tgggctcaaa 1920

```
cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcctacaaac     1980

ttcagttctt ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtat     2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160

tcagagcctc gccccattgg caccagatac ccgactcgta atctgtaa                  2208


<210> 232
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 232
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Glu Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Ser Gly Ser Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Leu Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480
```

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
485 490 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
530 535 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
580 585 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ser Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg Asn Leu
725 730 735

<210> 233
<211> 2208

<212> DNA
<213> Adeno-associated virus

<400> 233
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggagaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gccagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggtattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctcg tgggcggatt cggacttaaa 1920 caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact   1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg   2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac   2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat   2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa   2208

<210> 234
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 234
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Glu Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195   200   205

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp Tyr Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445


Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495


Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 235
<211> 2209
<212> DNA
```

<213> Adeno-associated virus

<400> 235
atggctgccg atggttatcc tccagattgg ctcgaggaca ctctctctga agggataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcggcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatcg ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

```
ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaat                 2209


<210> 236
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 236
Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Arg Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn Arg Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 237
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 237
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aggtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgtcga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa ggcggctccg 420

ggagaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

cattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccccca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

```
ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg    2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac    2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat    2160

tcagagcctc gccccattgg cgccagatac ctgactcgta atctgtaa                 2208


<210> 238
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 238
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Val
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Ala Ala Pro Gly Glu Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly His Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
```

```
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Pro Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Ala Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 239
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 239
atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga taacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccggcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

```
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 240
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 240
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495
```

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500   505   510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515   520   525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530   535   540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545   550   555   560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565   570   575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580   585   590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595   600   605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 241
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 241

```
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga      60
cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac     120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac     180
aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac     240
cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt     300
caggagcgcc ttaaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag     360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg     420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga     480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac     540
tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact     600
aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga     660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcgg cagagtcatc     720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc     780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg     840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc     900
aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc     960
aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt    1020
caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga    1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg    1140
aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct    1200
cagacgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc    1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag    1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt    1380
cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga    1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac    1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc    1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc    1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca    1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct    1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt    1800
cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag    1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa    1920
caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact    1980
ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg    2040
```

```
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 242
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 242
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Gly Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Thr Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 243
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 243
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60
```

```
cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180
aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga      480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac      540
tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600
aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720
accaccagca cccgcacctg ggccctgccc acctgcaaca accatctgta caagcaaatc      780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg      840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc      900
aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc      960
aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020
caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140
aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ttttccttct     1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc     1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag     1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt     1380
cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga     1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac     1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc     1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc     1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca     1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct     1740
acctacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt     1800
cttccaggca tggtctggca ggacagagac gtgtacctgc gggggcccat ctgggcaaag     1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa     1920
caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact     1980
ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg     2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac     2100
```

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 244
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 244
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Cys Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495
```

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Tyr Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
580 585 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 245
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 245
atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga 60

```
cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180
aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
cggcagctcg acagcggaga taacccgtac ctcaagtaca accacgccga cgcggagttt      300
caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga      480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac      540
tcagtacctg acccccggcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600
aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc      780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg      840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc      900
aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc      960
aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020
caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140
aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct     1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc     1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag     1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt     1380
cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga     1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac     1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc     1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc     1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca     1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct     1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt     1800
cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag     1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa     1920
caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact     1980
ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg     2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac     2100
```

```
acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 246
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 246
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
```

```
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445


Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495


Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
```

```
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 247
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 247

```
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120
```

ggcagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctca acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga gaccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accacaagca ctcgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactattttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct ccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagat gtgtaccttc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagattat gatcaaaaac actcccgttc cagccaatcc tcctacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacaataa tggcgtgtac 2160

```
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 248
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 248
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Gly Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asn Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Pro Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515   520   525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530   535   540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545   550   555   560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565   570   575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580   585   590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595   600   605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Asn Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 249
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 249
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga   60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac   120

```
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga      480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac      540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc      780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg      840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc      900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc      960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct     1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc     1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag     1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt     1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga     1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac     1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc     1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc     1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca     1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa     1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact     1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160
```

```
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 250
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 250
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
580 585 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 251
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 251
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

```
aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga      480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac      540
tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600
aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc      780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg      840
tatttcgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc      900
aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc      960
aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020
caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080
tgccttccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140
aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct     1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc     1260
catagcagct acgctcacgg ccaaagtctg gaccgtctca tgaatcctct catcgaccag     1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt     1380
cagttttctc aggccggagc aagtgacgtt cgggaccagt ctagaaactg gcttcctgga     1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac     1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc     1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc     1620
gtctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca     1680
gacgaagagg aaatcaggac caccaatccc gcggctacgg agcagtatgg ttctgtatct     1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt     1800
cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag     1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa     1920
caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact     1980
ttcagtgcgg caaagtttgt ttccttcatc acacagtact ccacggggca ggtcagcgtg     2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac     2100
acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208
```

<210> 252
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 252
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Gly Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Val Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
485 490 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Val Phe Gly Lys
    530                 535                 540


Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Ala Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Val Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 253
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 253
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga aactcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180
```

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttctgga acctctgagc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctccc gcagagccag attcctcctc cggaactgga 480

aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780

tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctagagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt caggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttcctcagag cggggttctt 1620

atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtcgggca agacagagac gtgtacctgc aggggcctac ttgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```
<210> 254
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 254
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Ser Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Gln Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
```

```
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Gly Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Thr Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 255
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 255
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
```

```
cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt      300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
gcaaaaaaga gggttctgga acctctgggc ctggttgagg agcctgttaa gacggctccg      420
ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga      480
aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac      540
tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600
aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720
accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata      780
tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg      840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc      900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc      960
aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020
caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140
aacaacggga gtcaggcagt aggacgctct tcattttact gcctagggta ctttccttct     1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc     1260
cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag     1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt     1380
cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga     1440
ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc     1560
ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttcctcagag cggggttctt     1620
atctttggga agcaaggccc agagaaaaca aatgtggata ttgaaaaggt catgattaca     1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct     1740
accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt     1800
cttccaggca tggtctggca agacagagac gtgtacctgc aggggcctat ttgggcaaag     1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa     1920
caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980
ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg     2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac     2100
acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208
```

<210> 256
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 256
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Gly Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530   535   540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545   550   555   560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565   570   575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580   585   590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595   600   605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 257
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 257
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305   310   315   320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325   330   335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340   345   350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355   360   365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370   375   380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385   390   395   400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405   410   415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420   425   430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435   440   445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450   455   460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465   470   475   480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485   490   495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500   505   510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515   520   525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530   535   540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545   550   555   560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565   570   575

```
Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 258
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 258
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

```
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 259
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 259
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac       120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac       240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt       300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag       360

gcgaaaaaga gggttcttga acctctgcgg cctggtttga ggaaacctgt taagacggct       420

ccgggaaaaa agaggccggt agagcactct cctgtggagc cagactcctc ctcgggaacc       480

ggaaaagcgg gccagcagcc tgcaagaaaa agattaaatt ttggtcagac tggagacgca       540

gactccgtac ctgaccccca gcctctcgga cagccaccag cagccccctc tggtctggga       600

tctactacaa tggctacagg cagtggcgca ccaatggcag acaataacga gggtgccgat       660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctgga cgacagagtc       720

atcgccacca gcacccgaac ctgggccctg cccacataca acaaccacct ctacaagcaa       780

atctccagcc aatcaggagc ctgcaacgac aaccactact ttggctacag caccccctgg       840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc       900

atcaacagca actggggatt ccggcccaaa agactcaact tcaagctctt taatattcaa       960

gtcaaagagg tcacgcagaa tgacggtacg acgacgattg ccaataacct taccagcacg      1020

gttcaggtgt ttactgactc ggagtaccag ctcccgtacg tcccgggctc ggcgcatcaa      1080
```

ggatgcctcc cgccgtttcc agcggacgtc ttcatggtcc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc ggtaggacgc tcttcctttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtactgg aaacaacttt cagttcagct acacttttga agacgtgcct 1260

ttccacagca gctacgctca ctgccagagt ctggatcggc tgatgaatcc tctgatcgac 1320

cagtacctgt attatctgaa caagacacaa acaaatagtg gaactcttca gcagtctcgg 1380

ctactgttta gccaagctgg accaaccaac atgtctcttc aagctaaaaa ctggctgcct 1440

ggaccttgct acagacagca gcgtctgtca aaacaggcaa acgacaataa caactgcaac 1500

tttccctgga ctgcagctac aaagtatcat ctaaatggcc gggactcgtt ggttaatcca 1560

ggaccagcta tggccagtca caaggatgac gaagaaaagt ttttccccat gcatggaacc 1620

ctgatatttg gtaaacaagg aacaaatgcc aacgacgcgg atttggaaaa tgtcatgatt 1680

acagatgaag aagaaatcag gcccaccaat cccgtggcta cggagcagta cgggactgtg 1740

tcaaataatt tgcaaaactc aaacactggt ccaactacag gaactgtcaa tcaccaagga 1800

gcgttacctg gtatggtgtg gcaggatcga gacgtgtacc tgcagggacc catttgggcc 1860

aagattcctc acaccgatgg acactttcat ccttctccac tgatgggagg ttttggactc 1920

aaacacccgc ctcctcagat catgatcaaa agcactcccg ttccagccaa tcctcccaca 1980

aacttcagtt ctgccaagtt tgcttcttcc atcacacagt attccacggg acaggtcagc 2040

gtggagatcg agtgggagct gcagaaggag aacagcaaac gctggaatcc cgaaattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtggacac taatggtgtg 2160

tattcagagc ctcgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 260
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 260
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Arg Pro Gly Leu Arg Lys Pro Val Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr
145                 150                 155                 160

Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Asp Asp Arg Val
225                 230                 235                 240

Ile Ala Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Cys Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Cys Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys
        435                 440                 445

Thr Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn
                485                 490                 495

Asn Asn Cys Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Met Ile Lys Ser Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Ser Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 261
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 261
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttctgga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480

aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780

tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

```
aacaacggga gtcaggcagt aggacgctct tcattttact gcctagagta ctttccttct     1200

cagatgctgc gtaccggaaa cagctttacc ttcagctaca cctttgagga cgttcctttc     1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag     1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt     1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga     1440

ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc     1560

ccggccatgg ccagccacaa agacgatgaa gaaaagttct ttcctcagag cggggttctt     1620

atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaaggt catgattaca     1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca agacagagac gtgtacctgc aggggcctat ttgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa     1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 262
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 262
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Ser Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445


Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

```
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 263
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 263
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140
```

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaattttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 264
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 264
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
```

370 375 380

Gly Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala

645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Ser Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 265
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 265
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtt cacagcccgc taaaaagaaa ctcaatttcg gtcagactgg cgacacagag 540

tcagtccccg accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atgggagcca ggccgtgggt cgttcgtcct ttttactgcct ggaatatttc 1200

```
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta     1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc     1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg     1380

ctaaaattca gcgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct     1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata     1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860

aaaattcctc acacggacgg caactttcac ccttctccgc taatgggagg gtttggaatg     1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980

gctttcaata aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040

gtggagattg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a              2211
```

```
<210> 266
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 266
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 267
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 267
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cggcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

```
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc     1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag     1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt     1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga     1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc     1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc     1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca     1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa     1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208
```

```
<210> 268
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 268
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Gly Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445


Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
```

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 269
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 269
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtccttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacgaga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260 cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 270
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 270
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Glu Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
```

```
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 271
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 271
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga      60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac     120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac     180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac     240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt     300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag     360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg     420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga     480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac     540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact     600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga     660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc     720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt     780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg     840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc     900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc     960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt    1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga    1080

tgcctcccgc cgttcccagc agacgtcttc atggtaccac agtatggata cctcaccctg    1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct    1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc    1260
```

```
cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag     1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt     1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga     1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc     1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc     1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca     1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa     1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208

<210> 272
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 272
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
```

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
```

385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln

```
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 273
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 273
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac       120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac       180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac       240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt       300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag       360

gcgaaaaaga gggtactcga acctctgggc ctggttgagg aacctgttaa gacggctccg       420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga       480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac       540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact       600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga       660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc       720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt       780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg       840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc       900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc       960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt      1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga      1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg      1140

aacaacggga gtcaggcagc aggacgctct tcattttact gcctggagta ctttccttct      1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc      1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag      1320
```

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc cgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 274
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 274
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Ala Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

```
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 275
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 275
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
```

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590


Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
```

```
Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 276
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 276
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct       420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc       480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca       540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga       600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac       660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc       720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa       780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc       840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag       900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac       960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc      1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg      1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac      1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat      1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac      1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc      1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc      1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg      1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac      1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta      1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt      1620
```

ggagtcctga tgttcggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccccg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 277
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 277
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln

```
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
```

```
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590


Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Cys His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
```

705   710   715   720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 278
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 278
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Arg
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195   200   205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Leu Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Ala Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Pro Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Arg Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485   490   495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500   505   510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515   520   525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530   535   540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545   550   555   560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565   570   575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580   585   590

Pro Thr Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595   600   605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610   615   620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625   630   635   640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645   650   655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660   665   670

Ile Ala Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Ala Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 279
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 279
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcggac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtt 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt atcttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcgcc 1020

agcaccatcc aggtgtttac ggactcggaa taccagccgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctcg ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ctgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860 tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatcg cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgcgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 280
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 280
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcgtc 900

aacaacaacc ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440 ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 281
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 281
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Val Asn Asn Asn Arg
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 282
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 282
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Ser Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly

```
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
```

465   470   475   480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485   490   495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500   505   510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515   520   525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530   535   540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545   550   555   560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565   570   575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580   585   590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595   600   605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610   615   620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625   630   635   640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645   650   655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660   665   670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 283
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 283
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgagct ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg ggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattctgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800 caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 284
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 284
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Pro Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190
```

```
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Val Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 285
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 285
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ccggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgccacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccgtcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

```
atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt      1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc      1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc      1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt      1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct      1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag      2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgttg gaacccagag      2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag      2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa         2217


<210> 286
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 286
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
```

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Ser Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590


Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Leu
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
```

```
Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 287
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 287
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca      540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga      600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac      660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa      780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc      840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag      900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac      960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc     1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg     1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac     1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat     1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac     1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc     1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc     1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg     1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aagcaacaac     1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta     1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt     1620
```

```
ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt      1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt      1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc      1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc      1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggactt      1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct      1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag      2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag      2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag      2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa         2217
```

<210> 288
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 288

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Pro Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160
```

```
Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Val Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700
```

```
Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720


Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735


Leu



<210> 289
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 289
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480
```

```
Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 290
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 290
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ccgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgcctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacaacca tcgctaataa ccttaccagc 1020

acggttcaag tcttctcgga ctcggagtac cagcttccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctctccaca gcagctacgc gcacagccag agcctggacc ggctgatgaa tcctctcatc 1320

gtccaatacc tgtattacct gaacagaact caaaatcagt ccggaagtgc ccaaaacaag 1380

gacttgctgt tcagccgtgg gtctccagct ggcatgtctg ttcagcccaa aaactggcta 1440

cctggaccct gttatcggca gcagcgcgtt tctaaaacaa aaacagacaa caacaacagc 1500

aattttacct ggactggtgc ttcaaaatat aacctcaatg ggcgtgaatc catcatcaac 1560

cctggcactg ctatggcctc acacaaagac gacgaagaca agttctttcc catgagcggt 1620

gtcatgattt ttggaaaaga gagcgccgga gcttcaaaca ctgcattgga caatgtcatg 1680

attacagacg aagaggaaat taaagccact aaccctgtgg ccaccgaaag atttgggacc 1740

gtggcagtca atttccagag cagcagcaca gaccctgcga ccggagatgt gcatgctatg 1800

```
ggagcattac ctggcatggt gtggcaagat agagacgtgt acctgcaggg tcccatttgg     1860

gccaaaattc ctcacacaga tggacacttt cacccgtctc ctcttatggg cggctttgga     1920

ctcaagaacc cgcctcctca gatcctcatc aaaaacacgc ctgttcctgc gaatcctccg     1980

gcggagtttt cagctacaaa gtttgcttca ttcatcaccc aatactccac aggacaagtg     2040

agtgtggaaa ttgaatggga gctgcagaaa gaaaacagca agcgctggaa tcccgaagtg     2100

cagtacacat ccaattatgc aaaatctgcc agcgttgatt ttactgtgga caacaatgga     2160

ctttatactg agcctcgccc cattggcacc cgttacctta cccgtcccct gtaa           2214


<210> 291
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 291
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Pro Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
```

```
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 292
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 292
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcagacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctga gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagggccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacccgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaaggtaga gacgtgtacc tgcagggtcc catttgggcc 1860

```
aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a              2211
```

```
<210> 293
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 293
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Pro Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
```

```
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

```
<210> 294
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 294
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 295
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 295
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
            20                  25                  30
```

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305   310   315   320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325   330   335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340   345   350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355   360   365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370   375   380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385   390   395   400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405   410   415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420   425   430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435   440   445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450   455   460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485   490   495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 296
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 296
atggctgccg atggctatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatagggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata ccccaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccgtgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 297
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 297
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
```

305   310   315   320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325   330   335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
            340   345   350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355   360   365

Val Phe Met Val Pro Gln Tyr Gly Tyr Pro Thr Leu Asn Asn Gly Ser
    370   375   380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385   390   395   400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405   410   415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420   425   430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435   440   445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450   455   460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465   470   475   480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485   490   495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500   505   510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Val Ala Ser His Lys Asp
        515   520   525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530   535   540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545   550   555   560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565   570   575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr

580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 298
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 298
atggctgccg acggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgggc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcccctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcactgc gattccacat ggctgggcga cagagtcatc 720 accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggccgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctctt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ctccacagca gctgcgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacagggac 1380

ttgctgttca gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccgcagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 299
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 299
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Pro Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Arg Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Ser Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590
```

```
Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Ala Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 300
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 300
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 301
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 301
atggctgccg atggctatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatagggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac      540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt      780

tccagccaat caggagcctc gaacgacagt cactactttg gctacagcac cccttggggg      840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc      900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc      960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140
```

```
aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct     1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc     1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag     1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctc     1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga     1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc     1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc     1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca     1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa     1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208

<210> 302
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 302
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
```

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Ser His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
```

```
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
```

```
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 303
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 303
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1               5                   10                  15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
            20                  25                  30

Pro Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu
        35                  40                  45

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
    50                  55                  60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110

Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu
        115                 120                 125

Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160
```

```
Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270


His Tyr Phe Gly Tyr Gly Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700
```

```
Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720


Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735


Leu



<210> 304
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 304
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Gly Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
```

465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485   490   495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 305

<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 305
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gccagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtactt caacgggggc cagcaacgac aaccactact tcggctacgg caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcgaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaacacaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcaccgctg tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaagcactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

```
aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a              2211


<210> 306
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 306
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1               5                   10                  15


Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
            20                  25                  30


Pro Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu
        35                  40                  45


Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
    50                  55                  60


Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80


Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95


Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110


Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu
        115                 120                 125


Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140


Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160


Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480
```

```
Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

```
<210> 307
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 307
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1               5                   10                  15


Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
            20                  25                  30


Pro Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu
        35                  40                  45


Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
    50                  55                  60


Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80


Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95


Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110


Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu
        115                 120                 125


Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140


Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160


Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510
```

```
Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu


<210> 308
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 308
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1               5                   10                  15
```

```
Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
            20                  25                  30

Pro Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu
        35                  40                  45

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
    50                  55                  60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110

Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu
        115                 120                 125

Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
405 410 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
435 440 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
450 455 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465 470 475 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
485 490 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
500 505 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
515 520 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
530 535 540

Gly Lys Glu Ser Ala Gly Ala Asn Ser Thr Ala Leu Asp Asn Val Met
545 550 555 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
565 570 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
580 585 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 309
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 309
atggctgccg atggttatct tccagattgg ctcaaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcgggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agtacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaacagga 480

aaagcgggcc agcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaag ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta caagcagatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc ccggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgagga tgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctactgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgcacctgc aggggcctat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcaaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtatt ccacagggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 310
<211> 735
<212> PRT
<213> Adeno-associated virus

```
<400> 310
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Lys Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Gly Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu Tyr Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Ser Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

```
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val His Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 311
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 311
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac       120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac       240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt       300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag       360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg       420
```

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcgcaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 312
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 312

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser Arg Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540
```

```
Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590


Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 313
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 313
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac       120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac       180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac       240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt       300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag       360

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgtcaa gacggctcca       420
```

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcggct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtacgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 314
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 314
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
```

```
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
```

545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 315
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 315
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa tcggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta cagacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

agcaacggga gtcaggcagt aggacgctct tcattttact gcccggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacctaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atttgtaa 2208

<210> 316
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 316
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Arg His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Ser Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445


Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
```

```
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Pro Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 317
<211> 2205
<212> DNA
<213> Adeno-associated virus

<400> 317

```
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac       120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac       180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac       240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt       300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag       360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg       420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga       480
```

aaagcgggcc agcagcctgc aagaaaaaga ctgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcagacag ccaccagcag cccccacaag tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accaccttta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtttg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctaaacag aacacaaaca gctagtggaa ctcagcagtc tcggctactg 1380

tttagccaag ctggacccac aagcatgtct cttcaagcta aaaactggct gcctggaccg 1440

tgttatcgcc agcagcgttt gtcaaagcag gcaaacgaca acaacaacag caactttccc 1500

tggactggag ctaccaagta ctacctcaat ggcagagact ctttggtgaa cccgggcccg 1560

gccatggcca gccacaagga cgatgaagaa aagtttttcc ccatgcatgg aaccctaata 1620

tttggtaaag aaggaacaaa tgctaccaac gcggaattgg aaaatgtcat gattacagat 1680

gaagaggaaa tcaggaccac caatcccgtg gctacagagc agtacggata tgtgtcaaat 1740

aatttgcaaa actcaaatac tgctgcaagt actgaaactg tgaatcacca aggagcatta 1800

cctggtatgg tgtggcagga tcgagacgtg tacctgcagg gacccatttg ggccaagatt 1860

cctcacaccg atggacactt tcatccttct ccactgatgg gaggttttgg actcaaacac 1920

ccgcctcctc agattatgat caaaaacact cccgttccag ccaatcctcc cacaaacttc 1980

agttctgcca agtttgcttc cttcatcaca cagtattcca cgggacaggt cagcgtggag 2040

atcgagtggg agctgcagaa ggagaacagc aaacgctgga atcccgaaat tcagtacact 2100

tccaactaca acaaatctgt taatgtggac tttactgtgg acactaatgg tgtgtattca 2160

gagcctcgcc ccattggcac cagatacctg actcgtaatc tgtaa 2205

<210> 318
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 318
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560
```

```
Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575


Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590


Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605


Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620


Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640


Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655


Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670


Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685


Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
    690                 695                 700


Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705                 710                 715                 720


Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210> 319
<211> 3160
<212> DNA
<213> Adeno-associated virus

<400> 319
acccttcact aaagggacta gtcctgcagg tttaaacgaa ttcgcccttg ctgcgtcaac        60

tggaccaatg agaactttcc cttcaacgac tgtgtcgaca agatggtgat ttggtgggag       120

gaggggaaga tgaccgccaa ggtcgtggag tcggccaaag ccattctcgg aggaagcaag       180

gtgcgcgtgg accagaaatg caagtcctcg gcccagatag atccgactcc cgtgatcgtc       240

acctccaaca ccaacatgtg cgccgtgatt gacgggaact caacgacctt cgaacaccag       300

cagccgttgc aagaccggat gttcaaattt gaactcaccc gccgtctgga tcatgacttt       360

gggaaggtca ccaagcggga agtcaaagac tttttccggt gggcaaagga tcacgtggtt       420

gaggtggagc atgaattcta cgtcaaaaag ggtggagcca agaaaagacc cgcccctagt       480

gacgcagata taagtgagcc caaacgggtg cgcgagtcag ttgcgcagcc atcgacgtca       540
```

gacgcggaag cttcgatcaa ctacgcggac aggtaccaaa acaaatgttc tcgtcacgtg 600

ggcatgaatc tgatgctgtt tccctgcaga caatgcgaga gaatgaatca aaattcaaat 660

atctgcttca ctcacggaca gaaagactgt ttagagtgct ttcccgtgtc agaatctcaa 720

cctgtttctg tcgtcaaaaa ggcgtatcag aaactgtgct acattcatca tatcatggga 780

aaggtgccag acgcttgcac tgcctgcgat ctggtcaatg tggatttgga tgactgcatc 840

tctgaacaat aaatgattta aatcaggtat ggctgccgat ggttatcttc cagattggct 900

cgaggacact ctctctgaag gaataagaca gtggtggaag ctcaaacctg gcccaccacc 960

accaaagccc gcagagcggc ataaggacga cagcaggggt cttgtgcttc ctgggtacaa 1020

gtacctcgga cccttcaacg gactcgacaa gggagagccg gtcaacgagg cagacgccgc 1080

ggccctcgag cacgacaagg cctacgaccg gcagctcgac agcggagaca acccgtacct 1140

caagtacaac cacgccgacg cggagtttca ggagcgtctt aaagaagata cgtcttttgg 1200

gggcaacctc ggacgagcag tcttccaggc gaaaaagagg gttcttgaac ctctgggcct 1260

ggttgaggaa cctgttaaga cggctccggg aaaaaagagg ccggtagagc actctcctgc 1320

ggagccagac tcctcctcgg gaaccggaaa agcgggccag cagcctgcaa gaaaaagact 1380

gaatttcggt cagactggag acgcagactc cgtacctgac ccccagcctc tcagacagcc 1440

accagcagcc cccacaagtt tgggatctac tacaatggct acaggcagtg gcgcaccaat 1500

ggcagacaat aacgagggtg ccgatggagt gggtaattcc tcaggaaatt ggcattgcga 1560

ttcccaatgg ctgggcgaca gagtcatcac caccagcacc cgaacctggg ccctgcccac 1620

ctacaacaac cacctttaca agcaaatctc cagccaatca ggagcctcaa acgacaacca 1680

ctactttggc tacagcaccc cctgggggta ttttgacttc aacagattcc actgccactt 1740

ttcaccacgt gactggcaaa gactcatcaa caacaactgg ggattccgac ccaagagact 1800

caacttcaag ctctttaaca ttcaagtcaa agaggtcacg cagaatgacg gtacgacgac 1860

gattgccaat aaccttacca gcacggttca ggtgtttact gactcggagt accagctccc 1920

gtacgtcctc ggctcggcgc atcaaggatg cctcccgccg tttccagcgg acgtcttcat 1980

ggtcccacag tatggatacc tcaccctgaa caacgggagt caggcggtag gacgctcttc 2040

cttttactgc ctggagtact ttccttctca gatgctgcgt actggaaaca actttcagtt 2100

cagctacact tttgaagacg tgcctttcca cagcagctac gctcacagcc agagtttgga 2160

tcggctgatg aatcctctga tcgaccagta cctgtattat ctaaacagaa cacaaacagc 2220

tagtggaact cagcagtctc ggctactgtt tagccaagct ggacccacaa gcatgtctct 2280

tcaagctaaa aactggctgc ctggaccgtg ttatcgccag cagcgtttgt caaagcaggc 2340

aaacgacaac aacaacagca actttccctg gactggagct accaagtact acctcaatgg 2400

cagagactct ttggtgaacc cgggcccggc catggccagc cacaaggacg atgaagaaaa 2460

gtttttcccc atgcatggaa ccctaatatt tggtaaagaa ggaacaaatg ctaccaacgc 2520

ggaattggaa aatgtcatga ttacagatga agaggaaatc aggaccacca atcccgtggc 2580

```
tacagagcag tacggatatg tgtcaaataa tttgcaaaac tcaaatactg ctgcaagtac     2640

tgaaactgtg aatcaccaag gagcattacc tggtatggtg tggcaggatc gagacgtgta     2700

cctgcaggga cccatttggg ccaagattcc tcacaccgat ggacactttc atccttctcc     2760

actgatggga ggttttggac tcaaacaccc gcctcctcag attatgatca aaaacactcc     2820

cgttccagcc aatcctccca caaacttcag ttctgccaag tttgcttcct tcatcacaca     2880

gtattccacg ggacaggtca gcgtggagat cgagtgggag ctgcagaagg agaacagcaa     2940

acgctggaat cccgaaattc agtacacttc caactacaac aaatctgtta atgtggactt     3000

tactgtggac actaatggtg tgtattcaga gcctcgcccc attggcacca gatacctgac     3060

tcgtaatctg taattgcttg ttaatcaata aaccgtttaa ttcgtttcag ttgaactttg     3120

gtctctgcga agggcgaatt cgcggccgct aaatcaatcg                           3160
```

<210> 320
<211> 734
<212> PRT
<213> Adeno-associated virus

```
<400> 320
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160
```

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Gly Leu Asp Arg
420 425 430

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445


Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460


Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480


Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495


Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Gly
            500                 505                 510


Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525


Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540


Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560


Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575


Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590


Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605


Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp
    610                 615                 620


Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640


Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655


Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670


Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685


Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
    690                 695                 700
```

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705   710   715   720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730

<210> 321
<211> 3157
<212> DNA
<213> Adeno-associated virus

<400> 321
ctcactaagg gactagtcct gcaggtttaa acgaattcgc ccttgctgcg tcaactggac 60

caatgagaac tttcccttca acgactgtgt cgacaagatg gtgatttggt gggaggaggg 120

gaagatgacc gccaaggtcg tggagtcggc caaagccact ctcggaggaa gcaaggtgcg 180

cgtggaccag aaacgcaagt cctcggccca gatagatccg actcccgtga tcgtcacctc 240

caacaccaac atgtgcgccg tgattgacgg gaactcaacg accttcgaac accagcagcc 300

gttgcaagac cgaatgttca aatttgaact cacccgccgt ctggatcatg acttcgggaa 360

ggtcaccaag caggaagtca aagacttttt ccggtgggca aaggatcacg tggttgaggt 420

ggagcatgaa ttctacgtca aaaagggtgg agccaagaaa agacccgccc ctagtgacgc 480

agatataagt gagcccaaac gggtgcgcga gtcagttgcg cagccatcga cgtcagacgc 540

ggaagcttcg atcaactacg cggacaggta ccaaaacaaa tgttctcgtc acgtgggcat 600

gaatctgatg ctgtttccct gcagacaatg cgagagaatg aatcaaaatt caaatatctg 660

cttcactcac ggacagaaag actgtttaga gtgctttccc gtgtcagaat ctcaacctgt 720

ttctgtcgtc aaaaaggcgt atcagaaact gtgctacatt catcatatca tgggaaaggt 780

gccagacgct tgcactgcct gcgatctggt caatgtggat ttggatgact gcatctctga 840

acaataaatg atttaaatca ggtatggctg ccgatggtta tcttccagat tggctcgagg 900

acactctctc tgaaggaata agacagtggt ggaagctcaa acctggccca ccaccaccaa 960

agcccgcaga gcggcataag gacgacagca ggggtcttgt gcttcctggg tacaagtacc 1020

tcggaccctt caacggactc gacaagggag agccggtcaa cgaggcagac gccgcggctc 1080

tcgagcacga caaggcctac gaccggcagc tcgacagcgg agacaacccg tacctcaagt 1140

acaaccacgc cgacgcggag tttcaggagc gtcttaaaga agatacgtct tttgggggca 1200

acctcggacg agcagtcttc caggcgaaaa agagggttct tgaacctctg ggcctggttg 1260

aggaacctgt taagacggct ccgggaaaaa agaggccggt agagcactct cctgcggagc 1320

cagactcctc ctcgggaacc ggaaaagcgg gccagcagcc tgcaagaaaa agactgaatt 1380

tcggtcagac tggagacgca gactccgtac ctgaccccca gcctctcgga cagccaccag 1440

cagcccccac aagtttggga tctactacaa tggctacagg cagtggcgca ccaatggcag 1500

acaataacga gggtgccgat ggagtgggta attcctcagg aaattggcat tgcgattccc 1560

aatggctggg cgacagagtc atcaccacca gcacccgaac ctgggccctg cccacctaca 1620 acaaccacct ttacaagcaa atctccagcc aatcaggagc ctcaaacgac aaccactact 1680

ttggctacag cacccccctgg gggtattttg acttcaacag attccactgc cgcttttcac 1740

cacgtgactg gcaaagactc atcaacaaca actggggatt ccgacccaag agactcaact 1800

tcaagctctt taacattcaa gtcaaagagg tcacgcagaa tgacggtacg acgacgattg 1860

ccaataacct taccagcacg gttcaggtgt ttactgactc ggagtaccag ctcccgtacg 1920

tcctcggctc ggcgcatcaa ggatgcctcc cgccgtttcc agcggacgtc ttcatggtcc 1980

cacagtatgg atacctcacc ctgaacaacg ggagtcaggc ggtaggacgc tcttcctttt 2040

actgcctgga gtactttcct tctcagatgc tgcgtactgg aaacaacttt cagttcagct 2100

acacttttga agacgtgcct ttccacagca gctacgctca cagccagggt ttggatcggc 2160

tgatgaatcc tctgatcgac cagtacctgt attatctaaa cagaacacaa acagctagtg 2220

gaactcagca gtctcggcta ctgtttagcc aagctggacc cacaagcatg tctcttcaag 2280

ctaaaaactg gctgcctgga ccgtgttatc gccagcagcg tttgtcaaag caggcaaacg 2340

acaacaacaa cagcaacttt ccctggactg gagctaccaa gtaccacctc aatggcggag 2400

actctttggt gaacccgggc ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt 2460

tccccatgca tggaacccta atatttggta aagaaggaac aaatgctacc aacgcggaat 2520

tggaaaatgt catgattaca gatgaagagg aaatcaggac caccaatccc gtggctacag 2580

agcagtacgg atatgtgtca aataatttgc aaaactcaaa tactgctgca agtactgaaa 2640

ctgtgaatca ccaaggagca ttacctggta tggtgtggca ggatcgagac gtgtacctgc 2700

ggggacccat ttgggccaag attcctcacg ccgatggaca ctttcatcct tctccactga 2760

tgggaggttt tggactcaaa cacccgcctc ctcagattat gatcaaaaac actcccgttc 2820

cagccaatcc tcccacaaac ttcagttctg ccaagtttgc ttccttcatc acacagtatt 2880

ccacgggaca ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct 2940

ggaatcccga aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg 3000

tggacactaa tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta 3060

atctgtaatt gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc 3120

tgcgaagggc gaattcgcgg ccgctaaatt caattcg 3157

<210> 322
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 322
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
```

```
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Cys Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
```

```
            580                 585                 590


Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605


Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620


Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640


Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655


Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670


Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685


Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
    690                 695                 700


Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705                 710                 715                 720


Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210> 323
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 323
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctggatac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

aaagcgggca accagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac      540

tccgtacctg acccccagcc tctcggacag ccaccagcat ccccctctgg tctgggaact      600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcgtc      720
```

accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcagatt 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcgccac gcgactggca gagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctgtttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgacttgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gcaccggaaa caactttacc ttcagctaca cttttgaaga cgttcctttc 1260

cacagcagct acgctcacag tcaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccactacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaaa 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct cattaagaat accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagcgcgg caaagtttgc ttccttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggggtgtat 2160

tcagagcctc gccctattgg caccagatac ctgactcgta atctgtaa 2208

<210> 324
<211> 3159
<212> DNA
<213> Adeno-associated virus

<400> 324
gattgattta gcggccgcga attcgccctt gctgcgtcaa ctggaccaat gagaactttc 60

ccttcaacga ttgcgtcgac aagatggtga tctggtggga ggagggaaag atgaccgcca 120

aggtcgtgga gtcggccaaa gccattctcg gaggaagcaa ggtgcgtgtg gaccaaaagt 180

gcaagtcttc ggcccagatc gacccgactc ccgtgatcgt cacctccaac accaacatgt 240

gcgccgtgat tgatggaaac tcaacgacct tcgagcacca gcagccgttg caagaccgga 300 tgttcaaatt tgaacttacc cgccgtctgg atcatgactt tggaaaggtc accaagcagg 360

aagtgaaaga ctttttccgg tgggcaaagg atcacgtggt tgaggtggag catgagttct 420

acgtcaaaaa gggtggagcc aaaaaaagac ccgcccccag tgacgcagat ataagtgagc 480

ccaaacgggc gcgcgagtca gttgcgcagc catcgacgtc agacgcggaa gcttcgatca 540

actacgcgga caggtaccaa aacaaatgtt ctcgtcacgt gggcatgaat ctgatgctgt 600

ttccctgcag acaatgcgag agaatgaatc agaattcaaa tatctgcttc actcacggac 660

agaaagactg tccatagtgc tttcccgtgt cagaatctca acccgtttct gtcgtcaaaa 720

aggcgtatca gaaactgtgc tacattcatc acatcatggg aaaggtgcca gacgcttgca 780

ctgcttgcga cctggtcaat gtggatttgg atgactgcat ctctgaacaa taaatgattt 840

aaatcaggta tggctgccga tggttatctt ccagattggc tcgaggacac tctctctgaa 900

ggaataagac agtggtggaa gctcaaacct ggcccaccac caccaaagcc cgcagagcgg 960

cataaggacg acagcagggg tcttgtgctt cctggataca agtacctcgg acccttcaac 1020

ggactcgaca agggagagcc ggtcaacgag gcagacgccg cggccctcga gcacgacaag 1080

gcctacgacc ggcagctcga cagcggagac aacccgtacc tcaagtacaa ccacgccgac 1140

gcggagtttc aggagcgcct taaagaagat acgtcttttg gggcaacct cggacgagca 1200

gtcttccagg cgaaaaagag ggttcttgaa cctctgggcc tggttgagga acctgttaag 1260

acggctccgg gaaaaaagag gccggtagag cactctcctg tggagccaga ctcctcctcg 1320

ggaaccggaa aagcgggcaa ccagcctgca agaaaaagat tgaatttcgg tcagactgga 1380

gacgcagact ccgtacctga cccccagcct ctcggacagc caccagcatc cccctctggt 1440

ctgggaacta atacgatggc tacaggcagt ggcgcaccaa tggcagacaa taacgagggc 1500

gccgacggag tgggtaattc ctcgggaaat tggcattgcg attccacatg gatgggcgac 1560

agagtcgtca ccaccagcac ccgcacctgg gccctgccca cctacaacaa ccacctctac 1620

aagcagattt ccagccaatc aggagccagc aacgacaacc actactttgg ctacagcacc 1680

ccttgggggt attttgactt caacagattc cactgccact tttcgccacg cgactggcag 1740

agactcatca acaacaactg gggattccgg cccaaaagac tcaacttcaa gctgtttaac 1800

attcaagtca aggaggtcac gcagaatgac ggtacgacga cgattgccaa taaccttacc 1860

agcacggttc aggtgtttac tgacttggag taccagctcc cgtacgtcct cggctcggcg 1920

catcaaggat gcctcccgcc gttcccagca gacgtcttca tggtgccaca gtatggatac 1980

ctcaccctga acaacgggag tcaggcggta ggacgctctt ccttttactg cctggagtac 2040

tttccttctc agatgcttcg caccggaaac aactttacct tcagctacac ttttgaagac 2100

gttcctttcc acagcagcta cgctcacagt caaagtctgg accgtctcat gaatcctctc 2160

atcgaccagt acctgtatta cttgagcaga acaaacactc caagcggaac cactacgcag 2220

tccaggcttc agttttctca ggccggagcg agtgacattc gggaccagtc taggaactgg 2280

cttcctggac cctgttaccg ccagcagcga gtatcaaaga cagctgcgga taacaacaac 2340 agtgaatact cgtggactgg agctaccaag taccacctca atggcagaga ctctctggtg 2400

aatccgggcc cggccatggc cagccacaag gacgatgaag aaaagttttt tcctcaaagc 2460

ggggttctca tctttgggaa gcaaggctca gagaaaacaa atgtggacat tgaaaaggtc 2520

atgattacag acgaagagga aatcaggacc accaatcccg tggctacgga gcagtatggt 2580

tctgtatcta ccaacctcca gagcggcaac acacaagcag ctacctcaga tgtcaacaca 2640

caaggcgttc ttccaggcat ggtctggcag gacagagacg tgtacctgca ggggcccatc 2700

tgggcaaaaa ttccacacac ggacggacat tttcacccct ctcccctcat gggcggattt 2760

ggacttaaac accctcctcc acagattctc attaagaata ccccggtacc tgcgaatcct 2820

tcgaccacct tcagcgcggc aaagtttgct tccttcatca cacagtattc cacggggcag 2880

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaatcccgaa 2940

attcagtaca cttccaacta caacaaatct gttaatgtgg actttactgt ggacactaat 3000

ggggtgtatt cagagcctcg ccctattggc accagatacc tgactcgtaa tctgtaattg 3060

cttgttaatc aataaaccgt ttaattcgtt tcagttgaac tttggtctct gcgaagggcg 3120

aattcgttta aacctgcagg actagtccct ttagtgagg 3159

<210> 325
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 325
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ser Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
```

405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
580 585 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys

```
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 326
<211> 2205
<212> DNA
<213> Adeno-associated virus

<400> 326

```
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagtggtgga agctcaaacc tggcccacca ccaaagcccg cagagcggca taaggacgac       120

agcaggggtc ttgtgcttcc tggatacaag tacctcggac ccttcaacgg actcgacaag       180

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaggc ctacgaccgg       240

cagctcgaca gcggagacaa cccgtacctc aagtacaacc acgccgacgc ggagtttcag       300

gagcgcctta aagaagatac gtcttttggg ggcaacctcg gacgagcagt cttccaggcg       360

aaaaagaggg ttcttgaacc tctgggcctg gttgaggaac ctgttaagac ggctccggga       420

aaaaagaggc ccgtagagca ctctcctgtg gagccagact cctcctcggg aaccggaaaa       480

gcgggcaacc agcctgcaag aaaaagattg aatttcggtc agactggaga cgcagactcc       540

gtacctgacc cccagcctct cggacagcca ccagcagccc cctctggtct gggaactaat       600

acgatggcta caggcagtgg cgcaccaatg gcagacaata acgagggcgc cgacggagtg       660

ggtaattcct cgggagattg gcattgcgat tccacatgga tgggcgacag agtcatcacc       720

accagcaccc gcacctgggc cctgcccacc tacaacaacc acctctacaa gcagatttcc       780

agccaatcag gagccagcaa tgacaaccac tactttggct acagcacccc ttgggggtat       840

tttgacttca acagattcca ctgccacttt tcgccacgcg actggcagag actcatcaac       900

aacaactggg gattccggcc caaaagactc aacctcaagc tgtttaacat tcaagtcaag       960

gaggtcacgc agaatgacgg tacgacgacg attgccaata accttaccag cacggttcag      1020

gtgtttactg acttggagta ccagctcccg tacgtcctcg gctcggcgca tcaaggatgc      1080

ctcccgccgt tcccagcaga cgtcttcatg gtgccacagt atggatacct caccctgaac      1140

aacgggagtc aggcggtagg acgctcttcc ttttactgcc tggagtactt tccttctcag      1200

atgcttcgta ccggaaacaa ctttaccttc agctacactt ttgaagacgt tcctttccac      1260

agcagctacg ctcacagtca aagtctggac cgtctcatga atcctctcat cgaccagtac      1320

ctgtattact tgagcagaac aaacactcca agcggaacca ctacgcagtc caggcttcag      1380

ttttctcagg ccggagcgag tgacattcgg gaccagtcta ggaactggct tcctggaccc      1440
```

```
tgttaccgcc agcagcgagt atcaaagaca gctgcggata acaacaacgg tgaatactcg     1500

tggactggag ctaccaagta ccacctcaat ggcagagact ctctggtgaa tccgggcccg     1560

gccatggcca gccacaagga cgatgaagaa aagttttttc ctcaaagcgg ggttctcatc     1620

tttgggaagc aaggctcaga gaaaacaaat gtggacattg aaaaggtcat gattacagac     1680

gaagaggaaa tcaggaccac caatcccgtg gctacggagc agtatggttc tgtatctacc     1740

aacctccaga gcggcaacac acgagcagct acctcagatg tcaacacaca aggcgttctt     1800

ccaggcatgg tctggcagga cagagacgtg tacctgcagg ggcccatctg ggcaaaaatt     1860

ccacacacgg acggacattt tcacccctct cccctcatgg gcggatttgg acttaaacac     1920

cctcctccac agattctcat taagaatacc ccggtacctg cgaatccttc gaccaccttc     1980

agcgcggcaa agtttgcttc cttcatcaca cagtattcca cggggcaggt cagcgtggag     2040

atcgagtggg agctgcagaa ggagaacagc aaacgctgga atcccgaaat tcagtacact     2100

tccaactaca acaaatctgt taatgtggac tttactgtgg acactaatgg ggtgtattca     2160

gagcctcgcc ctattggcac cagatacctg actcgtaatc tgtaa                     2205


<210> 327
<211> 3156
<212> DNA
<213> Adeno-associated virus

<400> 327
cgattgaatt tagcggccgc gaattcgccc ttgctgcgtc aacggaccaa tgagaacttt       60

cccttcaacg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc      120

aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgtgt ggaccaaaag      180

tgcaagtctt cggcccagat cgacccgact cccgtgatcg tcacctccaa caccaacatg      240

tgcgccgtga ttgatggaaa ctcaacgacc ttcgagcacc agcagccgtt gcaagaccgg      300

atgttcaaat ttgaacttac ccgccgtctg gatcatgact ttggaaaggt caccaagcag      360

gaagtgaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgagttc      420

tacgtcaaaa agggtggagc caaaaaaaga cccgcccccca gtgacgcaga tataagtgag      480

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc      540

aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg      600

tttccctgca gacaatgcga gcgaatgaat cagaattcaa atatctgctt cactcacgga      660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa      720

aaggcgtatc agaaactgtg ctacattcat cacatcatgg gaaaggtgcc agacgcttgc      780

actgcttgcg acctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt      840

taaatcaggt atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga      900

aggaataaga cagtggtgga agctcaaacc tggcccacca ccaaagcccg cagagcggca      960

taaggacgac agcaggggtc ttgtgcttcc tggatacaag tacctcggac ccttcaacgg     1020
```

actcgacaag ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaggc 1080

ctacgaccgg cagctcgaca gcggagacaa cccgtacctc aagtacaacc acgccgacgc 1140

ggagtttcag gagcgcctta aagaagatac gtcttttggg ggcaacctcg gacgagcagt 1200

cttccaggcg aaaaagaggg ttcttgaacc tctgggcctg gttgaggaac ctgttaagac 1260

ggctccggga aaaaagaggc ccgtagagca ctctcctgtg gagccagact cctcctcggg 1320

aaccggaaaa gcgggcaacc agcctgcaag aaaaagattg aatttcggtc agactggaga 1380

cgcagactcc gtacctgacc cccagcctct cggacagcca ccagcagccc cctctggtct 1440

gggaactaat acgatggcta caggcagtgg cgcaccaatg gcagacaata acgagggcgc 1500

cgacggagtg ggtaattcct cgggagattg gcattgcgat tccacatgga tgggcgacag 1560

agtcatcacc accagcaccc gcacctgggc cctgcccacc tacaacaacc acctctacaa 1620

gcagatttcc agccaatcag gagccagcaa tgacaaccac tactttggct acagcacccc 1680

ttgggggtat tttgacttca acagattcca ctgccacttt tcgccacgcg actggcagag 1740

actcatcaac aacaactggg gattccggcc caaaagactc aacctcaagc tgtttaacat 1800

tcaagtcaag gaggtcacgc agaatgacgg tacgacgacg attgccaata accttaccag 1860

cacggttcag gtgtttactg acttggagta ccagctcccg tacgtcctcg gctcggcgca 1920

tcaaggatgc ctcccgccgt tcccagcaga cgtcttcatg gtgccacagt atggatacct 1980

caccctgaac aacgggagtc aggcggtagg acgctcttcc ttttactgcc tggagtactt 2040

tccttctcag atgcttcgta ccggaaacaa ctttaccttc agctacactt ttgaagacgt 2100

tcctttccac agcagctacg ctcacagtca aagtctggac cgtctcatga atcctctcat 2160

cgaccagtac ctgtattact tgagcagaac aaacactcca agcggaacca ctacgcagtc 2220

caggcttcag ttttctcagg ccggagcgag tgacattcgg gaccagtcta ggaactggct 2280

tcctggaccc tgttaccgcc agcagcgagt atcaaagaca gctgcggata acaacaacgg 2340

tgaatactcg tggactggag ctaccaagta ccacctcaat ggcagagact ctctggtgaa 2400

tccgggcccg gccatggcca gccacaagga cgatgaagaa aagtttttc ctcaaagcgg 2460

ggttctcatc tttgggaagc aaggctcaga gaaaacaaat gtggacattg aaaaggtcat 2520

gattacagac gaagaggaaa tcaggaccac caatcccgtg gctacggagc agtatggttc 2580

tgtatctacc aacctccaga gcggcaacac acgagcagct acctcagatg tcaacacaca 2640

aggcgttctt ccaggcatgg tctggcagga cagagacgtg tacctgcagg ggcccatctg 2700

ggcaaaaatt ccacacacgg acggacattt tcacccctct cccctcatgg gcggatttgg 2760

acttaaacac cctcctccac agattctcat taagaatacc ccggtacctg cgaatccttc 2820

gaccaccttc agcgcggcaa agtttgcttc cttcatcaca cagtattcca cggggcaggt 2880

cagcgtggag atcgagtggg agctgcagaa ggagaacagc aaacgctgga atcccgaaat 2940

tcagtacact tccaactaca acaaatctgt taatgtggac tttactgtgg acactaatgg 3000

ggtgtattca gagcctcgcc ctattggcac cagatacctg actcgtaatc tgtaattgct 3060

```
tgttaatcaa taaaccgttt aattcgtttc agttgaactt tggtctctgc gaagggcgaa     3120

ttcgtttaaa cctgcaggac tagtcccttt agtgag                               3156


<210> 328
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 328
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Lys
                20                  25                  30


Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60


Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Arg
65                  70                  75                  80


Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125


Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140


Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly Lys
145                 150                 155                 160


Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
                165                 170                 175


Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
            180                 185                 190


Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly Ala
        195                 200                 205


Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220


Gly Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile Thr
```

```
225                 230                 235                 240


Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255


Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr Phe
            260                 265                 270


Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285


His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300


Phe Arg Pro Lys Arg Leu Asn Leu Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320


Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335


Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350


Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365


Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380


Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400


Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415


Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430


Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Asn
        435                 440                 445


Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln Ala
    450                 455                 460


Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly Pro
465                 470                 475                 480


Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn Asn
                485                 490                 495


Gly Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg
```

500 505 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
515 520 525

Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys Gln
530 535 540

Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr Asp
545 550 555 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
565 570 575

Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Arg Ala Ala Thr Ser
580 585 590

Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
690 695 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 329
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 329
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtacg accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgatgg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta caagcagatt 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960

agagaggtca cgcagaatga tggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta cttcccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga tgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggatcagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg acaacaacaa cagtgaatac 1500

tcgtggattg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggcaatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggaa aacaaggatc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca tctactgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcctat ctgggcaaag 1860

attccgcaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacagattct catcaaaaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtatt ccacggggcg ggtcagcgtg 2040

gagatcgagt gggagctaca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

```
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                2208


<210> 330
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 330
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asp His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Asp Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Ile Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515   520   525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530   535   540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545   550   555   560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565   570   575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ser Thr
            580   585   590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595   600   605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Arg Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 331
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 331
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagacag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaaccccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattccg catggctggg cgacagagtc 720

atcaccacca gcacccgacc ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080

caccagggct gcccgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaacggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgcggag aacgggcaac aactttgagt tcagctacca gtttgaggac 1260

gtgccttttc acagcagcta cgcgcatagc caaagcctgg accggctgat gaacccccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aataacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cttggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacgcacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttga tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aatcaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcatcctt cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc caagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160 ggtacttatt cagagcctcg ccccattggc acccgttacc tcacccgtaa cctgtaa   2217

<210> 332
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 332
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195   200   205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210   215   220

Ser Ser Gly Asn Trp His Cys Asp Ser Ala Trp Leu Gly Asp Arg Val
225   230   235   240

```
Ile Thr Thr Ser Thr Arg Pro Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 333
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 333
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
```

```
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445


Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460


Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
```

```
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 334
<211> 3158
<212> DNA
<213> Adeno-associated virus

<400> 334
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt        60

cctttcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc       120

aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgcgc ggaccagaaa       180

tgcaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccaacatg       240

tgcgccgtga ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg       300

atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag       360

gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc       420

tacgtcaaaa agggtggagc taagaaaaga cccgccccca gtgacgcaga tataagtgag       480
```

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 540

aactacgcgg gcaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600

tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga 660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780

actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

taaatcaggt atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga 900

aggaataaga cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg 960

gcataaggac gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa 1020

cggactcgac aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa 1080

ggcctacgac cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga 1140

cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc 1200

agtcttccag gcaaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa 1260

aacggctccg ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc 1320

gggaaccgga aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg 1380

agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg 1440

tctgggatct actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg 1500

tgccgatgga gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga 1560

cagagtcatc accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta 1620

caagcaaatc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac 1680

cccctggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca 1740

aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa 1800

cattcaagtc aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac 1860

cagcacggtt caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc 1920

gcatcaagga tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata 1980

cctcaccctg aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta 2040

ctttccttct cagatgctgc gtaccggaaa caactttcaa ttcagctaca cttttgaaga 2100

cgtgcctttc cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct 2160

ggtcgaccag tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca 2220

gtctcggcta ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg 2280

gctgcctgga ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa 2340

cagcaacttt ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt 2400

taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca 2460

tggaaccctt atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt 2520 catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg 2580

aactgtatca aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca 2640

ccaaggagcg ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat 2700

ttgggccaag attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt 2760

tggactcaaa cacccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc 2820

tcccacaaac ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca 2880

ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga 2940

aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa 3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt 3060

gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc tgcgaagggc 3120

gaattcgttt aaacctgcag gactagtccc tttagtga 3158

<210> 335
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 335
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Pro Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

```
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445


Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460


Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Arg Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590


Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 336
<211> 3159
<212> DNA
<213> Adeno-associated virus

<400> 336
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60

cctttcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc 120

aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa 180

tgcaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccgacatg 240

tgcgccgtga ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg 300

atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag 360

gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 420

tacgtcaaaa agggtggagc taagaaaaga cccgcccccca gtgacgcaga tataagtgag 480

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 540

aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600

tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga 660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780

actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

taaatcaggt atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga 900

aggaataaga cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg 960

gcataaggac gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa 1020

cggactcgac aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa 1080

ggcctacgac cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga 1140

cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc 1200

agtcttccag gcaaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa 1260

aacggctccg ggaaaaaaga ggccggtaga gcaccctcct gtggagccag actcctcctc 1320

gggaaccgga aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg 1380

agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg 1440

tctgggatct actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg 1500

tgccgatgga gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga 1560

```
cagagtcatc accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta     1620

caagcaaatc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac     1680

cccctggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca     1740

aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa     1800

cattcaagtc aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac     1860

cagcacggtt caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc     1920

gcatcaagga tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata     1980

cctcaccctg aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta     2040

ctttccttct cagatgctgc gtaccggaaa caactttcag ttcagctaca cttttgaaga     2100

cgtgcctttc cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct     2160

gatcgaccag tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca     2220

gtctcggcta ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaaccg     2280

gctgcctgga ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa     2340

cagcaacttt ccctggaccg cagctacaaa gtatcatcta aatggccggg actcgttggt     2400

taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca     2460

tggaaccctt atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt     2520

catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg     2580

aactgtatca aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca     2640

ccaaggagcg ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat     2700

ttgggccaag attcctcaca ccgatggaca ctttcatcct tctccactgg tgggaggttt     2760

tggactcaaa cacccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc     2820

tcccacaaac ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca     2880

ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga     2940

aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa     3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt     3060

gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc tgcgaagggc     3120

gaattcgttt aaacctgcag gactagtccc tttagtgag                             3159
```

```
<210> 337
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 337
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
```

cggcagctcg acagcggaga caacccgtac cccaagtaca accacgccga cgcggagttc 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caagcagatt 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcgccac gtgactggca aagactcatc 900

aacaacaatt ggggattccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgcccacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtgtggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcccc cgcagattct catcaagaac accccggtac ctgcgaatcc ttcgactacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccaggtac ctgactcgta atctgtaa 2208

```
<210> 338
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 338
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Pro Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 339
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 339
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
```

```
cggcagctcg acggcggaga caacccgtac ctcaagtaca accacgccga cgcggagttc      300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420
ggaaaaaaga ggccggtaga gcactctctt gcggagccag actcctcctc gggaaccgga      480
aaagcgggcc agcagcctgc aagaaggaga ttgaatttcg gtcagactgg agacgcagac      540
tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600
aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720
accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caggcagatt      780
tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg      840
tattttgact tcaacagatt ccactgccac ttttcgccac gtgactggca aagactcatc      900
aacaacaatt ggggatcccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc      960
aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020
caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140
aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct     1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc     1260
cacagcagct acgcccacag ccagagtttg gaccgtctca tgaatcctct cgtcgaccag     1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtcaaggctt     1380
cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga     1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500
tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc     1560
ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc     1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt catgattaca     1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct     1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt     1800
cttccaggca tggtgtggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag     1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa     1920
caccctcccc cgcagattct catcaagaac accccggtac ctgcgaatcc ttcgactacc     1980
ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg     2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtac     2100
acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat     2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208
```

<210> 340

```
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 340
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Leu Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Arg Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Ser Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530   535   540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545   550   555   560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565   570   575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580   585   590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595   600   605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 341
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 341
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ala Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
```

```
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Glu Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Cys Ala His Ser Gln Ser
            420                 425                 430

Ser Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Arg Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
```

```
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 342
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 342
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac      120

gacggccggg gtctggtgct tcttggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaatgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct      420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca      540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga      600
```

```
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac      660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720
atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa      780
atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc      840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag      900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac      960
atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc     1020
agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg     1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac     1140
cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat     1200
tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac     1260
gtgcctttcc acagcggcta cgcacacagc cagagcttgg accgactgat gaatcctctc     1320
atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc     1380
cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg     1440
ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac     1500
agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta     1560
aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt     1620
ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt     1680
atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt     1740
gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc     1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc     1860
tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt     1920
ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct     1980
ccaacgacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag     2040
gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag     2100
attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag     2160
ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa        2217
```

<210> 343
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 343

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Leu
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
580 585 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 344
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 344
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Pro Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445


Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460


Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590


Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
```

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 345
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 345
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

```
Leu Gly Leu Val Glu Gly Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 346
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 346
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg gacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320 tacctgtatt atctgaacaa aacacaatca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcaccta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggca tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 347
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 347
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 348
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 348
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaacaaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540 tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa aacacaatca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtaccaccta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggca tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 349
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 349
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccacctg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg agggagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac tgccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 350
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 350
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Thr Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
530 535 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
580 585 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 351
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 351
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac 120

aacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccctccaa cggactcgac 180 aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctgcagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtacccgctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctt gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 352
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 352
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Gln Asp Asn Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Ser Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Cys Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Pro Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
```

```
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Cys Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 353
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 353
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120
```

```
aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180
aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240
cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag      360
gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct      420
ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc      480
aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag      540
tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct      600
aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg      660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780
tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc      840
tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga      900
ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc      960
caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc     1020
accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac     1080
cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg     1140
acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc     1200
ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg     1260
cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt     1320
gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag     1380
actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg     1440
ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc     1500
aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat     1560
cctggcatcg ctatggcaac acacaaagac gacgaggagc gtttttttcc cagtaacggg     1620
atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg     1680
ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc     1740
gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag     1800
ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg     1860
gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc     1920
ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg     1980
accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc     2040
agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc     2100
cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt     2160
```

```
gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa          2214


<210> 354
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 354
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495
```

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500   505   510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515   520   525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530   535   540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545   550   555   560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565   570   575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580   585   590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595   600   605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610   615   620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625   630   635   640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645   650   655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660   665   670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675   680   685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690   695   700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705   710   715   720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725   730   735

Leu

<210> 355
<211> 2211

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 355
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc   60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac   120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac   180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac   240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt   300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag   360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct   420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc   480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag   540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct   600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga   660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc   720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc   780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg   840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc   900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa   960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg   1020

gttcaagtct tctcggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag   1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca   1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct   1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct   1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac   1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact   1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca   1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaat   1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaacccct   1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc   1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt   1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg   1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga   1800

```
gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc     1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a              2211


<210> 356
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 356
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
435 440 445

```
Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720
```

```
Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 357
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 357
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga 60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac 180

aagggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

```
ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt     1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg     1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg     1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca     1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg     1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg     1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc     2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag     2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt     2160

tatagtgaac ctcgccccat tggcacccgt taccttaccc gtcccctgta a              2211
```

```
<210> 358
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 358
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145   150   155   160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260   265   270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275   280   285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290   295   300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305   310   315   320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325   330   335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340   345   350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355   360   365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370   375   380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385   390   395   400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405   410   415

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 359
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 359
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380 cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 360
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 360
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385   390   395   400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405   410   415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420   425   430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435   440   445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450   455   460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485   490   495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr

```
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 361
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 361
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc      480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca      540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga      600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat      660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc      720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa      780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccccttgg     840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc      900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa      960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg     1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag     1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg     1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct     1200
```

```
tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct      1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc cctcatcgac      1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg      1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct      1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac      1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct      1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc      1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc      1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg      1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga      1800

gccttacctg gaatggtgtg gcaagacaga gacgtgtacc tgcagggtcc tatttgggcc      1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt      1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca      1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagt      2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag      2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt      2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a               2211


<210> 362
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 362
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 363
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 363
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc        60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac       120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac       180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac       240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag       360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct       420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc       480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag       540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct       600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg       660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat gactggggga cagagtcatc       720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc       780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc       840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga       900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc       960
```

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gtttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 364
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 364
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 365
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 365
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780 tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

ccttttcaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gtttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 366
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 366

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270


Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460


Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480


Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495


Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510


Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525


Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540


Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560


Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

```
Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590


Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
```

<210> 367
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 367

```
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420
```

```
ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc      480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca      540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caaccccgc tgctgtggga      600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat      660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc      720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa      780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag caccccttgg      840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc      900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa      960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg     1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag     1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg     1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct     1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct     1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac     1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg     1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct     1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat     1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct     1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt     1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga     1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc     1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a              2211
```

<210> 368
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

```
      polypeptide

<400> 368
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
```

            260   265   270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275   280   285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290   295   300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305   310   315   320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325   330   335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340   345   350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355   360   365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370   375   380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385   390   395   400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405   410   415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420   425   430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435   440   445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450   455   460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485   490   495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly

```
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 369
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 369
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tccgggttac aaatacctcg gacccggtaa cggactcgac      180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg agcacgacaa ggcctacgac      240
```

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctccc 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctctac gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaatttcg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aacacctact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

```
<210> 370
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 370
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510
```

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 371
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 371

atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa 1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc 1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct 1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct 1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt 1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac 1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca 1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt 1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatctg ggccaagatt 1860

cctcacacgg acggcaactt ccacccgtct ccgctgatgg gcggctttgg cctgaaacat 1920

cctccgcctc agatcctgat caagaacacg cctgtacctg cggatcctcc gaccaccttc 1980

aaccagtcaa agctgaactc tttcatcacg caatacagca ccggacaggt cagcgtggaa 2040 attgaatggg agctgcagaa ggaaaacagc aagcgctgga atcccgaagt gcagtataca 2100

tctaactatg caaaatctgc caacgttgat ttcactgtgg acaacaatgg actttatact 2160

gagcctcgcc ccattggcac ccgttacctc acccgtcccc tgtaa 2205

<210> 372
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 372
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415

Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460

Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480
```

```
Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
545                 550                 555                 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
                565                 570                 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
            580                 585                 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
                645                 650                 655

Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685

Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr Ala
    690                 695                 700

Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr Thr
705                 710                 715                 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730
```

<210> 373
<211> 2211
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 373
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagt gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

accgacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

```
aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a              2211


<210> 374
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 374
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Trp Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720
```

```
Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 375
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 375
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc        60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac       120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac       180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac       240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag       360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct       420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc       480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag       540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct       600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg       660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc       720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc       780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc       840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga       900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc       960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc      1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctcggcgcac      1080

cagggctgcc tccctccgtt cccggcggac gtcttcatgg tgccacagta tggatacctg      1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc      1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg      1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt      1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag      1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg      1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc      1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat      1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gtttttttcc cagtaacggg      1620
```

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggacttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 376
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 376
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly

145   150   155   160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260   265   270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275   280   285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290   295   300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305   310   315   320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325   330   335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340   345   350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355   360   365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370   375   380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385   390   395   400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405   410   415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu

```
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Asp Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
```

690   695   700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705   710   715   720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725   730   735

Leu

<210> 377
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 377
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aactgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

accaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

```
tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa     1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc     1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct     1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct     1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt     1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac     1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca     1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt     1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatctg ggccaagatt     1860

cctcacacgg acggcaactt ccacccgtct ccgctgatgg gcggctttgg cctgaaacat     1920

cctccgcctc agatcctgat caagaacacg cctgttcctg cgaatcctcc ggcggagttt     1980

tcagctacaa agtttgcttc attcatcacc cagtactcca caggacaagt gagtgtggaa     2040

attgaatggg agctgcagaa agaaaacagc aagcgctgga atcccgaagt gcagtacaca     2100

tccaattatg caaaatctgc caacgttgat tttactgtgg acaacaatgg actttatact     2160

gagcctcgcc ccattggcac ccgttacctt accaaacctc tgtaa                     2205


<210> 378
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 378
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Cys Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Thr Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415

Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460

Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480

Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
545                 550                 555                 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
                565                 570                 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
            580                 585                 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655
```

Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr Ala
690 695 700

Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr Thr
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Lys Pro Leu
725 730

<210> 379
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 379
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag caccccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080 ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 380
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 380
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 381
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 381
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900 ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gtttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 382
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 382
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270


Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590
```

```
Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu


<210> 383
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 383
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt        60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac       120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac       180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac       240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc       300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct       420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc       480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag       540
```

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa 1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc 1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct 1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct 1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt 1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac 1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca 1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt 1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatttg ggccaaaatt 1860

cctcacacgg acggcaactt tcacccttct ccgctgatgg gagggtttgg aatgaaacac 1920

ccgcctcctc agatcctcat caaaaacaca cctgtacctg cggatcctcc aacggccttc 1980

aacaaggaca agctgaactc tttcatcacc cagtattcta ctggccaagt cagcgtggag 2040

atcgagtggg agctgcagaa ggaaaacagc aagcgctgga accccgagat ccagtacacc 2100

tccaactact acaaatctac aagtgtggac tttgctgtta atacagaagg cgtgtactct 2160

gaaccccgcc ccattggcac ccgttacctc acccgtaatc tgtaa 2205

<210> 384
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 384
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
```

```
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415

Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460

Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480

Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
```

545 550 555 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
565 570 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
580 585 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys His
625 630 635 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
645 650 655

Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr
690 695 700

Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 385
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 385
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccct ctcccctcat gggtggattc 1920

ggacttaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 386
<211> 738
<212> PRT
<213> Artificial Sequence

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 386
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 387
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 387
```

atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga 60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac 180

aagggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caggtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040 gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 388
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 388
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 389
<211> 2211
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 389
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga 60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac 180

aagggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

```
aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg     1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg     1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc     2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag     2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt     2160

tatagtgaac ctcgccccat tggcacccgt accttaccc gtcccctgta a              2211


<210> 390
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 390
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445
```

```
Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460


Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720
```

```
Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 391
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 391
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt        60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac       120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac       180

aaaggagagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct       420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc       480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag       540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct       600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga       660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc       720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc       780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccсctgg       840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc       900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa       960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg      1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag      1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg      1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct      1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct      1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac      1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac      1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct      1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat      1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct      1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc      1620
```

```
atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt     1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga     1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc     1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt     1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca     1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc     2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag     2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a              2211


<210> 392
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 392
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
```

```
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
```

420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn

690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 393
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 393
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggatgca acggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaaccaccag cagcccccac aagtttggga 600

tctaatacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa ccgcttccac tgccacttct cgccaagaga ctggcaaaga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta tggatacctc 1140

accctgaaca acggaagtca agcggtggga cgctcatcct tttactgcct ggagtacttc 1200

ccttcgcaga tgctaaggac tggaaataac ttccaattca gctatacctt cgaggatgta 1260

ccttttcaca gcagctacgc tcacagccag agtttggatc gcttgatgaa tcctcttatt 1320

gatcagtatc tgtactacct gaacagaacg caaggaacaa cctctggaac aaccaaccaa 1380

tcacggctgc tttttagcca ggctgggcct cagtctatgt ctttgcaggc cagaaattgg 1440

```
ctacctgggc cctgctaccg gcaacagaga ctttcaaaga ctgctaacga caacaacaac     1500

agtaactttc cttggacagc agccagcaaa tatcatctca atggccgcga ctcgctggtg     1560

aatccaggac cagctatggc cagtcacaag gacgatgaag aaaaattttt ccctatgcac     1620

ggcaatctaa tatttggcaa agaagggaca acggcaagta acgcagaatt agataatgta     1680

atgattacgg atgaagaaga gattcgtacc accaatcctg tggcaacaga gcagtatgga     1740

actgtggcaa ataacttgca gagctcaaat acagctccca cgactagaac tgtcaatgat     1800

caggggggcct tacctggcat ggtgtggcaa gatcgtgacg tgtaccttca ggggcccatc     1860

tgggcaaaga ttccacacac ggacggacat tttcacccct ctcccctcat gggtggattc     1920

ggacttaaac accctcctcc gcagattctc atcaagaaca ccccggtacc tgcgaatcct     1980

tcgaccacct tcagtgcggc aaagtttgct tccttcatca cacagtactc cacgggacag     2040

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag     2100

atccagtaca cttccaacta ttacaagtct aataatgttg aatttgctgt taatactgaa     2160

ggtgtatata gtgaaccccg ccccattggc accagatacc tgactcgtaa tctgtaa        2217
```

<210> 394
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 394

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Thr Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn
                485                 490                 495

Asp Asn Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser
        515                 520                 525

His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile
    530                 535                 540

Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val
545                 550                 555                 560

Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala
            580                 585                 590

Pro Thr Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe
            660                 665                 670
```

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 395
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 395
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgatt tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaggaggtca cgcagaatga aggcaccaag accatcgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcggctcggc gcatcaagga 1080 tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg   1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct   1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc   1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct gattgaccag   1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt   1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga   1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac   1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc   1560

ccggccatgg caagccacaa ggactatgaa gaaaagtttt ttcctcagag cggggttctc   1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca   1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct   1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt   1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag   1860

attccacaca cggacggaca ttttcacccg tctccgctga tgggcggctt tggcctgaaa   1920

catcctccgc ctcagatcct gatcaagaac acgcctgtac ctgcggatcc tccgaccacc   1980

ttcaaccagt caaagctgaa ctctttcatc actcagtatt ctactggcca agtcagcgtg   2040

gagatcgagt gggagctgca gaaggaaaac agcaagcgct ggaaccccga gatccagtac   2100

acctccaact actacaaatc tacaagtgtg gactttgctg ttaatacaga aggcgtgtac   2160

tctgaacccc gccccattgg cacccgttac ctcacccgta atctgtaa   2208

<210> 396
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 396
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Tyr Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
645 650 655

Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 397
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 397
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900 ctcatcaaca acaattgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacgac aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca gcagcgagta tcaaagacat ttgcggataa caacaacagt 1500

gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agtttttttcc tcagagcggg 1620

gttctcatct ttgggaagca aggctcagag aaaacaaatg tggacattga aaaggtcatg 1680

attacagacg aagaggaaat caggacaacc aatcccgtgg ctacggagca gtatggttct 1740

gtatctacca acctccagag aggcaacaga caagcagcta ccgcagatgt caacacacaa 1800

ggcgttcttc caggcatggt ctggcaggac agagatgtgt accttcaggg gcccatctgg 1860

gcaaagattc cacacacgga cggacatttt cacccctctc ccctcatggg tggattcgga 1920

cttaaacacc ctccgcctca gatcctgatc aagaacacgc ctgtacccgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcaccc agtattctac tggccaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 398
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 398
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Phe Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590
```

```
Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu


<210> 399
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 399
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct       420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc       480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca       540
```

gagtcagttc cagaccctca acctctcgga gaaccaccag cagcccccac aagtttggga 600

tctaatacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa ccgcttccac tgccacttct cgccaagaga ctggcaaaga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta tggatacctc 1140

accctgaaca acggaagtca agcggtggga cgctcatcct tttactgcct ggagtacttc 1200

ccttcgcaga tgctaaggac tggaaataac ttccaattca gctatacctt cgaggatgta 1260

ccttttcaca gcagctacgc tcacagccag agtttggatc gcttgatgaa tcctcttatt 1320

gatcagtatc tgtactacct gaacagaacg caaggaacaa cctctggaac aaccaaccaa 1380

tcacggctgc tttttagcca ggctgggcct cagtctatgt ctttgcaggc cagaaattgg 1440

ctacctgggc cctgctaccg gcaacagaga ctttcaaaga ctgctaacga caacaacaac 1500

agtaactttc cttggacagc agccagcaaa tatcatctca atggccgcga ctcgctggtg 1560

aatccaggac cagctatggc cagtcacaag gacgatgaag aaaaattttt ccctatgcac 1620

ggcaatctaa tatttggcaa agaagggaca acggcaagta acgcagaatt agataatgta 1680

atgattacgg atgaagaaga gattcgtacc accaatcctg tggcaacaga gcagtatgga 1740

actgtggcaa ataacttgca gagctcaaat acagctccca cgactagaac tgtcaatgat 1800

caggggggcct tacctggcat ggtgtggcaa gatcgtgacg tgtaccttca ggggcccatc 1860

tgggcaaaga ttccacacac ggacggacat tttcacccct ctcccctcat gggtggattc 1920

ggacttaaac accctcctcc gcagattctc atcaagaaca ccccggtacc tgcgaatcct 1980

tcgaccacct tcagtgcggc aaagtttgct tccttcatca cacagtactc cacgggacag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag 2100

atccagtaca cttccaacta ttacaagtct aataatgttg aatttgctgt taatactgaa 2160

ggtgtatata gtgaaccccg ccccattggc accagatacc tgactcgtaa tctgtaa 2217

<210> 400
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 400
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser

```
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270


His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

```
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445


Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn
                485                 490                 495


Asp Asn Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser
        515                 520                 525


His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile
    530                 535                 540


Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val
```

```
545                 550                 555                 560


Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala
            580                 585                 590


Pro Thr Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu


<210> 401
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 401
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac      240
```

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```
<210> 402
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 402
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 403
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 403

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc caaaaagaga ctcaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacagca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac gactactttg gctacagcac cccttggggg 840

tattttgatt tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgagg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

```
gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208


<210> 404
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 404
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Ser Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn Asp Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Glu Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 405
<211> 2208
<212> DNA
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 405
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttc 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcaacttca agctctttaa catccaggtc 960

aaggaggtca cgcagaatga aggcaccaag accatcgcca ataacctcac cagcaccatc 1020

caggtgttta cggactcgga gtaccagctg ccgtacgttc tcggctctgc ccaccagggc 1080

tgcctgcctc cgttcccggc ggacgtgttc atgattcccc agtacggcta cctaacactc 1140

aacaacggta gtcaggccgt gggacgctcc tccttctact gcctggaata ctttccttcg 1200

cagatgctga gaaccggcaa caacttccag tttacttaca ccttcgagga cgtgcctttc 1260

cacagcagct acgcccacag ccagagcttg gaccggctga tgaatcctct gattgaccag 1320

tacctgtatt acttgtctcg gactcaaaca acaggaggca cgacaaatac gcagactctg 1380

ggcttcagcc aaggtgggcc taatacaatg gccaatcagg caaagaactg gctgcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acagggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc agggtcccat ttgggccaaa 1860

```
attcctcaca cagatggaca ctttcacccg tcccctctta tgggcggctt tggactcaag     1920

aacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag     1980

ttttcagcta caaagtttgc ttcattcatc acccaatact ccacaggaca agtgagtgtg     2040

gaaattgaat gggagctgca gaaagaaaac agcaagcgct ggaatcccga agtgcagtac     2100

acatccaatt atgcaaaatc tgccaacgtt gattttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctcacccgta atctgtaa                  2208


<210> 406
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 406
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

```
Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe Ser Gln
    450                 455                 460


Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 407
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 407
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacgac aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca gcagcgagta tcaaagacat ttgcggataa caacaacagt 1500

gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agtttttcc tcagagcggg 1620

```
gttctcatct ttgggaagca aggctcagag aaaacaaatg tggacattga aaaggtcatg     1680

attacagacg aagaggaaat caggacaacc aatcccgtgg ctacggagca gtatggttct     1740

gtatctacca acctccagag aggcaacaga caagcagcta ccgcagatgt caacacacaa     1800

ggcgttcttc caggcatggt ctggcaggac agagatgtgt accttcaggg gcccatctgg     1860

gcaaagattc cacacacgga cggacatttt cacccctctc ccctcatggg tggattcgga     1920

cttaaacacc ctccgcctca gatcctgatc aagaacacgc ctgtacccgc ggatcctccg     1980

accaccttca accagtcaaa gctgaactct ttcatcaccc agtattctac tggccaagtc     2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc     2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc     2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa           2214


<210> 408
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 408
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
```

```
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
```

```
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460


Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480


Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Phe Ala Asp
                485                 490                 495


Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510


Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525


Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540


Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560


Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590


Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
```

690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 409
<211> 2196
<212> DNA
<213> Adeno-associated virus

<400> 409
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag 480

cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc 540

caacctctct cagaaccacc cgcaggtccc tctggtctgg gatctggtac aatggctgct 600

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca 660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840

tttaacagat tccactgcca cttttcacca cgtgactggc agcgactcat caacaacaac 900

tgggggttcc ggcccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc 960

acccagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggtcttt 1020

acggactcgg agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140

agccaggccg tggggcgatc ctccttctac tgcctggagt actttccctc gcagatgctg 1200

agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260

tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac 1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440 cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500

gcgaccaagt accacctgaa cggccgagac tccctggtga gccccggtgt cgccatggca 1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggcaag 1620

cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680

atcaagacca ccaaccctgt ggccacggag cagtacggcg tggtggctga caatctgcag 1740

cagaccaact cagctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct 1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaaccccgc 2160

cccattggca ctcgttacct cacccgtaat ctgtaa 2196

<210> 410
<211> 731
<212> PRT
<213> Adeno-associated virus

<400> 410
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln
145                 150                 155                 160

Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
                165                 170                 175

Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190

Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255

Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415
```

```
Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Ser Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
                645                 650                 655

Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685
```

```
Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
    690                 695                 700


Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705                 710                 715                 720


Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210> 411
<211> 2196
<212> DNA
<213> Adeno-associated virus

<400> 411
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt       300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag       360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct       420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccggcag       480

cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc       540

caacctctct cagaaccacc cgcaggtccc tctggtctgg gatctggtac aatggctgca       600

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgcctca       660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg       720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg       780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac       840

tttaacagat tccactgcca cttttcacca cgtgactggc agcgactcat caacaacaac       900

tggggattcc ggcccaagag gctcaacttc aagctcttca acatccaggt caaggaggtc       960

acccagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggtcttt      1020

acggactcga agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct      1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg      1140

agccaggccg tggggcgatc ctccttctac tgcctggagt actttccctc gcagatgctg      1200

agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc      1260

tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac      1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag      1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg      1440
```

```
cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg     1500

gcgaccaagt accacctgaa cggccgagac tccctggtga accccggtgt cgccatggca     1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg ggtcctgat gtttggcaag     1620

cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag     1680

atcaagacca ccaaccctgt ggccacggag cagtacggtg tggtggctga caatctgcag     1740

cagaccaact cggctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg     1800

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg     1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc     1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct     1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg     2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat     2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaaccccgc     2160

cccattggca ctcgttacct cacccgtaat ctgtaa                               2196
```

<210> 412
<211> 731
<212> PRT
<213> Adeno-associated virus

<400> 412

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Arg Gln
145                 150                 155                 160

Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
                165                 170                 175

Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190

Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255

Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Thr Asp Ser Lys Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415
```

```
Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
                645                 650                 655

Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685
```

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
    690   695   700

Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705   710   715   720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730

<210> 413
<211> 2196
<212> DNA
<213> Adeno-associated virus

<400> 413
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag 480

cccgcgaaaa agagactgaa ttttgggccg actggcgact cagagtcagt gcctgacccc 540

caacctctct cagaaccacc tgcaggtccc tctggtctgg gatctggtac aatggctgca 600

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca 660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840

tttaacagat tccactgcca cttttcacca cgcgactggc agcgactcat caacaacaac 900

tggggattcc ggcccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc 960

acccagaatg aaggcaccaa gaccaccgcc aataacctca ccagcacggt gcaggtcttt 1020

acggactcgg agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140

agccaggccg tggggcgatc ctccttctac tgcctggagt actttccctc gcagatgctg 1200

agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260

tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac 1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440

cagcagcgcg tctctacggc agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500 gcgaccaagt accacctgaa cggccgagac tccctggtga accccggtgt cgccatggca 1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggcaag 1620

cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680

atcaagacca ccaaccctgt ggccacggag cagtacggtg tggtggctga caatctgcag 1740

cagaccaact cggctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct 1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag cgaaccccgc 2160

cccattggca ctcgttacct cacccgtaat ctgtaa 2196

<210> 414
<211> 731
<212> PRT
<213> Adeno-associated virus

<400> 414
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

```
Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln
145                 150                 155                 160

Pro Ala Lys Lys Arg Leu Asn Phe Gly Pro Thr Gly Asp Ser Glu Ser
                165                 170                 175

Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190

Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255

Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Gln Asn Glu Gly Thr Lys Thr Thr Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415
```

```
Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Ala Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
                645                 650                 655

Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685
```

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
690 695 700

Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 415
<211> 4404
<212> DNA
<213> Adeno-associated virus

<400> 415
atggctgccg atggttatct tccagattgg ctcgagggca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaacggccag 480

ccgcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct 600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 840

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1140

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1200

acgggcgata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1260

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1320

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500 aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

gccggacccc agacacagac tgtcaacagc caggggggctc tgcccggcat ggtctggcag 1800

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 1860

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 1920

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 1980

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2040

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2100

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2160

acccgttacc tcacccgtaa cctgtaaatg gctgccgatg gttatcttcc agattggctc 2220

gaggacaacc tctctgaggg cattcgcgag tggtgggact tgaaacctgg agccccgaaa 2280

cccaaagcca accagcaaaa gcaggacgac ggccggggtc tggtgcttcc tggctacaag 2340

tacctcggac ccttcaacgg actcgacaag ggggagcccg tcaacgcggc ggacgcagcg 2400

gccctcgagc acgacaaggc ctacgaccag cagctcaaag cgggtgacaa tccgtacctg 2460

cggtataacc acgccgacgc cgagtttcag gagcgtctgc aagaagatac gtcttttggg 2520

ggcaacctcg ggcgagcagt cttccaggcc aagaagcggg ttctcgaacc tctcggtctg 2580

gttgaggaag gcgctaagac ggctcctgga aagaagagac cggtagagcc atcaccccag 2640

cgttctccag actcctctac gggcatcggc aagaaaggcc agcagcccgc gaaaaagaga 2700

ctcaactttg ggcagactgg cgactcagag tcagtgcccg accctcaacc aatcggagaa 2760

ccccccgcag gcccctctgg tctgggatct ggtacaatgg ctgcaggcgg tggcgctcca 2820

atggcagaca ataacgaagg cgccgacgga gtgggtagtt cctcaggaaa ttggcattgc 2880

gattccacat ggctgggcga cagagtcatc accaccagca cccgaacctg ggccctcccc 2940

acctacaaca accacctcta caagcaaatc tccaacggga cttcgggagg aagcaccaac 3000

gacaacacct acttcggcta cagcaccccc tgggggtatt ttgactttaa cagattccac 3060

tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg attccggccc 3120

aagagactca acttcaagct cttcaacatc caggtcaagg aggtcacgca gaatgaaggc 3180

accaagacca tcgccaataa ccttaccagc acgattcagg tctttacgga ctcggaatac 3240

cagctcccgt acgtcctcgg ctctgcgcac cagggctgcc tgcctccgtt cccggcggac 3300

gtcttcatga ttcctcagta cgggtacctg actctgaaca atggcagtca ggccgtgggc 3360

cgttcctcct tctactgcct ggagtacttt ccttctcaaa tgctgagaac gggcaacaac 3420

tttgagttca gctaccagtt tgaggacgtg ccttttcaca gcagctacgc gcacagccaa 3480

agcctggacc ggctgatgaa cccccctcatc gaccagtacc tgtactacct gtctcggact 3540 cagtccacgg gaggtaccgc aggaactcag cagttgctat tttctcaggc cgggcctaat 3600

aacatgtcgg ctcaggccaa aaactggcta cccgggccct gctaccggca gcaacgcgtc 3660

tccacgacac tgtcgcaaaa taacaacagc aactttgcct ggaccggtgc caccaagtat 3720

catctgaatg gcagagactc tctggtaaat cccggtgtcg ctatggcaac ccacaaggac 3780

gacgaagagc gatttttccc gtccagcgga gtcttaatgt ttgggaaaca gggagctgga 3840

aaagacaacg tggactatag cagcgttatg ctaaccagtg aggaagaaat taaaaccacc 3900

aacccagtgg ccacagaaca gtacggcgtg gtggccgata acctgcaaca gcaaaacgcc 3960

gctcctattg taggggccgt caacagtcaa ggagccttac ctggcatggt ctggcagaac 4020

cgggacgtgt acctgcaggg tcctatctgg gccaagattc ctcacacgga cggaaacttt 4080

catccctcgc cgctgatggg aggctttgga ctgaaacacc cgcctcctca gatcctgatt 4140

aagaatacac ctgttcccgc ggatcctcca actaccttca gtcaagctaa gctggcgtcg 4200

ttcatcacgc agtacagcac cggacaggtc agcgtggaaa ttgaatggga gctgcagaaa 4260

gaaaacagca aacgctggaa cccagagatt caatacactt ccaactacta caaatctaca 4320

aatgtggact ttgctgttaa cacagatggc acttattctg agcctcgccc catcggcacc 4380

cgttacctca cccgtaatct gtaa 4404

<210> 416
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 416
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670
```

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705   710   715   720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 417
<211> 3129
<212> DNA
<213> Adeno-associated virus

<400> 417
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg gggcgggcac ccgagattgc ttgctcggcc 780

tgcgatctgg tcaacgtgga cctagatgac tgtgtttctg agcaataaat gacttaaacc 840

aggtatggct gccgatggtt atcttccaga ttggctcgag gacaacctct ctgagggcat 900

tcgcgagtgg tgggacttga aacctggagc cccgaaaccc aaagccaacc agcaaaagca 960

ggacgacggc cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact 1020

cgacaagggg gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta 1080

cgaccagcag ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga 1140

gtttcaggag cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt 1200

ccaggccaag aagcgggttc tcgaacctct cggtctggtt gaggaaggcg ctaagacggc 1260

```
tcctggaaag aagagaccgg tagagccatc accccagcgt tctccagact cctctacggg     1320
catcggcaag aaaggccagc agcccgcgaa aaagagactc aactttgggc agactggcga     1380
ctcagagtca gtgcccgacc ctcaaccaat cggagaaccc cccgcaggcc cctctggtct     1440
gggatctggt acaatggctg caggcggtgg cgctccaatg gcagacaata acgaaggcgc     1500
cgacggagtg ggtagttcct caggaaattg gcattgcgat tccacatggc tgggcgacag     1560
agtcatcacc accagcaccc gaacctgggc cctccccacc tacaacaacc acctctacaa     1620
gcaaatctcc aacgggactt cgggaggaag caccaacgac aacacctact tcggctacag     1680
caccccctgg gggtattttg actttaacag attccactgc cacttctcac cacgtgactg     1740
gcagcgactc atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt     1800
caacatccag gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct     1860
taccagcacg attcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc     1920
tgcgcaccag ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg     1980
gtacctgact ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga     2040
gtactttcct tctcaaatgc tgagaacggg caacaacttt gagttcagct accagtttga     2100
ggacgtgcct tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc     2160
cctcatcgac cagtacctgt actacctgtc tcggactcag tccacgggag gtaccgcagg     2220
aactcagcag ttgctatttt ctcaggccgg gcctaataac atgtcggctc aggccaaaaa     2280
ctggctaccc gggccctgct accggcagca acgcgtctcc acgacactgt cgcaaaataa     2340
caacagcaac tttgcctgga ccggtgccac caagtatcat ctgaatggca gagactctct     2400
ggtaaatccc ggtgtcgcta tggcaaccca caaggacgac gaagagcgat tttttccgtc     2460
cagcggagtc ttaatgtttg ggaaacaggg agctggaaaa gacaacgtgg actatagcag     2520
cgttatgcta accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta     2580
cggcgtggtg gccgataacc tgcaacagca aaacgccgct cctattgtag gggccgtcaa     2640
cagtcaagga gccttacctg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc     2700
tatctgggcc aagattcctc acacggacgg aaactttcat ccctcgccgc tgatgggagg     2760
ctttggactg aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgga     2820
tcctccaact accttcagtc aagctaagct ggcgtcgttc atcacgcagt acagcaccgg     2880
acaggtcagc gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc     2940
agagattcaa tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac     3000
agatggcact tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctgta     3060
attgcttgtt aatcaataaa ccggttgatt cgtttcagtt gaactttggt ctctgcgaag     3120
ggcgaattc                                                             3129
```

<210> 418
<211> 738

```
<212> PRT
<213> Adeno-associated virus

<400> 418
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu



<210> 419
<211> 733
<212> PRT
<213> Adeno-associated virus

<400> 419
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Arg Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
    290                 295                 300
```

```
Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575
```

```
Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590


Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605


Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620


Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640


Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
                645                 650                 655


Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670


Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
        675                 680                 685


Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
    690                 695                 700


Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705                 710                 715                 720


Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210> 420
<211> 2501
<212> DNA
<213> Adeno-associated virus

<400> 420
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc        60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc       120

aaggccattc atcatctgct ggggcgggct cccgagattg cttgctcggc ctgcgatctg       180

gtcaacgtgg acctggatga ctgtgtttct gagcaataaa tgacttaaac caggtatggc       240

tgccgatggt tatcttccag attggctcga ggacaacctc tctgagggca ttcgcgagtg       300

gtgggacttg agacctggag ccccgaaacc caaagccaac cagcaaaagc aggacgacgg       360

ccggggtctg gtgcttcctg gctacaagta cctcggaccc ttcaacggac tcgacaaggg       420

agagccggtc aacgaggcag acgccgcggc cctcgagcac gacaaggcct acgacaagca       480

gctcgagcag gggacaacc cgtacctcaa gtacaaccac gccgacgccg agtttcagga       540

gcgtcttcaa gaagatacgt cttttggggg caacctcggg cgagcagtct tccaggccaa       600
```

```
gaagcgggtt ctcgaacctc tcggtctggt tgaggaaggc gctaagacgg ctcctggaaa      660

gaagagaccc atagaatccc ccgactcctc cacgggcatc ggcaagaaag gccagcagcc      720

cgctaaaaag agactcaact ttgggcagac tggcgactca gagtcagtgc ccgaccctca      780

accaatcgga gaaccccccg caggcccctc tggtctggga tctggcacaa tggctgcagg      840

cggtggcgct ccaatggcag acaataacga aggcgccgac ggagtgggta gttcctcagg      900

aaattggcat tgcgattcca catggctggg cgacagagtc atcaccacca gcacccgaac      960

ctgggccctc cccacctaca acaaccacct ctacaagcaa atctccaacg ggacatcggg     1020

aggaagcacc aacgacaaca cctacttcgg ctacagcacc ccctgggggt attttgactt     1080

taacagattc cactgccact tctcaccacg tgactggcag cgactcatca acaacaactg     1140

gggattccgg cccaagagac tcaacttcaa gctcttcaac atccaggtca aggaggtcac     1200

gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc agcacgattc aggtctttac     1260

ggactcggaa taccagctcc cgtacgtcct cggctctgcg caccagggct gcctgcctcc     1320

gttcccggcg gacgtcttca tgattcctca gtacgggtac ctgactctga acaacggcag     1380

tcaggccgtg ggccgttcct ccttctactg cctggagtac tttccttctc aaatgctgag     1440

aacgggcaac aactttgagt tcagctacca gtttgaggac gtgccttttc acagcagcta     1500

tgcgcacagc caaagcctgg accggctgat gaaccccctc atcgaccagt acctgtacta     1560

cctgtctcgg actcagtcca cgggaggtac cgcaggaact cagcagttgc tattttctca     1620

ggccgggcct aataacatgt cggctcaggc caaaaactgg ctacccgggc cctgctaccg     1680

gcagcaacgc gtctccacga cagtgtcgca aaataacaac agcaactttg cttggaccgg     1740

tgccaccaag tatcatctga atggcagaga ctctctggta aatcccggtg tcgctatggc     1800

aacgcacaag ggcgacgaag agcgattttt tccatccagc ggagtcttga tgtttgggaa     1860

acagggagct ggaaaagaca acgtagacta tagcagcgtt atgctaacca gtgaggaaga     1920

aatcaaaacc accaacccag tggccacaga acagtacggc gtggtggccg ataacctgca     1980

acagcaaaac gccgctccta ttgtaggggc cgtcaacagt caaggagcct tacctggcat     2040

ggtctggcag aaccgggacg tgtacctgca gggtcctatc tgggccaaga ttcctcacac     2100

ggacggcaac tttcatcctt cgccgctgat gggaggcttt ggactgaaac acccgcctcc     2160

tcagatcctg attaagaata cacctgttcc cgcggatcct ccaactacct tcagtcaagc     2220

caagctggcg tcgttcatca cgcagtacag caccggacag gtcagcgtgg aaattgaatg     2280

ggagctgcag aaagagaaca gcaagcgctg gaacccagag attcagtata cttccaacta     2340

ctacaaatct acaaatgtgg actttgctgt caatactgag ggtacttatt cagagcctcg     2400

ccccattggc acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg     2460

ttgattcgtt tcagttgaac tttggtctca agggcgaatt c                         2501
```

<210> 421
<211> 2187
<212> DNA

<213> Adeno-associated virus

<400> 421
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 480

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct 600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 840

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1140

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1200

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1260

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1320

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg cgaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

gccggacccc agacacagac tgtcaacagc caggggggctc tgcccggcat ggtctggcag 1800

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 1860

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 1920

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 1980

```
tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag     2040

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct     2100

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc     2160

acccgttacc tcacccgtaa cctgtaa                                         2187


<210> 422
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 422
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190


Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205
```

```
Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480
```

```
Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Glu Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 423
<211> 728
<212> PRT
<213> Adeno-associated virus

```
<400> 423
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190


Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205


Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220


His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255


Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270
```

```
Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285


Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300


Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320


Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335


Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350


Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365


Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380


Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400


Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415


His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430


Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445


Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460


Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480


Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495


Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510


Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525


Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540
```

```
Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560


Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575


Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590


Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 424
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 424
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320
```

```
Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590
```

```
Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 425
<211> 733
<212> PRT
<213> Adeno-associated virus

<400> 425
Met Ala Ala Asp Gly His Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380
```

```
Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
                645                 650                 655
```

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 426
<211> 3113
<212> DNA
<213> Adeno-associated virus

<400> 426
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg cttccctgca 600

agacatgcga gagaatgaat cagaatttca gcatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtca tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200 caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga accccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500

tcctcaggaa attggcattg cgattccaca tagctgggcg acagagtcat caccaccagc 1560

acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaat ctccaacggg 1620

acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740

aacagctggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaggtcaag 1800

gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860

gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acgggtacct gactctgaac 1980

aacggcagtc aggccgtggg ccgttcctcc ttctactgcc tggagtactt tccttctcaa 2040

atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gccttttcac 2100

agcagctacg cgcacagcca aagcctggac cggctgatga accccctcat cgaccagtac 2160

ctgtactacc tgtctcggac tcagtccacg ggaggtaccg caggaactca gcagttgcta 2220

ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280

tgctaccggc agcaacgcgt ctccacgaca ctgtcgcaaa ataacaacag caactttgct 2340

tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccggtgtc 2400

gctatggcaa cgcacaagga cgacgaagag cgattttttc catccagcgg agtcttgatg 2460

tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520

gaggaagaaa tcaaaaccac caacccagtg gccacagaac agtacggcgt ggtggccgat 2580

aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700

cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820

agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggt cagcgtggaa 2880

attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact 2940

tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg tacttattca 3000

gagcctcgcc ccattggcac ccgttacctc acccgtaacc tgtaattgcc tgttaatcaa 3060

taaaccggtt aattcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 427
<211> 731
<212> PRT

```
<213> Adeno-associated virus

<400> 427
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Arg Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190


Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205


Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220


His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255


Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
```

```
            260                 265                 270


Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285


Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Arg Gly Phe Arg Pro
    290                 295                 300


Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320


Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335


Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350


Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365


Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380


Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400


Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
                405                 410                 415


His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430


Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
        435                 440                 445


Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
    450                 455                 460


Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480


Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495


Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510


Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525


Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
```

    530   535   540

Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545   550   555   560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565   570   575

Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
            580   585   590

Ser Gln Gly Ala Leu Pro Gly Met Ala Trp Gln Asn Arg Asp Val Tyr
        595   600   605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610   615   620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625   630   635   640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
                645   650   655

Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660   665   670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675   680   685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
    690   695   700

Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705   710   715   720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730

<210> 428
<211> 3106
<212> DNA
<213> Adeno-associated virus

<400> 428
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgattg 60

cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 120

cgccaaggcc attctcggcg gcagcaaggt gcgcgtggac caaaagtgca agtcgtccgc 180

ccagatcgac cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 300

actcacccgc cgtctggagc atgactttgg caaggcgaca aagcaggaag tcaaagagtt 360 cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttctacg tcagaaaggg 420

tggagccaac aagagacccg cccccgatga cgcggataaa agcgagccca agcgggcccg 480

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600

aacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660

ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720

gaaactctgt gccattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 900

gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 1020

acaagggaga gccggtcaac gaggcagacg ccgcggccct cgagcacgac aaggcctacg 1080

acaagcagct cgagcagggg gacaacccgt acctcaagta caaccacgcc gacgccgagt 1140

ttcaggagcg tcttcaagaa gatacgtctt ttgggggcaa cctcgggcga gcagtcttcc 1200

gggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc 1260

ctggaaagaa gagacccata gaatcccccg actcctccac gggcatcggc aagaaaggcc 1320

agcagcccgc taaaaagaag ctcaactttg ggcagactgg cgactcagag tcagtgcccg 1380

acccccaacc tctcggagaa cctcccgccg cgccctcagg tctgggatct ggtacaatgg 1440

ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga gtgggtaatg 1500

cctccggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc accaccagca 1560

cccgcacctg ggccctgccc acctacaaca accacctcta caagcagata tcaagtcaga 1620

gcggggctac caacgacaac cacttcttcg gctacagcac cccctggggc tattttgact 1680

tcaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc aacaacaacc 1740

ggggattccg gcccagaaag ctgcggttca agttgttcaa catccaggtc aaggaggtca 1800

cgacgaacga cggcgttacg accatcgcta ataaccttac cagcacgatt caggtcttct 1860

cggactcgga gtaccaactg ccgtacgtcc tcggctctgc gcaccagggc tgcctccctc 1920

cgttccctgc ggacgtgttc atgattcctc agtacggata tctgactcta aacaacggca 1980

gtcagtctgt gggacgttcc tccttctact gcctggagta ctttccttct cagatgctga 2040

gaacgggcaa taactttgaa ttcagctacc agtttgagga cgtgcccttt cacagcagct 2100

acgcgcacag ccaaagcctg gaccggctga tgaacccccct catcgaccag tacctgtact 2160

acctgtctcg gactcagtcc acgggaggta ccgcaggaac tcagcagttg ctattttctc 2220

aggccgggcc taataacatg tcggctcagg ccaaaaactg gctacccggg ccctgctacc 2280

ggcagcaacg cgtctccacg acactgtcgc aaaataacaa cagcaacttt gcttggaccg 2340

gtgccaccaa gtatcatctg aatggcagag actctctggt aaatcccggt gtcgctatgg 2400

```
caacgcacaa ggacgacgaa gagcgatttt ttccatccag cggagtcttg atgtttggga     2460

aacagggagc tggaaaagac aacgtggact atagcagcgt tatgctaacc agtgaggaag     2520

aaatcaaaac caccaaccca gtggccacag aacagtacgg cgtggtggcc gataacctgc     2580

aacagcaaaa cgccgctcct attgtagggg ccgtcaacag tcaaggagcc ttacctggca     2640

tggcctggca gaaccgggac gtgtacctgc agggtcctat ctgggccaag attcctcaca     2700

cggacggcaa ctttcatcct tcgccgctga tgggaggctt tggactgaaa cacccgcctc     2760

ctcagatcct gattaagaat acacctgttc ccgcggatcc tccaactacc ttcagtcaag     2820

ccaagctggc gtcgttcatc acgcagtaca gcaccggaca ggtcagcgtg gaaattgaat     2880

gggagctgca gaaagagaac agcaagcgct ggaacccaga gattcagtat acttccaact     2940

actacaaatc tacaaatgtg gactttgctg tcaatactga gggtacttat tcagagcctc     3000

gccccattgg cacccgttac ctcacccgta acctgtaatt gcctgttaat caataaaccg     3060

gttaattcgt ttcagttgaa ctttggtctc tgcgaagggc gaattc                    3106
```

```
<210> 429
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 429
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415
```

```
Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

```
Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 430
<211> 3197
<212> DNA
<213> Adeno-associated virus

<400> 430

```
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt        60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt       120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg       180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg       240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg       300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt       360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg       420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct       480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg       540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca       600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact       660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc       720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct       780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca       840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt       900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag       960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc      1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac      1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag      1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc      1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct      1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc      1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac      1380
```

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

accccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattcgt ttaaacctgc aggactagtc cctttagtga gggttaattc tgagcttggc 3180

gtaatcatgg gtcatag 3197

<210> 431
<211> 735
<212> PRT
<213> Adeno-associated virus

```
<400> 431
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Arg Lys Leu Arg Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asp Asp Gly Val Thr Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Glu Leu Gln Phe His
    450                 455                 460

Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
        515                 520                 525

Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
    530                 535                 540
```

Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545 550 555 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
565 570 575

Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
580 585 590

Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Asp Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Ala Lys Ser Asn Asn Val Glu Phe Ala Val Asn Asn Glu Gly Val Tyr
705 710 715 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 432
<211> 3276
<212> DNA
<213> Adeno-associated virus

<400> 432
gaattcgccc ttcgcagaga ccaaagttca actgaaacga attaaccggt ttattgatta 60

acaggcaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa 120

accccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgaggtgtac 180

tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg 240

ctgacctggc cggtgctgta ctgcgtgata aatgaggcaa acttggcagg agtaaacacc 300

tctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg 360

agtccaaatc cgtccatcag ggagacgggg tgaaagttgc cgtccgtgtg aggaattttg 420

gcccagatgg gaccctgcag gtacacgtcc cggttctgcc agaccatgcc gggcagagcc 480
ccctggctgt tgacagtctg tgtctggggt ccggccgtag acgattgcag gttgctggag 540
accacaccgt attcttctgt agccacggga ttggtggttt tgatctcctc ctcgctggtc 600
attagcacgt tttccagcgt tgtcttgttg gcagcccccg ttttgccaaa aaccagcact 660
ccgttgatgg gaaagaactg gtcctcgtcg tccttgttgg tggccatggc tacgcccggg 720
ttggttaatg aatttctacc attcagatgg tatttagtgg ccccggtcca ggcaaagtta 780
ctgttgttgt tgctgtctat gtttttgac agtctctgct gccgataaca gggtccgggc 840
agccagttct ttgattgctc ggccatggtg ttgggcccag cctgatggaa ctgcagctcc 900
cttgtggacc ccgtagtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgagg 960
ggattcatca gccggtccag gctctggcta tgcgcatagc tgctgtggaa aggcacttcc 1020
tcaaaggtgt agctgaattc aaagttattg cccgttctca gcatctgaga aggaaagtac 1080
tccaggcagt agaaggagga acgtcccaca gactgactgc cgttgtttag agtcagatat 1140
ccgtactgag gaatcatgaa cacgtccgca gggaacggag ggaggcagcc ctggtgcgca 1200
gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta 1260
aggttattag cgatggtcgt aacgccgtcg tccgtcgtga cctccttgac ctggatgttg 1320
aacaacttga accgcagctt tctgggccgg aatccccagt tgttgttgat gagtcgctgc 1380
cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccagggggtg 1440
ctgtagccga agtaggtgtt gtcgttggtg cttcctcccg atgtcccgtt ggagatttgc 1500
ttgtagaggt ggttgttgta ggtggggagg gcccaggttc gggtgctggt ggtgatgact 1560
ctgtcgccca gccatgtgga atcgcaatgc caatttcctg aggaactacc cactccgtcg 1620
gcgccttcgt tattgtctgc cattggagcg ccaccgcctg cagccattgt accagatccc 1680
agaccagagg ggcctgcggg gggttctccg attggttgag ggtcgggcac tgactctgag 1740
tcgccagtct gcccaaagtt gagtctcttt ttcgcgggct gctggcctgt cttgccgatg 1800
cccgtagagg agtctggaga acgctggggt gatggctcta ccggtctctt ctttccagga 1860
gccgtcttag cgccttcctc aaccagaccg agaggttcga gaacccgctt cttggcctgg 1920
aagactgctc gcccgaggtt gcccccaaaa gacgtatctt cttgaagacg ctcctgaaac 1980
tcggcgtcgg cgtggttgta cttgaggtac gggttgtccc cctgctcgag ctgcttgtcg 2040
taggccttgt cgtgctcgag ggccgcggcg tctgcctcgt tgaccggctc tcccttgtcg 2100
agtccgttga agggtccgag gtacttgtag ccaggaagca ccagaccccg gccgtcgtcc 2160
tgcttttgct ggttggcttt gggtttcggg gctccaggtt tcaagtccca ccactcgcga 2220
atgccctcag agaggttgtc ctcgagccaa tctggaagat aaccatcggc agccatacct 2280
ggtttaagtc atttattgct cagaaacaca gtcatccagg tccacgttga ccagatcgca 2340
ggccgagcaa gcaatctcgg gagcccgccc cagcagatga tgaatggcac agagtttccg 2400
atacgtcctc tttctgacga ccggttgaga ttctgacacg ccggggaaac attctgaaca 2460

```
gtctctggtc ccgtgcgtga agcaaatgtt gaaattctga ttcattctct cgcatgtctt     2520

gcagggaaac agcatctgaa gcatgcccgc gtgacgagaa cacttgtttt ggtacctgtc     2580

ggcaaagtcc accggagctc cttccgcgtc tgacgtcgat ggatgcaaaa tgtcgcaaaa     2640

gcactcacgt gacagctaat acaggaccac tcccctatga cgtgatttac gtcagcgcta     2700

tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc ggagctcctt     2760

ccgcgtctga cgtcgatgga tccgcgactg aggggcaggc ccgcttgggc tcgcttttat     2820

ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag aactcatgcg     2880

ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc tgctttgtca     2940

ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc cggtcctgca     3000

acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac atgttggtgt     3060

tggaagtgac gatcacgggg gtgggatcga tctgggcgga agacttgcac ttttggtcca     3120

cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg gccgtcatct     3180

tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga aagttctcat     3240

tggtccagtt gacgcagccg tagaaagggc gaattc                               3276
```

```
<210> 433
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 433
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670
```

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 434
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 434
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165   170   175

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
```

```
Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 435
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 435
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 436
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 436
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Arg Lys Gly Gln
145   150   155   160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165   170   175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180   185   190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195   200   205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210   215   220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225   230   235   240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245   250   255

```
Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525
```

```
Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 437
<211> 2489
<212> DNA
<213> Adeno-associated virus

<400> 437
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt        60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtgaagt       120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg       180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt       240
```

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcag gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 1200

acgaacgacg gcgttacgac catcgccaat aaccttacca gcacgattca ggtcttctcg 1260

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1320

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1380

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1440

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1500

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1560

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1620

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1680

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1740

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1800

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1980

gccggacccc agacacagac tgtcaacagc cagggggctc tgcccggcat ggtctggcag 2040

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 2100

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 2160

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 2220

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2280 aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct   2340

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc   2400

acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcgtt   2460

tcagttgaac tttggtcaag ggcgaattc   2489

<210> 438
<211> 728
<212> PRT
<213> Adeno-associated virus

<400> 438
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145   150   155   160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165   170   175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180   185   190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195   200   205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp

```
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Arg Gln
465                 470                 475                 480

Arg Leu Ser Lys Asp Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
```

```
                485                 490                 495


Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510


Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525


Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540


Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560


Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575


Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590


Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 439
<211> 3098
<212> DNA
<213> Adeno-associated virus

<400> 439
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accggagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga accccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtaat 1500

gcctccggaa attggcattg cgattccaca tggctgggcg acagagtcat caccaccagc 1560

acccgcacct gggccctgcc cacctacaac aaccacctct acaagcagat atcaagtcag 1620

agcggggcta ccaacgacaa ccacttcttc ggctacagca ccccctgggg ctattttgac 1680

ttcaacagat tccactgcca cttctcacca cgtgactggc agcgactcat caacaacaac 1740

tggggattcc ggcccagaaa gctgcggttc aagttgttca acatccaggt caaggaggtc 1800

acgacgaacg acggcgttac gaccatcgct aataacctta ccagcacgat tcaggtcttc 1860

tcggactcgg agtaccaact gccgtacgtc ctcggctctg cgcaccaggg ctgcctccct 1920

ccgttccctg cggacgtgtt catgattcct cagtacggat atctgactct aaacaacggc 1980

agtcagtctg tgggacgttc ctccttctac tgcctggagt actttccttc tcagatgctg 2040

```
agaacgggca ataactttga attcagctac acctttgagg aagtgccttt ccacagcagc     2100

tatgcgcaca gccagagcct ggaccggctg atgaatcccc tcatcgacca gtacctgtac     2160

tacctggccc ggacccagag cactacgggg tccacaaggg agctgcagtt ccatcaggct     2220

gggcccaaca ccatggccga gcaatcaaag aactggctgc ccggaccctg ttatcggcgg     2280

cagagactgt caaaagacat agacagcaac aacaacagta actttgcctg gaccggggcc     2340

actaaatacc atctgaatgg tagaaattca ttaaccaacc cgggcgtagc catggccacc     2400

aacaaggacg acgaggacca gttctttccc atcaacggag tgctggtttt tggcaaaacg     2460

ggggctgcca acaagacaac gctggaaaac gtgctaatga ccagcgagga ggagatcaaa     2520

accaccaatc ccgtggctac agaagaatac ggtgtggtct ccagcaacct gcaatcgtct     2580

acggccggac cccagacaca gactgtcaac agccaggggg ctctgcccgg catggtctgg     2640

cagaaccggg acgtgtacct gcagggtccc atctgggcca aaattcctca cacggacggc     2700

aactttcacc cgtctcccct gatgggcgga tttggactca aacacccgcc tcctcaaatt     2760

ctcatcaaaa acaccccggt acctgctaat cctccagagg tgtttactcc tgccaagttt     2820

gcctcattta tcacgcagta cagcaccggc caggtcagcg tggagatcga gtgggaactg     2880

cagaaagaga acagcaaacg ctggaatcca gagattcagt acacctcaaa ttatgccaag     2940

tctaataatg tggaatttgc tgtcaacaac gaaggggttt atactgagcc tcgccccatt     3000

ggcacccgtt acctcacccg taacctgtaa ttacttgtta atcaataaac cggttgattc     3060

gtttcagttg aactttggtc tctgcgaagg gcgaattc                             3098

<210> 440
<211> 685
<212> PRT
<213> Adeno-associated virus

<400> 440
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Gly Leu Gln Phe His
    450                 455                 460


Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
                485                 490                 495


Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
        515                 520                 525


Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
    530                 535                 540


Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545                 550                 555                 560


Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575


Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
            580                 585                 590


Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

```
His Pro Pro Pro Gln Ile Leu Ile Lys Tyr Thr Ser Asn Tyr Tyr Lys
                645                 650                 655


Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
            660                 665                 670


Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
        675                 680                 685


<210> 441
<211> 2969
<212> DNA
<213> Adeno-associated virus

<400> 441
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt        60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt       120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg       180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg       240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg       300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt       360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg       420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct       480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg       540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca       600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact       660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc       720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct       780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca       840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatc       900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag       960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc      1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac      1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag      1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc      1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct      1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc      1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac      1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg      1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc      1500
```

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

accccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gacgaacccc 2160

ctcatcgacc agtacctgta ctacctggcc cggacccaga gcactacggg gtccacaagg 2220

gggctgcagt tccatcaggc tgggcccaac accatggccg agcaatcaaa gaactggctg 2280

cccggacccct gttatcggca gcagagactg tcaaaaaaca tagacagcaa caacaacagt 2340

aactttgcct ggaccggggc cactaaatac catctgaatg gtagaaattc attaaccaac 2400

ccgggcgtag ccatggccac caacaaggac gacgaggacc agttctttcc catcaacgga 2460

gtgctggttt ttggcaaaac gggggctgcc aacaagacaa cgctggaaaa cgtgctaatg 2520

accagcgagg aggagatcaa aaccaccaat cccgtggcta cagaagaata cggtgtggtc 2580

tccagcaacc tgcaatcgtc tacggccgga ccccagacac agactgtcaa cagccagggg 2640

gctctgcccg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 2700

aaaattcctc acacggacgg caactttcac ccgtctcccc tgatgggcgg atttggactc 2760

aaacacccgc ctcctcaaat tctcatcaag tatacttcca actactacaa atctacaaat 2820

gtggactttg ctgtcaatac tgagggtact tattcagagc ctcgccccat tggcacccgt 2880

tacctcaccc gtaacctgta attgcctgtt aatcaataaa ccggttaatt cgtttcagtt 2940

gaactttggt ctctgcgaag ggcgaattc 2969

<210> 442
<211> 733
<212> PRT
<213> Adeno-associated virus

<400> 442
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320
```

```
Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590
```

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595   600   605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610   615   620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625   630   635   640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
                645   650   655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
            660   665   670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
        675   680   685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
    690   695   700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705   710   715   720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Ser Leu
                725   730

<210> 443
<211> 3113
<212> DNA
<213> Adeno-associated virus

<400> 443
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780 gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga acccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500

tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat caccaccagc 1560

acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaat ctccaacggg 1620

acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaggtcaag 1800

gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860

gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acgggtacct gactctgaac 1980

aacggcagtc aggccgtggg ccgttcctcc ttctactgcc tggagtactt tccttctcaa 2040

atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gccttttcac 2100

agcagctatg cgcacagcca aagcctggac cggctgatga accccctcat cgaccagtac 2160

ctgtactacc tgtctcggac tcagtccacg ggaggtaccg caggaactca gcagttgcta 2220

ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280

tgctaccggc agcaacgcgt ctccacgaca gtgtcgcaaa ataacaacag caactttgct 2340

tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccggtgtc 2400

gctatggcaa cgcacaaggg cgacgaagag cgattttttc catccagcgg agtcttgatg 2460

tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520

gaggaagaaa tcaaaaccac caacccagtg gccacagaac agtacggcgt ggtggccgat 2580

aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700

cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820

```
agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggt cagcgtggaa     2880

attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact     2940

tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg tacttattca     3000

gagcctcgcc ccattggcac ccgttacctc acccgtagcc tgtaattgcc tgttaatcaa     3060

taaaccggtt gattcgtttc agttgaactt tggtctctgc gaagggcgaa ttc            3113


<210> 444
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 444
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 445
<211> 3128
<212> DNA
<213> Adeno-associated virus

<400> 445
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcgcggg accagagact 660

gttcagaatg tttcccgggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

accccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800 aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcccgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgcg gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcat agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 446
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 446
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu


<210> 447
<211> 1933
<212> DNA
<213> Adeno-associated virus


<220>
<221> modified_base
<222> (1302)..(1302)
<223> a, c, t or g

<400> 447
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc        60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg       120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc       180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg       240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga       300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc       360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg       420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat       480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat       540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcaccccctg       600
```

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat gnaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 448
<211> 733
<212> PRT
<213> Adeno-associated virus

<400> 448
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
```

```
Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Ser Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Gly Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala Tyr Ser Gln Ser Pro Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605
```

```
Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620


His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640


Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655


Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670


Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685


Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700


Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720


Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730


<210> 449
<211> 3105
<212> DNA
<213> Adeno-associated virus

<400> 449
gaattcgccc ttgctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg       60

acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca      120

aggccattct gggcggaagc aaggtgcgcg tggaccaaaa gtgcaagtca tcggcccaga      180

tcgaccccac gcccgtgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga      240

acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca      300

cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc      360

gctgggctca ggatcacgtg actgaggtgg cgcatgagtt ctacgtcaga aagggcggag      420

ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgcccct      480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc      540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg      600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt      660

gcttccccgg cgcgtcagaa tctcaacccg tcgtcagaaa aaagacgtat cagaaactgt      720

gcgcgattca tcatctgctg ggcgggcac ccgagattgc gtgttcggcc cgcgatctcg      780

tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct      840
```

gctgacggtt atcttccaga ttggctcgag gacaacctct ctgagggcat tcgcgagtgg 900

tgggacctga aacctggagc ccccaagccc aaggccaacc agcagaagca ggacgacggc 960

cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact cgacaagggg 1020

gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag 1080

ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag 1140

cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag 1200

aagagggtac tcgaacctct gggcctggtt gaagaaggtg ctaagacggc tcctggaaag 1260

aagagaccgt tagagtcacc acaagagccc gactcctcct caggaatcgg caaaaaaggc 1320

aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc 1380

cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc 1440

ggaaatgctg tcgatgcggg acaaggttcc gatggagtgg gtaatgcctc gggtgattgg 1500

cattgcgatt ccacctggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc 1560

ttgcccacct acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc 1620

tacaacggat tctccacccc ctggggatac tttgacttta acagattcca ctgtcacttc 1680

tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg 1740

cgcgttaaaa tcttcaatat ccaagttaag gaggtcacaa cgtcgaacgg cgagactacg 1800

gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg 1860

tacgtgatgg acgctggaca agagggaagt ctgtctcctt tccccaatga cgtcttcatg 1920

gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga 1980

aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt 2040

gaaatggctt acaactttgg gaaggtgccg ttccactcaa tgtatgctta cagccagagc 2100

ccggacagac tgatgaatcc cctcctggac cagtacctgt ggcacttaca gtcgaccacc 2160

tctggagaga ctctgaatca aggcaatgca gcaaccacat ttggaaaaat caggagtgga 2220

gactttgcct tttacagaaa gaactggctg cctgggcctt gtgttaaaca gcagagactc 2280

tcaaaaactg ccagtcaaaa ttacaagatt cctgccagcg gggcaacgc tctgttaaag 2340

tatgacaccc actatacctt aaacaaccgc tggagcaaca tagcgcctgg acctccaatg 2400

gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca 2460

tcagtcaccg gaaacacaac aacctcagca aacaatctgt tgtttacatc agaagaagaa 2520

attgctgcca ccaacccaag agacacggac atgtttggtc agattgctga caataatcag 2580

aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgct tcctggcatg 2640

gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg 2700

gacggacatt ttcatccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc 2760

cagatattta tcaaaaacac ccccgtacct gccaatcctg cgacaacctt cactgcagcc 2820

agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg 2880

```
gaaatcgaaa aggaacgctc caaacgctgg aatcctgaag tgcagtttac ttcaaactat     2940

gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg     3000

gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt     3060

gtgattcgtt tcagttgaac tttggtctct gcgaagggcg aattc                     3105


<210> 450
<211> 733
<212> PRT
<213> Adeno-associated virus

<400> 450
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160


Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175


Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190


Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205


Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
```

```
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
```

```
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730
```

<210> 451
<211> 3105
<212> DNA
<213> Adeno-associated virus

<400> 451
gaattcgccc ttgctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg 60

acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca 120

aggccattct gggcggaagc aaggtgcgcg tggaccaaaa gtgcaagtca tcggcccaga 180

tcgaccccac gcccgtgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga 240

acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca 300

cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc 360

gctgggctca ggatcacgtg actgaggtgg cgcatgagtt ctacgtcaga aagggcggag 420

ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgcccct 480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc 540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg 600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt 660

gcttccccgg cgcgtcagaa tctcaacccg tcgtcagaaa aaagacgtat cagaaactgt 720

gcgcgattca tcatctgctg gggcgggcac ccgagattgc gtgttcggcc tgcgatctcg 780

tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct 840

gctgacggtt atcttccaga ttggctcgag gacaacctct ctgagggcat tcgcgagtgg 900

tgggacctga aacctggagc cccaaagctc aaggccaacc agcagaagca ggacgacggc 960

cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tccacggact cgacaagggg 1020

gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag 1080

ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag 1140

cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag 1200

aagagggtac tcgaaccact gggcctggtt gaagaaggtg ctaagacggc tcctggaaag 1260

aagagaccgt tagagtcacc acaagagccc gactcctcct caggaatcgg caaaaaaggc 1320

aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc 1380

cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc 1440

ggaaatgctg tcgatgcggg acaaggttcc gatggagtgg gtaatgcctc gggtgattgg 1500

cattgcgatt ccacctggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc 1560

ttgcccacct acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc 1620

tacaacggat tctccacccc ctggggatac tttgacttta acagattcca ctgtcacttc 1680

tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg 1740

cgcgttaaaa tcttcaatat ccaagttaag gaggtcacaa cgtcgaacgg cgagactacg 1800

gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg 1860

tacgtgatgg acgctggaca agagggaagt ctgcctcctt tccccaatga cgtcttcatg 1920

gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga 1980

aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt 2040 gaaatggctt acaactttga gaaggtgccg ttccactcaa tgtatgctca cagccagagc 2100

ctggacagac tgatgaatcc cctcctggac cagtacctgt ggcacttaca gtcgaccacc 2160

tctggagaga ctctgaatca aggcaatgca gcaaccacat ttggaaaaat caggagtgga 2220

gactttgcct tttacagaaa gaactggctg cctgggcctt gtgttaaaca gcagagattc 2280

tcaaaaactg ccagtcaaaa ttacaagatt cctgccagcg gggcaacgc tctgttaaag 2340

tatgacaccc actatacctt aaacaaccgc tggagcaaca tagcgcctgg acctccaatg 2400

gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca 2460

tcagtcaccg gaaacacaac aacctcagca aacaatctgt tgtttacatc agaaggagaa 2520

attgctgcca ccaacccaag agacacggac atgtttggtc agattgctga caataatcag 2580

aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgct tcctggcatg 2640

gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg 2700

gacggacatt ttcatccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc 2760

cagatattta tcaaaaacac cccgtacct gccaatcctg cgacaacctt cactgcagcc 2820

agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg 2880

gaaatcgaaa aggaacgctc caaacgccgg aatcctgaag tgcagtttac ttcaaactat 2940

gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg 3000

gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt 3060

gtgattcgtt tcagttgaac tttggtctct gcgaagggcg aattc 3105

<210> 452
<211> 733
<212> PRT
<213> Adeno-associated virus

<400> 452
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Glu Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160


Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175


Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190


Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205


Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220


Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240


Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255


Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320


Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335


Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350


Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365
```

```
Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Thr Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Gly Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640
```

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Tyr Pro Ala
645 650 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Cys Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 453
<211> 3105
<212> DNA
<213> Adeno-associated virus

<400> 453
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcacacggt ttattgatta 60

actaggcagt tacaaatgat tagtcaaata acgagagcca ataacccgcg gctctgtata 120

cttcccagtt gtatcgggag cccacaacat agaagactgg ttcccacagt ttgaagtaaa 180

ctgcacttca ggattccagc gtttggagcg ttccttttcg atttcccatt caatctgaac 240

agcgacctgg ccggtgctgt attgtgtgat gaaagagtcc actctggctg cagtgaaggt 300

tgtcgcagga taggcaggta cgggggtgtt tttgataaat atctggggag gcggatgttt 360

cagtccaaaa ccgccaatta gcggtgaagg atgaaaatgt ccgtccgcgt gtgggatctt 420

ggcccaaatt ggcccttggt agtaaatgtc tctgttttgc cacaccatgc caggaagcac 480

tcccatagca gtcacgttgc cggttatggg agcagttgta gcattctgat tattgtcagc 540

aatctgacca aacatgtccg tgtctcttgg gttggtggca gcaatttctt cttctgatgt 600

aaacaacaga ttgtttgctg aggttgttgt gtttccggtg actgatggtc cagggaagat 660

gagctgggcg ttgctgaagt ccccatctga aggtccagct gttgccattg gaggtccagg 720

cgctatgttg ctccagcggt tgtttaaggt atagtgggtg tcatacttta acagagcgtt 780

gccccccgctg gcaggaatct tgtaattttg actggcagtt tttgagaatc tctgctgttt 840

aacacaaggc ccaggcagcc agttctttct gtaaaaggca aagtctccac tcctgatttt 900

tccaaatgtg gttgctgcat tgccttgatt cagagtctct ccagaggtgg tcgactgtaa 960

gtgccacagg tactggtcca ggaggggatt catcagtccg tccaggctct ggctgtgagc 1020

atacattgag tggaacggca ccttctcaaa gttgtaagcc gtttcaaagt tattgccagt 1080

tctcagcatt tgtgaaggaa aatactccag gcagtagaaa gcatttctgt ccgtctggtt 1140 ctgattttcg ccagtcacaa tgccacagta gccatattga ggcaccatga agacgtcatt 1200

ggggaaagga ggcagacttc cctcttgtcc agcgtccatc acgtacggga gctcatacga 1260

cgagtccgca aatatctgaa ccgtgctggt aaggttatta gcgaccgtag tctcgccgtt 1320

cgacgttgtg acctccttaa cttggatatt gaagatttta acgcgcatgg cttttggtcg 1380

tagtccccag ttgttgttga tgagtctttg ccagtcacgt ggtgagaagt gacagtggaa 1440

tctgttaaag tcaaagtatc cccagggggt ggagaatccg ttgtaggtgt tgctgtttga 1500

tgttgttccg agccgcaggt acaagtggtt gttgtaggtg ggcaagaccc aggttctggt 1560

cgaggttgtt gtgaccttgc cctcagacca ggtggaatcg caatgccaat cacccgaggc 1620

attacccact ccatcggaac cttgtcccgc atcgacagca tttccgcccg gtgctgcacg 1680

catttcaatg tctgaagaca tggcgctggt atctgatcct tcagggggtc cgtctccggc 1740

tccagtgtcc tcttcaaagt tgagtctctt tttggctggt tgtttgcctt ttttgccgat 1800

tcctgaggag gagtcgggct cttgtggtga ctctaacggt ctcttctttc caggagccgt 1860

cttagcacct tcttcaacca ggcccagagg ttcgagtacc ctcttcttgg cctggaagac 1920

tgctcgcccg aggttgcccc caaaagacgt atcttcttgc agacgctcct gaaactcggc 1980

gtcggcgtgg ttataccgca ggtacggatt gtcacccgct ttgagctgct ggtcgtaggc 2040

cttgtcgtgc tcgagggccg ctgcgtccgc cgcgttgacg ggctccccct tgtcgagtcc 2100

gttgaagggt ccgaggtact cgtagccagg aagcaccaga ccccggccgt cgtcctgctt 2160

ctgctggttg gccttgggct tgggggctcc aggtttcagg tcccaccact cgcgaatgcc 2220

ctcagagagg ttgtcctcga gccaatctgg aagataaccg tcagcagcca tacctggttt 2280

aagtcattta ttgctcagaa acacagtcat ccaagtccac gttgacgaga tcgcaggccg 2340

aacacgcaat ctcgggtgcc cgccccagca gatgatgaat cgcgcacagt ttctgatacg 2400

tctttttct gacgacgggt tgagattctg acgcgccggg gaagcactct gagcagtctc 2460

tgaccccgtg cgtgaagcag acgttgaaat tctgattcat tctctcgcat gtcttgcagg 2520

gaaacagcat ctgaagcatg cccgcgtgac gagaacattt gttttggtac ctgtccgcaa 2580

ggtccaccgg tgcttccgcg tctgacgtcg atggctccgc aactgagggg caggcccgct 2640

tgggctcgct tatatccgcg tcactggggg cgggtctttt ggtggctccg ccctttctga 2700

cgtagaactc atgcgccacc tcagtcacgt gatcctgagc ccagcggaag aactctttga 2760

cttcctgctt ggtcaccttg ccaaagtcgt gctccagacg gcgggtgagc tcgaacttga 2820

acatgcggtc ctgcagcggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg 2880

cgcacatgtt ggtgttggag gtgacgatca cgggcgtggg gtcgatctgg gccgatgact 2940

tgcacttttg gtccacgcgc accttgcttc cgcccagaat ggccttggcg gactccacga 3000

ccttggcggt catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga 3060

agggaaagtt ctcattggtc cagttgacgc agcaagggcg aattc 3105

<210> 454

<211> 729
<212> PRT
<213> Adeno-associated virus

<400> 454
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145   150   155   160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165   170   175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180   185   190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195   200   205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210   215   220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225   230   235   240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245   250   255

```
Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270


Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285


Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300


Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320


Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335


Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350


Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365


Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380


Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400


Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415


Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430


Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445


Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460


Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480


Gln Gly Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495


Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510


Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525
```

```
Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540


Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560


Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575


Leu Gln Pro Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590


Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605


Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620


Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640


Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655


Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670


Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685


Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700


Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720


Gly Thr Arg Tyr Leu Pro Arg Asn Leu
                725


<210> 455
<211> 3094
<212> DNA
<213> Adeno-associated virus

<400> 455
gaattcgccc ttgctgcgtc aactggacca agagaacttt cccttcaacg attgcgtcga        60

caagatggtg atctggtggg aggagggcaa gatgacggcc aaggtcgtgg agtccgccaa       120

agccattctg ggcggaagca aggtgcgcgt cgaccaaaag tgcaagtcct cggcccagat       180

cgatcccacc cccgtgatcg tcacctccaa caccaacatg tgcgccgtga tcgacgggaa       240

cagcaccacc ttcgagcacc agcagccgtt gcaggaccgg atgttcaaat ttgaactcac       300
```

```
ccgccgtctg gaacacgact ttggcaaggt gaccaagcag gaagtcaaag agttcttccg      360
ctgggctagt gatcacgtga ctgaggtgac gcatgagttc tacgtcagaa agggcggagc      420
cagcaaaaga cccgcccccg atgacgcgga tataagcgag cccaagcggg cctgtccctc      480
agtcacggac ccatcgacgt cagacgcgga aggagctccg gtggactttg ccgacaggta      540
ccaaaacaaa tgttctcgtc acgcgggcat gcttcagatg ctgtttccct gcaaaacgtg      600
cgagagaatg aatcagaatt tcaacatttg cttcacgcac ggggtcagag actgtttaga      660
atgtttcccc ggcgtgtcag aatctcaacc ggtcgtcaga aaaaagacgt atcggaagct      720
gtgtgcgatt catcatctgc tggggcgggc acccgagatt gcttgctcgg cctgcgacct      780
ggtcaacgtg gacctggacg actgtgtttc tgagcaataa atgacttaaa ccgggtatgg      840
ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt      900
ggtgggacct gaaacctgga gccccgaaac ccaaagccaa ccagcaaaag caggacgacg      960
gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga ctcgacaagg     1020
gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc     1080
agctcaaagc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg     1140
agcgtctgca agaagatacg tcatttgggg gcaacctcgg gcgagcagtc ttccaggcca     1200
agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg gctcctggaa     1260
agaagagacc catagactct ccagactcct ccacgggcat cggcaaaaaa ggccagcagc     1320
ccgctaaaaa gaagctcaat tttggtcaga ctggcgactc agagtcagtc cccgaccctc     1380
aacctcttgg agaacctcca gcagcgccct ctagtgtggg atctggtaca atggctgcag     1440
gcggtggcgc accaatggca gacaataacg aaggtgccga cggagtgggt aatgcctcag     1500
gaaattggca ttgcgattcc acatggctgg gcgacagagt catcaccacc agcaccagaa     1560
cctgggccct ccccacctac aacaaccacc tctacaagca aatctccagc agcagctcag     1620
gagccaccaa tgacaaccac tacttcggct acagcacccc ctgggggtat tttgacttta     1680
acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac aacaactggg     1740
gattccggcc caagaagctg cggttcaagc tcttcaacat ccaggtcaag gaggtcacaa     1800
cgaatgacgg cgtcacgacc atcgctaata accttaccag cacggttcag gtcttctcgg     1860
actcggaata ccagctgccg tacgtcctcg gctctgcgca ccagggctgc ctgcctccgt     1920
tcccggcgga cgtcttcatg attcctcagt acggctacct gactctgaac aacggcagcc     1980
aatcggtggg ccgttcctcc ttctactgcc tggaatattt cccctctcaa atgctgagaa     2040
cgggcaacaa ctttgagttc agttacagct tcgaggacgt gcctttccac agcagctacg     2100
cgcacagcca gagcctagac cggctgatga accctctcat cgaccagtac ctgtactacc     2160
tggcccggac ccagagcacc acgggttcca ccagggaact gcaatttcat caagctgggc     2220
ccaatactat ggccgagcag tcaaagaact ggctgcctgg accctgctat aggcaacagg     2280
gactgtcaaa gaacttggac tttaacaaca acagcaattt tgcctggact gctgccacta     2340
```

```
aatatcatct gaatggcaga aactctttga ccaatcctgg cattcccatg gcaaccaaca     2400

aggatgatga ggaccagttc tttcccatca acggggtact ggtttttggc aagacgggag     2460

ctgccaacaa aactacgctg gaaaacgttc tgatgaccag cgaggaggag atcaagacca     2520

ctaaccctgt ggctacagaa gaatacggtg tggtctccag caacctgcag ccgtctacag     2580

ccgggcctca atcacagact atcaacagcc agggagcact gcctggcatg gtctggcaga     2640

accgggacgt gtatctgcag ggtcccatct gggccaaaat tcctcacacg gatggcaact     2700

ttcacccgtc tcctctgatg ggcggttttg gactcaaaca cccgcctcca cagatcctga     2760

tcaaaaacac acctgtacct gctaatcctc cggaggtgtt tactcctgcc aagtttgcct     2820

ccttcatcac gcagtacagc accggacaag tcagcgtgga aatcgagtgg gagctgcaga     2880

aagaaaacag caagcgctgg aacccagaaa ttcagtatac ttccaattat gccaagtcta     2940

ataatgttga atttgctgtg aaccctgatg gtgtttatac tgagcctcgc cccattggca     3000

ctcgttacct cccccgtaat ctgtaattgc ttgttaatca ataaaccggt tgattcgttt     3060

cagttgaact ttggtctctg cgaagggcga attc                                 3094


<210> 456
<211> 1458
<212> PRT
<213> Adeno-associated virus

<400> 456
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
260 265 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
275 280 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
290 295 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305 310 315 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
325 330 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
340 345 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
355 360 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
370 375 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385 390 395 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
405 410 415

```
Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685
```

```
Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700


Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720


Gly Thr Arg Tyr Leu Thr Arg Asn Leu Met Ala Ala Asp Gly Tyr Leu
                725                 730                 735


Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu Gly Ile Arg Glu Trp Trp
            740                 745                 750


Asp Leu Lys Pro Gly Ala Pro Lys Pro Lys Ala Asn Gln Gln Lys Gln
        755                 760                 765


Asp Asp Gly Arg Gly Leu Val Leu Pro Gly Tyr Lys Tyr Leu Gly Pro
    770                 775                 780


Phe Asn Gly Leu Asp Lys Gly Glu Pro Val Asn Ala Ala Asp Ala Ala
785                 790                 795                 800


Ala Leu Glu His Asp Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp
                805                 810                 815


Asn Pro Tyr Leu Arg Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg
            820                 825                 830


Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe
        835                 840                 845


Gln Ala Lys Lys Arg Val Leu Glu Pro Leu Gly Leu Val Glu Glu Gly
    850                 855                 860


Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro Ile Gly Ser Pro Asp Ser
865                 870                 875                 880


Ser Thr Gly Ile Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Lys Leu
                885                 890                 895


Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro
            900                 905                 910


Leu Gly Glu Pro Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met
        915                 920                 925


Ala Ala Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp
    930                 935                 940


Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu
945                 950                 955                 960
```

```
Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr
                965                 970                 975

Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ser Ser Ser Gly Ala
            980                 985                 990

Thr Asn Asp Asn His Tyr Phe Gly  Tyr Ser Thr Pro Trp  Gly Tyr Phe
        995                 1000                 1005

Asp Phe  Asn Arg Phe His Cys  His Phe Ser Pro Arg  Asp Trp Gln
    1010                 1015                 1020

Arg Leu  Ile Asn Asn Asn Trp  Gly Phe Arg Pro Lys  Lys Leu Arg
    1025                 1030                 1035

Phe Lys  Leu Leu Asn Ile Gln  Val Lys Glu Val Thr  Thr Asn Asp
    1040                 1045                 1050

Gly Val  Thr Thr Ile Ala Asn  Asn Leu Thr Ser Thr  Val Gln Val
    1055                 1060                 1065

Phe Ser  Asp Ser Glu Tyr Gln  Leu Pro Tyr Val Leu  Gly Ser Ala
    1070                 1075                 1080

His Gln  Gly Cys Leu Pro Pro  Phe Pro Ala Asp Val  Phe Met Ile
    1085                 1090                 1095

Pro Gln  Tyr Gly Tyr Leu Thr  Leu Asp Asn Gly Ser  Gln Ser Val
    1100                 1105                 1110

Gly Arg  Ser Ser Phe Tyr Cys  Leu Glu Tyr Phe Pro  Ser Gln Met
    1115                 1120                 1125

Leu Arg  Thr Gly Asn Asn Phe  Glu Phe Ser Tyr Ser  Phe Glu Asp
    1130                 1135                 1140

Val Pro  Phe His Ser Ser Tyr  Ala His Ser Gln Ser  Leu Asp Arg
    1145                 1150                 1155

Leu Met  Asn Pro Leu Ile Asp  Gln Tyr Leu Tyr Tyr  Leu Ala Arg
    1160                 1165                 1170

Thr Gln  Ser Thr Thr Gly Ser  Thr Arg Glu Leu Gln  Phe His Gln
    1175                 1180                 1185

Ala Gly  Pro Asn Thr Met Ala  Glu Gln Ser Lys Asn  Trp Leu Pro
    1190                 1195                 1200

Gly Pro  Cys Tyr Arg Gln Gln  Arg Leu Ser Lys Asn  Leu Asp Phe
    1205                 1210                 1215
```

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Ala Thr Lys Tyr His
1220 1225 1230

Leu Asn Gly Arg Asn Ser Leu Thr Asn Pro Gly Ile Pro Met Ala
1235 1240 1245

Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val
1250 1255 1260

Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu
1265 1270 1275

Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro
1280 1285 1290

Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu Gln Ser
1295 1300 1305

Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln Gly Ala
1310 1315 1320

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
1325 1330 1335

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
1340 1345 1350

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln
1355 1360 1365

Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val
1370 1375 1380

Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr
1385 1390 1395

Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
1400 1405 1410

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala
1415 1420 1425

Lys Ser Asn Asn Val Glu Phe Ala Val Asn Pro Asp Gly Val Tyr
1430 1435 1440

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
1445 1450 1455

<210> 457
<211> 3095

<212> DNA
<213> Adeno-associated virus

<400> 457
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagcaatt acagattacg ggtgaggtaa cgagtgccaa tggggcgagg ctcagtataa 120

acaccatcag ggttcacagc aaattcaaca ttattagact tggcataatt ggaagtatac 180

tgaatttctg ggttccagcg cttgctgttt tctttctgca gctcccactc gatttccacg 240

ctgacttgtc cggtgctgta ctgcgtgatg aaggaggcaa acttggcagg agtaaacacc 300

tccggaggat tagcaggtac aggtgtgttt ttgatcagga tctgtggagg cgggtgtttg 360

agtccaaaac cgcccatcag aggagacggg tgaaagttgc catccgtgtg aggaattttg 420

gcccagatgg gaccctgcag atacacgtcc cggttctgcc agaccatgcc aggcagtgct 480

ccctggctgt tgatagtctg tgattgaggc ccggctgtag acgactgcag gttgctggag 540

accacaccgt attcttctgt agccacaggg ttagtggtct tgatctcctc ctcgctggtc 600

atcagaacgt tttccagcgt agttttgttg gcagctcccg tcttgccaaa aaccagtacc 660

ccgttgatgg gaaagaactg gtcctcatca tccttgttgg ttgccatggg aatgccagga 720

ttggtcaaag agtttctgcc attcagatga tatttagtgg cagcagtcca ggcaaaattg 780

ctgttgttgt taaagtccaa gttctttgac agtctctgtt gcctatagca gggtccaggc 840

agccagttct ttgactgctc ggccatagta ttgggcccag cttgatgaaa ttgcagttcc 900

ctggtggaac ccgtggtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgaga 960

gggttcatca gccggtctag gctctggctg tgcgcgtagc tgctgtggaa aggcacgtcc 1020

tcgaagctgt aactgaactc aaagttgttg cccgttctca gcatttgaga ggggaaatat 1080

tccaggcagt agaaggagga acggcccacc gattggctgc cgttgtccag agtcaggtag 1140

ccgtactgag gaatcatgaa gacgtccgcc gggaacggag gcaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ctggtattcc gagtccgaga agacctgaac cgtgctggta 1260

aggttattag cgatggtcgt gacgccgtca ttcgttgtga cctccttgac ctggatgttg 1320

aggagcttga accgcagctt cttgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccaggggggtg 1440

ctgtagccga agtagtggtt gtcattggtg gctcctgagc tgctgctgga gatttgcttg 1500

tagaggtggt tgttgtaggt ggggagggcc caggttctgg tgctggtggt gatgactctg 1560

tcgcccagcc atgtggaatc gcaatgccaa tttcctgagg cattacccac tccgtcggca 1620

ccttcgttat tgtctgccat tggtgcgcca ccgcctgcag ccattgtacc agatcccaca 1680

ctagagggcg ctgctggagg ttctccaaga ggttgagggt cggggactga ctctgagtcg 1740

ccagtctgac caaaattgag cttcttttta gcgggctgct ggcctttttt gccgatgccc 1800

gtggaggagt ctggagagcc tatgggtctc ttctttccag gagccgtctt agcgccttcc 1860

tcaaccagac cgagaggttc gagaacccgc ttcttggcct ggaagactgc tcgcccgagg 1920 ttgcccccaa atgacgtatc ttcttgcaga cgctcctgaa actcggcgtc ggcgtggtta 1980

taccgcaggt acggattgtc acccgctttg agctgctggt cgtaggcctt gtcgtgctcg 2040

agggccgctg cgtccgccgc gttgacgggc tccccttgt cgagtccgtt gaagggtccg 2100

aggtacttgt agccaggaag caccagaccc cggccgtcgt cctgcttttg ctggttggct 2160

ttgggtttcg gggctccagg tttcaggtcc caccactcgc gaatgccctc agagaggttg 2220

tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag tcatttattg 2280

ctcagaaaca cagtcgtcca ggtccacgtt gaccaggtcg caggccgagc aagcaatctc 2340

gggtgcccgc cccagcagat gatgaatcgc acacagcttc cgatacgtct tttttctgac 2400

gaccggttga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgtgcgt 2460

gaagcaaatg ttgaaattct gattcattct ctcgcacgtt ttgcagggaa acagcacctg 2520

aagcatgccc gcgtgacgag aacatttgtt ttggtacctg tcggcaaagt ccaccggagc 2580

tccttccgcg tctgacgtcg atgggtccgt gactgaggga cgggcccgct tgggctcgct 2640

tatatccgcg tcatcggggg cgggtctttt gctggctccg ccctttctga cgtagaactc 2700

atgcgtcacc tcagtcacgt gatcactagc ccagcggaag aactctttga cttcctgctt 2760

tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820

ctgcaacggt tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg cgcacatgtt 2880

ggtgttggag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgcacttttg 2940

gtccacgcgc accttgctgc cgccgagaat ggccttggcg gactccacga ccttggccgt 3000

catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga agggaaagtt 3060

ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> 458
<211> 3095
<212> DNA
<213> Adeno-associated virus

<400> 458
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagcaatt acagattacg ggtgaggtaa cgagtgccaa tggggcgagg ctcagtataa 120

acaccatcag ggttcacagc aaattcaaca ttattagact tggcataatt ggaagtatac 180

tgaatttctg ggttccagcg cttgctgttt tctttctgca gctcccactc gatttccacg 240

ctgacttgtc cggtgctgta ctgcgtgatg aaggaggcaa acttggcagg agtaaacacc 300

tccggaggat tagcaggtac aggtgtgttt ttgatcagga tctgtggagg cgggtgttcg 360

agtccaaaac cgcccatcag aggagacggg tgaaagttgc catccgtgtg aggaattttg 420

gcccagatgg gaccctgcag atacacgtcc cggttctgcc agaccatgcc aggcagtgct 480

ccctggctgt tgatagtctg tgattgaggc ccggctgtag acgactgcag gttgctggag 540

accacaccgt attcttctgt agccacaggg ttagtggtct tgatctcctc ctcgctggtc 600

atcagaacgt tttccagcgt agttttgttg gcagctcccg tcttgccaaa aaccagtacc 660 ccgttgatgg gaaagaactg gtcctcatca tccttgttgg ttgccatggg aatgccagga 720

ttggtcaaag agtttctgcc attcagatga tatttagtgg cagcagtcca ggcaaaattg 780

ctgttgttgt taaagtccaa gttctttgac agtctctgtt gcctatagca gggtccaggc 840

agccagttct ttgactgctc ggccatagta ttgggcccag cttgatgaaa ttgcagttcc 900

ctggtggaac ccgtggtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgaga 960

gggttcatca gccggtctag gctctggctg tgcgcgtagc tgctgtggaa aggcacgtcc 1020

tcgaagctgt aactgaactc aaagttgttg cccgttctca gcatttgaga ggggaaatat 1080

tccaggcagt agaaggagga acggcccacc gattggctgc cgttgttcag agtcaggtag 1140

ccgtactgag gaatcatgaa gacgtccgcc gggaacggag gcaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ctggtattcc gagtccgaga agacctgaac cgtgctggta 1260

aggttattag cgatggtcgt gacgccgtca ttcgttgtga cctccttgac ctggatgttg 1320

aagagcttga accgcagctt cttgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccagggggtg 1440

ctgtagccga agtagtggtt gtcattggtg gctcctgagc tgctgctgga gatttgcttg 1500

tagaggtggt tgttgtaggt ggggagggcc caggttctgg tgctggtggt gatgactctg 1560

tcgcccagcc atgtggaatc gcaatgccaa tttcctgagg cattacccac tccgtcggca 1620

ccttcgttat tgtctgccgt tggtgcgcca ccgcctgcag ccattgtacc agatcccaca 1680

ctagagggcg ctgctggagg ttctccaaga ggttgagggt cggggactga ctctgagtcg 1740

ccagtctgac caaaattgag cttcttttta gcgggctgct ggcctttttt gccgatgccc 1800

gtggaggagt ctggagagtc tatgggtctc ttctttccag gagccgtctt agcgccttcc 1860

tcaaccagac cgagaggttc gagaacccgc ttcttggcct ggaagactgc tcgcccgagg 1920

ttgcccccaa atgacgtatc ttcttgcagg cgctcctgaa actcggcgtc ggcgtggtta 1980

taccgcaggt acggattgtc acccgctttg agctgctggt cgtaggcctt gtcgtgctcg 2040

agggccgctg cgtccgccgc gttgacgggc tccccttgt cgagtccgtt gaagggtccg 2100

aggtacttgt agccaggaag caccagaccc cggccgtcgt cctgcttttg ctggttggct 2160

ttgggtttcg gggctccagg tttcaggtcc caccactcgc gaatgccctc agagaggttg 2220

tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag ccatttattg 2280

ctcagaaaca cagtcgtcca ggtccacgtt gaccaggtcg caggccgagc aggcaatctc 2340

gggtgcccgc cccagcagat gatgaatcgc acacagcttc cgatacgtct tttttctgac 2400

gaccggttga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgtgcgt 2460

gaagcaaatg ttgaaattct gattcattct ctcgcacgtt ttgcagggaa acagcatctg 2520

aagcatgccc gcgtggcgag aacatttgtt ttggtacctg tcggcaaagt ccaccggagc 2580

tccttccgcg tctgacgtcg atgggtccgt gactgaggga caggcccgct tgggctcgct 2640

tatatccgcg tcatcggggg cgggtctttt gctggctccg ccctttctga cgtagaactc 2700

```
atgcgtcacc tcagtcacgt gatcactagc ccagcggaag aactctttga cttcctgctt     2760

tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc     2820

ctgcaacggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg cgcgcatgtt     2880

ggtgttggag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgcacttttg     2940

gtccacgcgc accttgctgc cgccgagaat ggccttggcg gactccacga ccttggccgt     3000

catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga agggaaagtt     3060

ctcattggtc cagttgacgc agcaagggcg aattc                                3095


<210>  459
<211>  729
<212>  PRT
<213>  Adeno-associated virus

<400>  459
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190
```

```
Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460
```

```
Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

```
<210> 460
<211> 729
<212> PRT
<213> Adeno-associated virus

<400> 460
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190


Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205


Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220


His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240
```

```
Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510
```

```
Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525


Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540


Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560


Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575


Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590


Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605


Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620


Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640


Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655


Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670


Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685


Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700


Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720


Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 461
<211> 729
<212> PRT
<213> Adeno-associated virus

<400> 461
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160


Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190


Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205


Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220


His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255


Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270


Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285


Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300
```

```
Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320


Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335


Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350


Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365


Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380


Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400


Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415


Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430


Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445


Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460


Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480


Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495


Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510


Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525


Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540


Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560


Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575
```

```
Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590


Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605


Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620


Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640


Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655


Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670


Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685


Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700


Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720


Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 462
<211> 2217
<212> DNA
<213> Adeno-associated virus

```
<400> 462
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt       300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct       420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc       480

ggcaagaaag gccagcggcc cgctaaaaag agactgaact ttggtcagac tggcgactca       540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga       600
```

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gcccttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgcacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgctacc tcacccgtaa tctgtaa 2217

<210> 463
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 463
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Arg Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Pro Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580   585   590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595   600   605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610   615   620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625   630   635   640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645   650   655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660   665   670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 464
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 464
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc   60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac   120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac   180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac   240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt   300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag   360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct   420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc   480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca   540 gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg ataacttgca gcaaaccaat acggggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 465
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 465
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590


Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 466
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 466
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asp Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Arg Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 467
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 467
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720 atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcaggatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcgggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg ttgctatggc aacgcataag gacgacgagg aacgtttctt tccatcgagc 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta tagcagcgtt 1680

atgctaacca gcgaggaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaagccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaaa ttcctcacac ggacggcaat tttcacccgt ctcctctgat gggcggcttt 1920

ggactgaagc acccacctcc ccagatcctg atcaagaata cgccggtacc tgcggatcct 1980

ccaacgacgt tcagccaggc aaaattggct tccttcatca cgcagtacag caccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgatg gaacccagaa 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caattctgag 2160

ggtacatatt cagagcctcg ccccattggt actcgttatc tgacacgtaa tctgtaa 2217

<210> 468
<211> 2211
<212> DNA
<213> Adeno-associated virus

<400> 468
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gcctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcg aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccagtaga gcagtcaccc caagaaccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gtttttttccc agtaacggga 1620

tcctgttttt ggcaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct acagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac ccgccccat tggcacccgt tacctcaccc gtaatctgta a 2211

<210> 469
<211> 736
<212> PRT
<213> Adeno-associated virus

```
<400> 469
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270
```

```
Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Val Thr Gly Ser Cys Phe Trp
    530                 535                 540
```

Gln Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545   550   555   560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565   570   575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580   585   590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 470
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 470
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc   60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac   120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac   180

aagggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgacaa ggcctgcgac   240

cagcggctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt   300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag   360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaagg gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaatcacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga cgaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 471
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 471
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Cys Asp
65   70   75   80

Gln Arg Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195   200   205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210   215   220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225   230   235   240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245   250   255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260   265   270

```
Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540
```

```
Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560


Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Glu Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 472
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 472
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300
```

```
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct      420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480
ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca      540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga      600
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac      660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720
atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa      780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc      840
tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg      900
ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc      960
caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc     1020
acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac     1080
cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg     1140
actctcaaca acggtagtca ggccgtggga cgttcctcct tctactgcct ggagtacttc     1200
ccctctcaga tgctgagaac gggcaacaac ttttccttca gctacacttt cgaggacgtg     1260
cctttccaca gcagctacgc gcacagccag agtttggaca ggctgatgaa tcctctcatc     1320
gaccagtacc tgtactacct gtcaagaacc cagtctacgg gaggcacagc gggaacccag     1380
cagttgctgt tttctcaggc cgggcctagc aacatgtcga ctcaggccag aaactggctg     1440
cctggaccct gctacagaca gcagcgcgtc tccacgacac tgtcgcaaaa caacaacagc     1500
aactttgcct ggactggtgc caccaagtat catctgaacg gcagagactc tctggtgaat     1560
ccgggcgtcg ccatggcaac caacaaggac gacgaggacc gcttcttccc atccagcggc     1620
atcctcatgt ttggcaagca gggagctgga aaagacaacg tggactatag caacgtgatg     1680
ctaaccagcg aggaagaaat caagaccacc aaccccgtgg ccacagaaca gtatggcgtg     1740
gtggctgata acctacagca gcaaaacacc gctcctattg tgggggccgt caacagccag     1800
ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatttgg     1860
gccaagattc ctcacacaga tggcaacttt cacccgtctc ctttaatggg cggctttgga     1920
cttaaacatc cgcctcctca gatccttatc aaaaacactc ctgttcctgc ggatcctcca     1980
acagcgttca accaggccaa gctgaattct ttcatcacgc agtacagcac cggacaagtc     2040
agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt     2100
cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgagggt     2160
gcttactctg agcctcgccc cattggcact cgttacctca cccgtaatct gtaa           2214
```

<210> 473
<211> 737

```
<212> PRT
<213> Adeno-associated virus

<400> 473
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Asn Met Ser Thr Gln Ala Arg Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr Asn
        515                 520                 525
```

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met Phe
    530   535   540

Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val Met
545   550   555   560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565   570   575

Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580   585   590

Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595   600   605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610   615   620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625   630   635   640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645   650   655

Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile
            660   665   670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675   680   685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690   695   700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705   710   715   720

Ala Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725   730   735

Leu

<210> 474
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 474
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaaggcc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 475
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 475
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195   200   205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210   215   220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225   230   235   240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His

```
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
```

        515   520   525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530   535   540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545   550   555   560

Met Leu Thr Ser Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr
                565   570   575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580   585   590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595   600   605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610   615   620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625   630   635   640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645   650   655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660   665   670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 476
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 476
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc   60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac   120 gacggccggg gtctggtgct tcctggctac aagcacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgctga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacggttc aggtcttttc ggactcggaa taccagctgc cctacgtcct cggctccgca 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

ctgactctga acaatggcag ccaatcggtg ggtcgttcct ctttctactg cctggaatat 1200

ttcccttctc aaatgctgag aacgggcaac aacttcacct tcagctacac cttcgaggac 1260

gttcccttcc acagcagcta cgcacacagc cagagcctgg accggctgat gaatcctctt 1320

atcgaccagt acctgtatta cctggccaga acacagagca acgcaggagg cacagctggc 1380

aatcgggaac tgcagtttta tcagggcggg cctaccacca tggccgaaca agccaaaaac 1440

tggctgcctg gaccttgctt ccggcaacaa agagtctcca agacgctgga tcaaaacaac 1500

aacagcaact ttgcttggac tggtgccacc aaataccatc taaatggaag aaattcattg 1560

gttaatcccg gtgtcgccat ggcaacccac aaggacgacg aggaacgctt cttcccttcg 1620

agcggagtcc tgatttttgg aaaaactgga gcagctaata agactacact ggaaaatgtg 1680

ttaatgacaa atgaagagga aattcgtcct accaacccgg tagccaccga ggaatacggg 1740

actgttagca gcaacctgca ggcggctaac actgcagccc agacacaagt tgtcaacaac 1800

cagggagcct tacctggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcacccgt ctccgctgat gggcggcttt 1920

ggactgaagc atccgcctcc tcagatcctg atcaaaaaca ctcctgttcc tgctaatccc 1980

ccggaggtgt ttacgcctgc caagtttgct tctttcatca cacagtacag caccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cctccaattt tgacaaacag actggtgtgg actttgccgt tgacagccag 2160

```
ggtgtttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa        2217


<210> 477
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 477
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys His Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu
    450                 455                 460

Gln Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn
465                 470                 475                 480

Trp Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu
                485                 490                 495

Asp Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr
            500                 505                 510
```

His Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala
515 520 525

Thr His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu
530 535 540

Ile Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val
545 550 555 560

Leu Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr
565 570 575

Glu Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala
580 585 590

Ala Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 478
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 478

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270
```

```
Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445


Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460


Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540
```

```
Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560


Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 479
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 479
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590
```

```
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 480
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 480
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270


Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445


Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460


Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540


Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560


Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620
```

```
His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 481
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 481
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270


Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670
```

```
Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 482
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 482
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct       420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc       480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca       540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga       600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacaa gggcgccgac       660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc       720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa       780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc       840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg       900

ctcatcaaca gcaactgggg attccggccc aagaagctca acttcaagct gttcaacatc       960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc      1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac      1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg      1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc      1200
```

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 483
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 483
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgcac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acttatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840 ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggcaac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acatgggcta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacgg caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 484
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 484
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro His Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Leu Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Asn Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Met Gly Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Gly Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 485
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 485
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct       420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc       480

ggcaagaaag gccagcagcc cgccggaaag agactcaatt tcggtcagac tggcgactca       540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga       600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac       660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc       720
```

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

gtcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gagcccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 486
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 486
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Gly Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590
```

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595   600   605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610   615   620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625   630   635   640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645   650   655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660   665   670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Ser Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 487
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 487
atggttgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcagggc 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctta aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagctt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgcg ccaatggcag acaataacga aggtgccgac 660 ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gccagcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagccgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 488
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 488
Met Val Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

```
Lys Ala Asn Gln Gln Lys Gln Gly Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Leu Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Gln Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

```
Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Pro Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu


<210> 489
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 489
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca      540
```

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa tagcctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactccca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgtcttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacttgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 490
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 490
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn

```
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Ser Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Ser Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
```

565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 491
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 491
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415


Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Val His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Ser Gly Val Ala Met Ala Thr
        515                 520                 525


Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg
                725                 730                 735


Asn Leu


<210> 492
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 492
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca      540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga      600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac      660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc      720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa      780
```

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgtgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aattcgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc ccacccgtaa tctgtaa 2217

<210> 493
<211> 734
<212> PRT
<213> Adeno-associated virus

<400> 493

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590
```

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
690 695 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 494
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 494
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct cttcaacatc 960

caagtcaagg aggtcacgac gaatgacggc gtcacgacca tcgctaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggagtac cagctgccgt acgtcctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctgaaca atggcagcca atcggtggga cgttcatcct tctactgcct ggaatacttc 1200

ccttctcagg tgctgagaac gggtaacaac ttcaccttca gttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctagacc ggctgatgaa tcccctcatc 1320

gaccagtacc tgtattacct ggctagaaca cagagtaacc caggaggcac atctggcaat 1380

cgggaactgc agttttacca gggcgggcct tccaccatgg ccgaacaagc caagaactgg 1440

ttacctggac cttgcttccg gcaacaaaga gtttccaaaa cactggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcattggtg 1560

aatcctggtg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca accaacaaga ctacattgga aaacgtgtta 1680

atgacaaatg aagaagaaat tcgtcctact aatcctgtgg ccacagaaga atacgggata 1740

gtcagcagca atttacaagc ggccaatact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaaaattc ctcacacaga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 495
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 495
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270


Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Val Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ser Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
```

```
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 496
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 496

```
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca      540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga      600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac      660

ggagtgggta gttcctcggg aaattggcat tgcgattcca cacggctggg cgacagagtc      720
```

atcaccacca gcacccggac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacgaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 497
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 497
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Arg Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590
```

```
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 498
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 498
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac       120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac       240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt       300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag       360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg       420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga       480

aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac       540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tttgggatct       600
```

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cttcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggcccagccc acctacaaca accacctcta caagcaaatc 780

tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa aacacaatca aatagtggag ctcttcagca gtctcggcta 1380

ctgtttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtaccaccta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccgaggagcg 1800

ttacctggca tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 499
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 499

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
```

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Gln Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445


Gln Ser Asn Ser Gly Ala Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460


Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
```

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
580 585 590

Gly Thr Val Asn His Arg Gly Ala Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 500
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 500
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgcg ccaatggcag acaataacga aggtgccgac 660

```
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc      720
atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa      780
acctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc      840
ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag      900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac      960
atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc     1020
agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc     1080
caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac     1140
ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac     1200
ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac     1260
gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc     1320
atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc     1380
cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg     1440
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac     1500
agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg     1560
aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc     1620
ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg     1680
atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc     1740
gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc     1800
cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt     1860
tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt     1920
ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct     1980
ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa     2040
gtcagcgcgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag     2100
attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag     2160
ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa        2217
```

<210> 501
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 501

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Thr Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580   585   590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595   600   605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610   615   620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625   630   635   640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645   650   655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660   665   670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Ala Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 502
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 502
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc   60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac   120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac   180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac   240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt   300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag   360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct   420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc   480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca   540 gagtcagtcc ccgaccctca accaatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggccgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagctgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaagca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagtgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 503
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 503
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
```

```
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
```

565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Cys Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 504
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 504
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415


Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 505
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 505
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

```
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg      900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc      960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccctaccagc     1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac     1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg     1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc     1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt     1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc     1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat     1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg     1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac     1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg     1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc     1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg     1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc     1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc     1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt     1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt     1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct     1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa     2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag     2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag     2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa        2217


<210> 506
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 506
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270


Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Pro Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590
```

```
Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210> 507
<211> 2208
<212> DNA
<213> Adeno-associated virus

<400> 507
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcac        60

gagtggtggg acccgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct       420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc       480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca       540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga       600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac       660
```

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacccaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaacg tctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgtcact tctcaccacg tgaccggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cggaaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc ctcagatcct gatcaaaaac actcctgttc ctgctaatcc cccggaggtg 1980

tttacgcctg ccaagtttgc ttctttcatc acacagtaca gcaccggcca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaagcgct ggaacccaga gattcagtat 2100

acctccaatt ttgacaaaca gactggtgtg gactttgccg ttgacagcca gggtgtttat 2160

tctgagcctc gccccattgg tactcgttac ctcacccgta atctgtaa 2208

<210> 508
<211> 735
<212> PRT
<213> Adeno-associated virus

<400> 508
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile His Glu Trp Trp Asp Pro Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr His Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
```

305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Glu Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
530 535 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
565 570 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala

580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Phe
690 695 700

Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 509
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 509
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Pro Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Pro Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asp Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Val Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 510
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 510
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaagg ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgacccatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020 agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctaccc tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaagac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcaggtcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 511
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 511
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttc 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggctgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gagccaccag caggcccctc tggtctggga 600 tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacaa gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gggtgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atgacagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 512
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 512
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Ala Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270


Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Gly Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Asp Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

```
Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu


<210> 513
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 513
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct       420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc       480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca       540
```

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgtgtg ggagctgcag aaggagaaca gcaagcgcag gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 514
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 514
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Arg Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 515
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 515
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195   200   205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210   215   220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225   230   235   240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245   250   255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260   265   270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275   280   285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290   295   300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305   310   315   320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325   330   335

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415


Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610   615   620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625   630   635   640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645   650   655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660   665   670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 516
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 516
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645   650   655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660   665   670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu
        675   680   685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 517
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 517
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415
```

```
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690   695   700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705   710   715   720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725   730   735

Asn Leu

<210> 518
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 518
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

```
gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat     1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg     1440

ctgcctagac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac     1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt     1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc     1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta     1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact     1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag     1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg     1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga     1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg     1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc     2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt     2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt     2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa           2214


<210> 519
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 519
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445


Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460


Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Arg Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540


Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560


Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670
```

```
Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 520
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 520
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accatgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcctccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct      420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca      540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga      600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac      660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa      780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg      900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc      960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc     1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac     1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg     1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc     1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt     1260
```

ccccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 521
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 521
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220


Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270


Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

```
Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 522
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 522
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Leu Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160
```

```
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700
```

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705   710   715   720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725   730   735

Leu

<210> 523
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 523
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

```
ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac     1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg     1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccacccagc     1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg     1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc     1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc     1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt     1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt     1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct     1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa     2040

gtcagcgtgg tgatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag     2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag     2160

ggtgtttact ctgagcttcg ccccattggc actcgttacc tcacccgtaa tctgtaa        2217
```

<210> 524
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 524

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415
```

```
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Pro Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Val Ile Glu Trp Glu
        675                 680                 685
```

```
Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Leu Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 525
<211> 2214
<212> DNA
<213> Adeno-associated virus

<400> 525

```
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct      420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca      540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga      600

tctggtacaa tggctgcagg cggtggcgcc ccaatggcag acaataacga aggcgccgac      660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc      720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa      780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg      900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc      960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc     1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac     1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg     1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc     1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccatca gctacacctt cgaggacgtt     1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc     1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat     1380
```

caggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacaga tggcaacttt cacccgtctc ctttaatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctcatc aaaaacactc ctgttcctgc ggatcctcca 1980

acagcgttca accaggccaa gctgaattct ttcatcacgc agtacagcac cggacaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgagggt 2160

gtttactctg agcctcgccc cattggcact cgttacctca cccgtaatct gtaa 2214

<210> 526
<211> 737
<212> PRT
<213> Adeno-associated virus

<400> 526
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Ile Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Gln Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile
            660                 665                 670
```

```
Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 527
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 527
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct       420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc       480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca       540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga       600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac       660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc       720

atcaccacca gcacccgaac ctgggccctg cccgcctaca acaaccacct ctacaagcaa       780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc       840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag       900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac       960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc      1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc      1080

caccagggct gcctgcctcc gttcccggcg gatgtcttca tgattcctca gtacggctac      1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac      1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac      1260
```

```
gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc     1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc     1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg     1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac     1500

agcaactttg cctggactgg tgccaccaag tatcatctga gcggcagaga ctctctggtg     1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc     1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg     1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc     1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc     1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt     1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt     1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct     1980

ccaacagcgt tcaaccaggc caagctgaat tcttccatca cgcagtacag caccggacaa     2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag     2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag     2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tttgtaa        2217


<210> 528
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 528
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
```

115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Ala Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr

```
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415


Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Ser Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Ser
```

```
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 529
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 529
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160
```

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 530
<211> 2217
<212> DNA
<213> Adeno-associated virus

<400> 530
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

```
ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt     1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt     1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc     1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc     1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt     1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct     1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag     2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag     2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag     2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa        2217
```

```
<210> 531
<211> 738
<212> PRT
<213> Adeno-associated virus

<400> 531
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160
```

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Arg Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

```
Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 532
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 532
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Leu Asn Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Asp Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Gly
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Lys Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160


Gly Lys Lys Ser Pro His Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Glu Ala Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ser Asp Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
        435                 440                 445

Thr Gln Gly Thr Asn Ala Thr Val Gln Gly Ala Lys Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Asn Met Arg Asp Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Glu Tyr Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met Asn Gly Thr Leu Val Phe Gly
    530                 535                 540

Lys Asn Gly Ala Gly Asn Ser Asn Val Asp Ile Glu Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Val Val Ser Asp Asn Leu Gln Ser Ser Asn Thr Arg Pro Ile
            580                 585                 590

Thr Gly Asp Val Asp Ser Gln Gly Val Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 533
<211> 736
```

```
<212> PRT
<213> Adeno-associated virus

<400> 533
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270


Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445


Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460


Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495


Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525
```

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
530 535 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
580 585 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 534
<211> 736
<212> PRT
<213> Adeno-associated virus

<400> 534
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270


Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590
```

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595   600   605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 535
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 535
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445


Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460


Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495


Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590


Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 536
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 536
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Arg Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 537
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 537
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160
```

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270


Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445


Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460


Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495


Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Ala Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590


Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 538
<211> 1803
<212> DNA
<213> Bovine adeno-associated virus

<400> 538
acggcgcctg cggcaaaaaa gaggcctcta gagcagagtc ctcaagagcc agactcctcg        60

agcggagttg gcaagaaagg caaacagcct gccagaaaga gactcaactt tgacgacgaa       120

cctggagccg gagacgggcc tcccccagaa ggaccatctt ccggagctat gtctactgag       180

actgaaatgc gtgcagcagc tggcggaaat ggtggcgatg cgggacaagg tgccgaggga       240

gtgggtaatg cctccggtga ttggcattgc gattccactt ggtcagagag ccacgtcacc       300

accacctcaa cccgcacctg ggtcctgccg acctacaaca accacctgta cctgcggctc       360

ggctcgagca acgccagcga caccttcaac ggattctcca ccccctgggg atactttgac       420

tttaaccgct tccactgcca cttctcgcca agagactggc aaaggctcat caacaaccac       480

tggggactgc gccccaaaag catgcaagtc cgcatcttca acatccaagt taaggaggtc       540

acgacgtcta acggggagac gaccgtatcc aacaacctca ccagcacggt ccagatcttt       600

gcggacagca cgtacgagct cccgtacgtg atggatgcag gtcaggaggg cagcttgcct       660

cctttcccca acgacgtgtt catggtgcct cagtacgggt actgcggact ggtaaccgga       720

ggcagctctc aaaaccagac agacagaaat gccttctact gtctggagta ctttcccagc       780

cagatgctga gaaccggaaa caactttgag atggtgtaca agtttgaaaa cgtgcccttc       840

cactccatgt acgctcacag ccagagcctg gataggctga tgaacccgct gctggaccag       900

tacctgtggg agctccagtc taccacctct ggaggaactc tcaaccaggg caattcagcc       960

accaactttg ccaagctgac caaaacaaac ttttctggct accgcaaaaa ctggctcccg      1020

gggcccatga tgaagcagca gagattctcc aagactgcca gtcaaaacta caagattccc      1080

cagggaagaa acaacagtct gctccattat gagaccagaa ctaccctcga cggaagatgg      1140

agcaattttg ccccgggaac ggccatggca accgcagcca acgacgccac cgacttctct      1200

caggcccagc tcatctttgc ggggcccaac atcaccggca acaccaccac agatgccaat      1260

aacctgatgt tcacttcaga agatgaactt agggccacca acccccggga cactgacctg      1320

tttggccacc tggcaaccaa ccagcaaaac gccaccaccg ttcctaccgt agacgacgtg      1380

gacggagtcg gcgtgtaccc gggaatggtg tggcaggaca gagacattta ctaccaaggg      1440

cccatttggg ccaaaattcc acacacggat ggacactttc acccgtctcc tctcattggc      1500

ggatttggac tgaaaagccc gcctccacaa atattcatca aaaacactcc tgtacccgcc      1560

aatcccgcaa cgaccttctc tccggccaga atcaacagct tcatcaccca gtacagcacc      1620
```

ggacaggtgg ctgtcaaaat agaatgggaa atccagaagg agcggtccaa gagatggaac 1680

ccagaggtcc agttcacgtc caactacgga gcacaggact cgcttctctg ggctcccgac 1740

aacgccggag cctacaaaga gcccagggcc attggatccc gatacctcac caaccacctc 1800

tag 1803

<210> 539
<211> 1617
<212> DNA
<213> Bovine adeno-associated virus

<400> 539
atgcgtgcag cagctggcgg aaatggtggc gatgcgggac aaggtgccga gggagtgggt 60

aatgcctccg gtgattggca ttgcgattcc acttggtcag agagccacgt caccaccacc 120

tcaacccgca cctgggtcct gccgacctac aacaaccacc tgtacctgcg gctcggctcg 180

agcaacgcca gcgacacctt caacggattc tccacccccct ggggatactt tgactttaac 240

cgcttccact gccacttctc gccaagagac tggcaaaggc tcatcaacaa ccactgggga 300

ctgcgcccca aaagcatgca agtccgcatc ttcaacatcc aagttaagga ggtcacgacg 360

tctaacgggg agacgaccgt atccaacaac ctcaccagca cggtccagat ctttgcggac 420

agcacgtacg agctcccgta cgtgatggat gcaggtcagg agggcagctt gcctcctttc 480

cccaacgacg tgttcatggt gcctcagtac gggtactgcg gactggtaac cggaggcagc 540

tctcaaaacc agacagacag aaatgccttc tactgtctgg agtactttcc cagccagatg 600

ctgagaaccg gaaacaactt tgagatggtg tacaagtttg aaaacgtgcc cttccactcc 660

atgtacgctc acagccagag cctggatagg ctgatgaacc cgctgctgga ccagtacctg 720

tgggagctcc agtctaccac ctctggagga actctcaacc agggcaattc agccaccaac 780

tttgccaagc tgaccaaaac aaacttttct ggctaccgca aaaactggct cccggggccc 840

atgatgaagc agcagagatt ctccaagact gccagtcaaa actacaagat tcccccaggga 900

agaaacaaca gtctgctcca ttatgagacc agaactaccc tcgacggaag atggagcaat 960

tttgccccgg gaacggccat ggcaaccgca gccaacgacg ccaccgactt ctctcaggcc 1020

cagctcatct ttgcggggcc caacatcacc ggcaacacca ccacagatgc caataacctg 1080

atgttcactt cagaagatga acttagggcc accaaccccc gggacactga cctgtttggc 1140

cacctggcaa ccaaccagca aaacgccacc accgttccta ccgtagacga cgtggacgga 1200

gtcggcgtgt acccgggaat ggtgtggcag gacagagaca tttactacca agggcccatt 1260

tgggccaaaa ttccacacac ggatggacac tttcacccgt ctcctctcat tggcggattt 1320

ggactgaaaa gcccgcctcc acaaatattc atcaaaaaca ctcctgtacc cgccaatccc 1380

gcaacgacct tctctccggc cagaatcaac agcttcatca cccagtacag caccggacag 1440

gtggctgtca aaatagaatg ggaaatccag aaggagcggt ccaagagatg gaacccagag 1500

gtccagttca cgtccaacta cggagcacag gactcgcttc tctgggctcc cgacaacgcc 1560

ggagcctaca aagagcccag ggccattgga tcccgatacc tcaccaacca cctctag 1617

<210> 540
<211> 1173
<212> DNA
<213> Bovine adeno-associated virus

<400> 540
atggcgctgg taagctggct ggtggaacat ggcatcactt ccgagaagca gtggattcag 60

gagaatcagg agagctacct gtccttcaac tccacgggaa actctcggag ccagattaaa 120

gccgcgcttg acaacgcgtc aaaaattatg agtctgacca aatctgcctc agactatctc 180

gtgggacaga ctgttccaga ggacatttct gaaaacagaa tctggcagat ttttgatctc 240

aacggctacg acccggcata cgcgggctct gttctctacg gctggtgcac tcgcgccttt 300

ggaaagagga acaccgtctg gctgtatgga cccgcgacca ccggaaagac caacatcgcg 360

gaagccatct ctcacaccgt gcccttttat ggctgtgtga actggactaa tgagaacttt 420

ccctttaatg actgtgtgga aaaaatgttg atctggtggg aggagggaaa gatgaccagc 480

aaggtggtgg aacccgccaa ggccatcttg ggggggtcta gagtacgagt ggatcaaaaa 540

tgtaaatcct ctgtacaagt agactctacc ccggtgatta tcacctccaa tactaacatg 600

tgtgtggtgg tggatgggaa ctccacgacc tttgaacacc agcagccgct ggaagaccgc 660

atgttcagat ttgaactcat gcggcggctc ccgccagatt ttggcaagat taccaagcag 720

gaagtcaaag actttttgc ttgggcaaag gtcaaccagg tgccggtgac tcacgagttt 780

atggttccca agaaagtggc gggaactgag agggcggaga cttctagaaa acgcccactg 840

gatgacgtca ccaataccaa ctataaaagt ccggagaagc gggcccggct ctcagttgtt 900

cctgagacgc ctcgcagttc agacgtgcct gtagagcccg ctcctctgcg acctctcaac 960

tggtcttcca ggtatgaatg cagatgtgac tatcatgcta aatttgactc tgtaacgggg 1020

gaatgtgacg agtgtgaata tttgaatcgg ggcaaaaatg gctgtatctt tcataatgct 1080

acacattgtc aaatttgtca cgctgttcct ccatgggaaa aggaaaatgt gtcagatttt 1140

aatgattttg atgactgtaa taaagagcag taa 1173

<210> 541
<211> 1833
<212> DNA
<213> Bovine adeno-associated virus

<400> 541
atggctacct tctatgaagt cattgttcgc gttccatttg atgtggaaga gcacctgcct 60

ggaatttctg acaactttgt agactgggta actggtcaaa tttgggagct gcctcccgag 120

tcagatttga atttgactct gattgagcag cctcagctga cggtggctga cagaattcgc 180

cgcgtgttcc tgtacgagtg gaacaaattt tccaagcagg agagcaaatt ctttgtgcag 240

tttgaaaagg gatctgaata ttttcatctg cacacgctcg tggagacctc cggcatctct 300

tctatggtcc ttggccgcta cgtgagtcag attcgcgccc agctggtgaa ggtggtgttc 360

cagaacattg agccgcggat taacgactgg gtcgccatca ccaaggtaaa gaagggcgga 420 gccaataagg tggtggattc tgggtatatt cccgcctacc tgctgccgaa ggtccaacca 480

gagcttcagt gggcgtggac taacctcgaa gagtataaat tggccgccct caatctggag 540

gagcgcaaac ggctcgtcgc tcagtttcag cttgagtcct cgcagcgctc gcaagaggca 600

tcttcccaga gggacgtttc ggctgacccg gtcatcaaga gcaagacttc ccagaaatac 660

atggcgctgg taagctggct ggtggaacat ggcatcactt ccgagaagca gtggattcag 720

gagaatcagg agagctacct gtccttcaac tccacgggaa actctcggag ccagattaaa 780

gccgcgcttg acaacgcgtc aaaaattatg agtctgacca aatctgcctc agactatctc 840

gtgggacaga ctgttccaga ggacatttct gaaaacagaa tctggcagat tttgatctc 900

aacggctacg acccggcata cgcgggctct gttctctacg gctggtgcac tcgcgccttt 960

ggaaagagga acaccgtctg gctgtatgga cccgcgacca ccggaaagac caacatcgcg 1020

gaagccatct ctcacaccgt gccctttat ggctgtgtga actggactaa tgagaacttt 1080

ccctttaatg actgtgtgga aaaaatgttg atctggtggg aggagggaaa gatgaccagc 1140

aaggtggtgg aacccgccaa ggccatcttg ggggggtcta gagtacgagt ggatcaaaaa 1200

tgtaaatcct ctgtacaagt agactctacc ccggtgatta tcacctccaa tactaacatg 1260

tgtgtggtgg tggatgggaa ctccacgacc tttgaacacc agcagccgct ggaagaccgc 1320

atgttcagat ttgaactcat gcggcggctc ccgccagatt ttggcaagat taccaagcag 1380

gaagtcaaag acttttttgc ttgggcaaag gtcaaccagg tgccggtgac tcacgagttt 1440

atggttccca agaaagtggc gggaactgag agggcggaga cttctagaaa acgcccactg 1500

gatgacgtca ccaataccaa ctataaaagt ccggagaagc gggcccggct ctcagttgtt 1560

cctgagacgc ctcgcagttc agacgtgcct gtagagcccg ctcctctgcg acctctcaac 1620

tggtcttcca ggtatgaatg cagatgtgac tatcatgcta aatttgactc tgtaacgggg 1680

gaatgtgacg agtgtgaata tttgaatcgg ggcaaaaatg gctgtatctt tcataatgct 1740

acacattgtc aaatttgtca cgctgttcct ccatgggaaa aggaaaatgt gtcagatttt 1800

aatgattttg atgactgtaa taaagagcag taa 1833

<210> 542
<211> 2211
<212> DNA
<213> Bovine adeno-associated virus

<400> 542
atgtcttttg ttgaccaccc tccagattgg ttggaatcga tcggcgacgg ctttcgtgaa 60

tttctcggcc ttgaggcggg tcccccgaaa cccaaggcca atcaacagaa gcaagataac 120

gctcgaggtc ttgtgcttcc tgggtacaag tatcttggtc ctgggaacgg ccttgataag 180

ggcgatcctg tcaattttgc tgacgaggtt gcccgagagc acgacctctc ctaccagaaa 240

cagcttgagg cgggcgataa cccttacctc aagtacaacc acgcggacgc agagtttcag 300

gagaaactcg cttctgacac ttcttttggg ggaaaccttg ggaaggctgt tttccaggct 360 aaaaagagga ttctcgaacc tcttggcctg gttgagacgc cggataaaac ggcgcctgcg 420

gcaaaaaaga ggcctctaga gcagagtcct caagagccag actcctcgag cggagttggc 480

aagaaaggca aacagcctgc cagaaagaga ctcaactttg acgacgaacc tggagccgga 540

gacgggcctc ccccagaagg accatcttcc ggagctatgt ctactgagac tgaaatgcgt 600

gcagcagctg gcggaaatgg tggcgatgcg ggacaaggtg ccgagggagt gggtaatgcc 660

tccggtgatt ggcattgcga ttccacttgg tcagagagcc acgtcaccac cacctcaacc 720

cgcacctggg tcctgccgac ctacaacaac cacctgtacc tgcggctcgg ctcgagcaac 780

gccagcgaca ccttcaacgg attctccacc ccctggggat actttgactt taaccgcttc 840

cactgccact tctcgccaag agactggcaa aggctcatca acaaccactg gggactgcgc 900

cccaaaagca tgcaagtccg catcttcaac atccaagtta aggaggtcac gacgtctaac 960

ggggagacga ccgtatccaa caacctcacc agcacggtcc agatctttgc ggacagcacg 1020

tacgagctcc cgtacgtgat ggatgcaggt caggagggca gcttgcctcc tttccccaac 1080

gacgtgttca tggtgcctca gtacgggtac tgcggactgg taaccggagg cagctctcaa 1140

aaccagacag acagaaatgc cttctactgt ctggagtact ttcccagcca gatgctgaga 1200

accggaaaca actttgagat ggtgtacaag tttgaaaacg tgcccttcca ctccatgtac 1260

gctcacagcc agagcctgga taggctgatg aacccgctgc tggaccagta cctgtgggag 1320

ctccagtcta ccacctctgg aggaactctc aaccagggca attcagccac caactttgcc 1380

aagctgacca aaacaaactt ttctggctac cgcaaaaact ggctcccggg gcccatgatg 1440

aagcagcaga gattctccaa gactgccagt caaaactaca agattcccca gggaagaaac 1500

aacagtctgc tccattatga gaccagaact accctcgacg gaagatggag caattttgcc 1560

ccgggaacgg ccatggcaac cgcagccaac gacgccaccg acttctctca ggcccagctc 1620

atctttgcgg ggcccaacat caccggcaac accaccacag atgccaataa cctgatgttc 1680

acttcagaag atgaacttag ggccaccaac ccccgggaca ctgacctgtt tggccacctg 1740

gcaaccaacc agcaaaacgc caccaccgtt cctaccgtag acgacgtgga cggagtcggc 1800

gtgtacccgg gaatggtgtg gcaggacaga gacatttact accaagggcc catttgggcc 1860

aaaattccac acacggatgg acactttcac ccgtctcctc tcattggcgg atttggactg 1920

aaaagcccgc ctccacaaat attcatcaaa aacactcctg tacccgccaa tcccgcaacg 1980

accttctctc cggccagaat caacagcttc atcacccagt acagcaccgg acaggtggct 2040

gtcaaaatag aatgggaaat ccagaaggag cggtccaaga gatggaaccc agaggtccag 2100

ttcacgtcca actacggagc acaggactcg cttctctggg ctcccgacaa cgccggagcc 2160

tacaaagagc ccagggccat tggatcccga tacctcacca accacctcta g 2211

<210> 543
<211> 4694
<212> DNA
<213> Bovine adeno-associated virus

<400> 543
gtggcactcc ccccctgtc gcgttcgctc gttcgctggc tcgattgggg gggtggcagc 60

tcaaagagct gccagacgac ggccctctgg gccgtcgccc ccccaatcga gccagcgaac 120

gagcgaacgc gacagggggg ggagtgccac actctctagc aagggggttt tgtaggtggt 180

gatgtcattg ttgatgtcat tatagttgtc acgcgatagt taatgattaa cagtcatgtg 240

atgtgtgtta tccaatagga tgaaagcgcg cgaatgagat ctcgcgagac ttccggggta 300

taaaaggggt gagtgaacga gcccgccgcc attctctgct ctggactgct agaggaccct 360

cgctgccatg gctaccttct atgaagtcat tgttcgcgtt ccatttgatg tggaagagca 420

cctgcctgga atttctgaca actttgtaga ctgggtaact ggtcaaattt gggagctgcc 480

tcccgagtca gatttgaatt tgactctgat tgagcagcct cagctgacgg tggctgacag 540

aattcgccgc gtgttcctgt acgagtggaa caaattttcc aagcaggaga gcaaattctt 600

tgtgcagttt gaaaagggat ctgaatattt tcatctgcac acgctcgtgg agacctccgg 660

catctcttct atggtccttg gccgctacgt gagtcagatt cgcgcccagc tggtgaaggt 720

ggtgttccag aacattgagc cgcggattaa cgactgggtc gccatcacca aggtaaagaa 780

gggcggagcc aataaggtgg tggattctgg gtatattccc gcctacctgc tgccgaaggt 840

ccaaccagag cttcagtggg cgtggactaa cctcgaagag tataaattgg ccgccctcaa 900

tctggaggag cgcaaacggc tcgtcgctca gtttcagctt gagtcctcgc agcgctcgca 960

agaggcatct tcccagaggg acgtttcggc tgacccggtc atcaagagca agacttccca 1020

gaaatacatg gcgctggtaa gctggctggt ggaacatggc atcacttccg agaagcagtg 1080

gattcaggag aatcaggaga gctacctgtc cttcaactcc acgggaaact ctcggagcca 1140

gattaaagcc gcgcttgaca acgcgtcaaa aattatgagt ctgaccaaat ctgcctcaga 1200

ctatctcgtg ggacagactg ttccagagga catttctgaa aacagaatct ggcagatttt 1260

tgatctcaac ggctacgacc cggcatacgc gggctctgtt ctctacggct ggtgcactcg 1320

cgcctttgga aagaggaaca ccgtctggct gtatggaccc gcgaccaccg gaaagaccaa 1380

catcgcggaa gccatctctc acaccgtgcc cttttatggc tgtgtgaact ggactaatga 1440

gaactttccc tttaatgact gtgtggaaaa aatgttgatc tggtgggagg agggaaagat 1500

gaccagcaag gtggtggaac ccgccaaggc catcttgggg gggtctagag tacgagtgga 1560

tcaaaaatgt aaatcctctg tacaagtaga ctctaccccg gtgattatca cctccaatac 1620

taacatgtgt gtggtggtgg atgggaactc cacgaccttt gaacaccagc agccgctgga 1680

agaccgcatg ttcagatttg aactcatgcg gcggctcccg ccagattttg gcaagattac 1740

caagcaggaa gtcaaagact tttttgcttg ggcaaaggtc aaccaggtgc cggtgactca 1800

cgagtttatg gttcccaaga aagtggcggg aactgagagg gcggagactt ctagaaaacg 1860

cccactggat gacgtcacca ataccaacta taaaagtccg gagaagcggg cccggctctc 1920

agttgttcct gagacgcctc gcagttcaga cgtgcctgta gagcccgctc ctctgcgacc 1980

tctcaactgg tcttccaggt atgaatgcag atgtgactat catgctaaat ttgactctgt 2040 aacgggggaa tgtgacgagt gtgaatattt gaatcggggc aaaaatggct gtatctttca 2100

taatgctaca cattgtcaaa tttgtcacgc tgttcctcca tgggaaaagg aaaatgtgtc 2160

agattttaat gattttgatg actgtaataa agagcagtaa ataaagtgag tagtcatgtc 2220

ttttgttgac caccctccag attggttgga atcgatcggc gacggctttc gtgaatttct 2280

cggccttgag gcgggtcccc cgaaacccaa ggccaatcaa cagaagcaag ataacgctcg 2340

aggtcttgtg cttcctgggt acaagtatct tggtcctggg aacggccttg ataagggcga 2400

tcctgtcaat tttgctgacg aggttgcccg agagcacgac ctctcctacc agaaacagct 2460

tgaggcgggc gataaccctt acctcaagta caaccacgcg gacgcagagt ttcaggagaa 2520

actcgcttct gacacttctt ttgggggaaa ccttgggaag gctgttttcc aggctaaaaa 2580

gaggattctc gaacctcttg gcctggttga gacgccggat aaaacggcgc ctgcggcaaa 2640

aaagaggcct ctagagcaga gtcctcaaga gccagactcc tcgagcggag ttggcaagaa 2700

aggcaaacag cctgccagaa agagactcaa ctttgacgac gaacctggag ccggagacgg 2760

gcctccccca gaaggaccat cttccggagc tatgtctact gagactgaaa tgcgtgcagc 2820

agctggcgga aatggtggcg atgcgggaca aggtgccgag ggagtgggta atgcctccgg 2880

tgattggcat tgcgattcca cttggtcaga gagccacgtc accaccacct caacccgcac 2940

ctgggtcctg ccgacctaca acaaccacct gtacctgcgg ctcggctcga gcaacgccag 3000

cgacaccttc aacggattct ccacccccctg ggatactttt gactttaacc gcttccactg 3060

ccacttctcg ccaagagact ggcaaaggct catcaacaac cactggggac tgcgccccaa 3120

aagcatgcaa gtccgcatct tcaacatcca agttaaggag gtcacgacgt ctaacgggga 3180

gacgaccgta tccaacaacc tcaccagcac ggtccagatc tttgcggaca gcacgtacga 3240

gctcccgtac gtgatggatg caggtcagga gggcagcttg cctcctttcc ccaacgacgt 3300

gttcatggtg cctcagtacg ggtactgcgg actggtaacc ggaggcagct ctcaaaacca 3360

gacagacaga aatgccttct actgtctgga gtactttccc agccagatgc tgagaaccgg 3420

aaacaacttt gagatggtgt acaagtttga aaacgtgccc ttccactcca tgtacgctca 3480

cagccagagc ctggataggc tgatgaaccc gctgctggac cagtacctgt gggagctcca 3540

gtctaccacc tctggaggaa ctctcaacca gggcaattca gccaccaact ttgccaagct 3600

gaccaaaaca aacttttctg gctaccgcaa aaactggctc ccggggccca tgatgaagca 3660

gcagagattc tccaagactg ccagtcaaaa ctacaagatt ccccagggaa gaaacaacag 3720

tctgctccat tatgagacca gaactaccct cgacggaaga tggagcaatt ttgccccggg 3780

aacggccatg gcaaccgcag ccaacgacgc caccgacttc tctcaggccc agctcatctt 3840

tgcggggccc aacatcaccg gcaacaccac cacagatgcc aataacctga tgttcacttc 3900

agaagatgaa cttagggcca ccaacccccg ggacactgac ctgtttggcc acctggcaac 3960

caaccagcaa aacgccacca ccgttcctac cgtagacgac gtggacggag tcggcgtgta 4020

cccgggaatg gtgtggcagg acagagacat ttactaccaa gggcccattt gggccaaaat 4080

```
tccacacacg gatggacact ttcacccgtc tcctctcatt ggcggatttg gactgaaaag      4140

cccgcctcca caaatattca tcaaaaacac tcctgtaccc gccaatcccg caacgacctt      4200

ctctccggcc agaatcaaca gcttcatcac ccagtacagc accggacagg tggctgtcaa      4260

aatagaatgg gaaatccaga aggagcggtc caagagatgg aacccagagg tccagttcac      4320

gtccaactac ggagcacagg actcgcttct ctgggctccc gacaacgccg gagcctacaa      4380

agagcccagg gccattggat cccgatacct caccaaccac ctctagccca attctgttgc      4440

ataccctcaa taaaccgtgt attcgtttca gtaaaatact gcctcttgtg gtcattcggc      4500

gtacaacagc ttacaacaac aacaaaaccc ccttgctaga gagtgtggca ctcccccccc      4560

tgtcgcgttc gctcgttcgc tggctcgatt ggggggggtgg cagctcaaag agctgccaga      4620

cgacggccct ctgggccgtc gcccccccaa tcgagccagc gaacgagcga acgcgacagg      4680

gggggagtg ccac                                                          4694
```

```
<210> 544
<211> 390
<212> PRT
<213> Bovine adeno-associated virus

<400> 544
Met Ala Leu Val Ser Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
1               5                   10                  15


Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
            20                  25                  30


Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
        35                  40                  45


Ile Met Ser Leu Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr
    50                  55                  60


Val Pro Glu Asp Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu
65                  70                  75                  80


Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys
                85                  90                  95


Thr Arg Ala Phe Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110


Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro
        115                 120                 125


Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140


Cys Val Glu Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser
145                 150                 155                 160
```

Lys Val Val Glu Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val
180 185 190

Ile Ile Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe
210 215 220

Glu Leu Met Arg Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225 230 235 240

Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
245 250 255

Thr His Glu Phe Met Val Pro Lys Lys Val Ala Gly Thr Glu Arg Ala
260 265 270

Glu Thr Ser Arg Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr
275 280 285

Lys Ser Pro Glu Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro
290 295 300

Arg Ser Ser Asp Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn
305 310 315 320

Trp Ser Ser Arg Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp
325 330 335

Ser Val Thr Gly Glu Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
340 345 350

Asn Gly Cys Ile Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala
355 360 365

Val Pro Pro Trp Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp
370 375 380

Asp Cys Asn Lys Glu Gln
385 390

<210> 545
<211> 610
<212> PRT
<213> Bovine adeno-associated virus

<400> 545

```
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1               5                   10                  15

Glu His Leu Pro Gly Ile Ser Asp Asn Phe Val Asp Trp Val Thr Gly
            20                  25                  30

Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Ile
        35                  40                  45

Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
    50                  55                  60

Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65                  70                  75                  80

Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
                85                  90                  95

Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110

Ala Gln Leu Val Lys Val Val Phe Gln Asn Ile Glu Pro Arg Ile Asn
        115                 120                 125

Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
    130                 135                 140

Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160

Glu Leu Gln Trp Ala Trp Thr Asn Leu Glu Glu Tyr Lys Leu Ala Ala
                165                 170                 175

Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Gln Leu Glu
            180                 185                 190

Ser Ser Gln Arg Ser Gln Glu Ala Ser Ser Gln Arg Asp Val Ser Ala
        195                 200                 205

Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
    210                 215                 220

Ser Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225                 230                 235                 240

Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
                245                 250                 255

Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys Ile Met Ser Leu
            260                 265                 270
```

```
Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr Val Pro Glu Asp
        275                 280                 285

Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu Asn Gly Tyr Asp
    290                 295                 300

Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys Thr Arg Ala Phe
305                 310                 315                 320

Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
                325                 330                 335

Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro Phe Tyr Gly Cys
            340                 345                 350

Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Glu Lys
        355                 360                 365

Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser Lys Val Val Glu
    370                 375                 380

Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg Val Asp Gln Lys
385                 390                 395                 400

Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val Ile Ile Thr Ser
                405                 410                 415

Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
            420                 425                 430

His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe Glu Leu Met Arg
        435                 440                 445

Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
    450                 455                 460

Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465                 470                 475                 480

Met Val Pro Lys Lys Val Ala Gly Thr Glu Arg Ala Glu Thr Ser Arg
                485                 490                 495

Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr Lys Ser Pro Glu
            500                 505                 510

Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro Arg Ser Ser Asp
        515                 520                 525

Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn Trp Ser Ser Arg
    530                 535                 540
```

```
Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp Ser Val Thr Gly
545                 550                 555                 560


Glu Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
                565                 570                 575


Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala Val Pro Pro Trp
            580                 585                 590


Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp Asp Cys Asn Lys
        595                 600                 605


Glu Gln
    610


<210> 546
<211> 538
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 546
Met Arg Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala
1               5                   10                  15


Glu Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
            20                  25                  30


Ser Glu Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro
        35                  40                  45


Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Ser Ser Asn Ala Ser
    50                  55                  60


Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
65                  70                  75                  80


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
                85                  90                  95


Asn His Trp Gly Leu Arg Pro Lys Ser Met Gln Val Arg Ile Phe Asn
            100                 105                 110


Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ser
        115                 120                 125


Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu
    130                 135                 140


Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe
145                 150                 155                 160
```

```
Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val
                165                 170                 175

Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys
            180                 185                 190

Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu
        195                 200                 205

Met Val Tyr Lys Phe Glu Asn Val Pro Phe His Ser Met Tyr Ala His
    210                 215                 220

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp Gln Tyr Leu
225                 230                 235                 240

Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn
                245                 250                 255

Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys Thr Asn Phe Ser Gly Tyr
            260                 265                 270

Arg Lys Asn Trp Leu Pro Gly Pro Met Met Lys Gln Gln Arg Phe Ser
        275                 280                 285

Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Gln Gly Arg Asn Asn Ser
    290                 295                 300

Leu Leu His Tyr Glu Thr Arg Thr Thr Leu Asp Gly Arg Trp Ser Asn
305                 310                 315                 320

Phe Ala Pro Gly Thr Ala Met Ala Thr Ala Ala Asn Asp Ala Thr Asp
                325                 330                 335

Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly Pro Asn Ile Thr Gly Asn
            340                 345                 350

Thr Thr Thr Asp Ala Asn Asn Leu Met Phe Thr Ser Glu Asp Glu Leu
        355                 360                 365

Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu Phe Gly His Leu Ala Thr
    370                 375                 380

Asn Gln Gln Asn Ala Thr Thr Val Pro Thr Val Asp Asp Val Asp Gly
385                 390                 395                 400

Val Gly Val Tyr Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Tyr
                405                 410                 415

Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His
            420                 425                 430
```

```
Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln
        435                 440                 445


Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe
    450                 455                 460


Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln
465                 470                 475                 480


Val Ala Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg
                485                 490                 495


Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser
            500                 505                 510


Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala
        515                 520                 525


Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
    530                 535


<210> 547
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 547
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1               5                   10                  15


Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
    50                  55                  60


Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110
```

```
Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125


Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
    130                 135                 140


Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175


Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190


Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205


Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220


His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255


Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270


Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285


Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300


Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320


Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val His Ile Phe
                325                 330                 335


Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350


Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365


Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380
```

```
Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400


Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415


His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430


Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445


Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Asn
    450                 455                 460


Lys Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480


Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495


Gln Gly Gly Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510


Asp Arg Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525


Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530                 535                 540


Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560


Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575


Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590


Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675                 680                 685


Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700


Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705                 710                 715                 720


Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730                 735


<210> 548
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 548
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1               5                   10                  15


Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
    50                  55                  60


Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125


Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
    130                 135                 140


Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160
```

```
Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175

Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190

Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205

Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255

Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285

Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300

Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320

Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
                325                 330                 335

Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350

Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365

Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430
```

```
Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445

Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys
    450                 455                 460

Thr Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480

Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495

Gln Gly Arg Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510

Asp Gly Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525

Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530                 535                 540

Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560

Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575

Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590

Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700
```

Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705 710 715 720

Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730 735

<210> 549
<211> 736
<212> PRT
<213> Bovine adeno-associated virus

<400> 549
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1 5 10 15

Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
50 55 60

Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
130 135 140

Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
165 170 175

Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
180 185 190

Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
195 200 205

```
Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220


His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255


Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270


Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285


Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300


Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320


Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
                325                 330                 335


Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350


Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365


Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380


Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400


Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415


His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430


Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445


Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys
    450                 455                 460


Thr Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480
```

```
Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495


Gln Gly Arg Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510


Asp Gly Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525


Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530                 535                 540


Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560


Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575


Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590


Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675                 680                 685


Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700


Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705                 710                 715                 720


Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730                 735


<210> 550
<211> 600
<212> PRT
<213> Bovine adeno-associated virus
```

```
<400> 550
Thr Ala Pro Ala Ala Lys Lys Arg Pro Leu Glu Gln Ser Pro Gln Glu
1               5                   10                  15


Pro Asp Ser Ser Ser Gly Val Gly Lys Lys Gly Lys Gln Pro Ala Arg
            20                  25                  30


Lys Arg Leu Asn Phe Asp Asp Glu Pro Gly Ala Gly Asp Gly Pro Pro
        35                  40                  45


Pro Glu Gly Pro Ser Ser Gly Ala Met Ser Thr Glu Thr Glu Met Arg
    50                  55                  60


Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala Glu Gly
65                  70                  75                  80


Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu
                85                  90                  95


Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr
            100                 105                 110


Asn Asn His Leu Tyr Leu Arg Leu Gly Ser Ser Asn Ala Ser Asp Thr
        115                 120                 125


Phe Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
    130                 135                 140


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn His
145                 150                 155                 160


Trp Gly Leu Arg Pro Lys Ser Met Gln Val Arg Ile Phe Asn Ile Gln
                165                 170                 175


Val Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ser Asn Asn
            180                 185                 190


Leu Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu Leu Pro
        195                 200                 205


Tyr Val Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe Pro Asn
    210                 215                 220


Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val Thr Gly
225                 230                 235                 240


Gly Ser Ser Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu
                245                 250                 255


Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Met Val
            260                 265                 270
```

```
Tyr Lys Phe Glu Asn Val Pro Phe His Ser Met Tyr Ala His Ser Gln
        275                 280                 285

Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp Glu
    290                 295                 300

Leu Gln Ser Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn Ser Ala
305                 310                 315                 320

Thr Asn Phe Ala Lys Leu Thr Lys Thr Asn Phe Ser Gly Tyr Arg Lys
                325                 330                 335

Asn Trp Leu Pro Gly Pro Met Met Lys Gln Gln Arg Phe Ser Lys Thr
            340                 345                 350

Ala Ser Gln Asn Tyr Lys Ile Pro Gln Gly Arg Asn Asn Ser Leu Leu
        355                 360                 365

His Tyr Glu Thr Arg Thr Thr Leu Asp Gly Arg Trp Ser Asn Phe Ala
    370                 375                 380

Pro Gly Thr Ala Met Ala Thr Ala Ala Asn Asp Ala Thr Asp Phe Ser
385                 390                 395                 400

Gln Ala Gln Leu Ile Phe Ala Gly Pro Asn Ile Thr Gly Asn Thr Thr
                405                 410                 415

Thr Asp Ala Asn Asn Leu Met Phe Thr Ser Glu Asp Glu Leu Arg Ala
            420                 425                 430

Thr Asn Pro Arg Asp Thr Asp Leu Phe Gly His Leu Ala Thr Asn Gln
        435                 440                 445

Gln Asn Ala Thr Thr Val Pro Thr Val Asp Asp Val Asp Gly Val Gly
    450                 455                 460

Val Tyr Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Tyr Gln Gly
465                 470                 475                 480

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser
                485                 490                 495

Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln Ile Phe
            500                 505                 510

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe Ser Pro
        515                 520                 525

Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ala
    530                 535                 540
```

```
Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg Trp Asn
545                 550                 555                 560


Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser Leu Leu
                565                 570                 575


Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala Ile Gly
            580                 585                 590


Ser Arg Tyr Leu Thr Asn His Leu
        595                 600


<210> 551
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 551
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga        60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac       120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac       180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac       240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt       300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct       420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctcctc gggcatcggc       480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag       540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct       600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga       660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc        720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc       780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc       840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga       900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc       960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc      1020

acggtccagg tcttcacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac      1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta      1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt      1200
```

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gtttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ttggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 552
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 552
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270


Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460


Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480


Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495


Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510


Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525


Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540


Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560


Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590


Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640
```

```
Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735


Leu



<210> 553
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 553
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
```

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
435 440 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
450 455 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
500 505 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
515 520 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
530 535 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545 550 555 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
580 585 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr

```
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 554
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 554
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160
```

```
Glu Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445


Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460


Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495


Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525


Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540


Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560


Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590


Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 555
<211> 2181
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 555
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcacaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgcacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact attggggctt cagaccccgg 900

tctctcagag tcaaaatctt caacatccaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccaa 1020

ctcccgtacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc cccgcaggtc 1080

tttacgctgc cgcagtacgg ctacgcgacg ctgaaccgag acaacggaga caacccgaca 1140

gagcggagca gcttcttttg cctagagtac tttcccagca agatgctgag gacgggcaac 1200

aactttgagt ttacctacag ctttgaagag gtgcccttcc actgcagctt cgccccgagc 1260

cagaacctct ttaagctggc caacccgctg gtggaccagt acctgtaccg cttcgtgagc 1320

acctcggcca cgggcgccat ccagttccaa aagaacctgg cgggcagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacac gagctctggg 1440

gtcagcagca ccaacagagt cagcgtcaac aacttttccg tctcaaaccg gatgaacctg 1500 gagggggcca gctaccaagt gaaccccag cccaacggga tgacaaacac gctccaaggc 1560

agcaaccgct acgcgctgga aaacaccatg atcttcaacg ctcaaaacgc cacgccggga 1620

actacctcgg tgtacccaga ggacaatcta ctgctgacca gcgagagcga gactcagccc 1680

gtcaaccggg tggcttacaa cacgggcggt cagatggcca ccaacgccca gaacgccacc 1740

acggctccca cggtcgggac ctacaacctc caggaagtgc ttcctggcag cgtatggatg 1800

gagagggacg tgtacctcca aggacccatc tgggccaaga tcccagagac gggggcgcac 1860

tttcacccct ctccggccat gggcggattc ggactcaaac acccgccgcc catgatgctc 1920

atcaaaaaca cgccggtgcc cggcaacatc accagcttct cggacgtgcc cgtcagcagc 1980

ttcatcaccc agtacagcac cgggcaggtc accgtggaga tggaatggga gctcaaaaag 2040

gaaaactcca agaggtggaa cccagagatc cagtacacca acaactacaa cgacccccag 2100

tttgtggact ttgctccaga cggctccggc gaatacagaa ccaccagagc catcggaacc 2160

cgatacctca cccgacccct t 2181

<210> 556
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 556
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335


Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350


Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365


Ala Thr Leu Asn Arg Asp Asn Gly Asp Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380


Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400
```

```
Asn Phe Glu Phe Thr Tyr Ser Phe Glu Glu Val Pro Phe His Cys Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Ser Ala Thr Gly Ala Ile Gln
        435                 440                 445

Phe Gln Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Thr Ser Ser Gly
465                 470                 475                 480

Ser Ser Thr Asn Arg Val Ser Val Asn Asn Phe Ser Val Ser Asn Arg
                485                 490                 495

Met Asn Leu Glu Gly Ala Ser Tyr Gln Val Asn Pro Gln Pro Asn Gly
            500                 505                 510

Met Thr Asn Thr Leu Gln Gly Ser Asn Arg Tyr Ala Leu Glu Asn Thr
        515                 520                 525

Met Ile Phe Asn Ala Gln Asn Ala Thr Pro Gly Thr Thr Ser Val Tyr
    530                 535                 540

Pro Glu Asp Asn Leu Leu Leu Thr Ser Glu Ser Glu Thr Gln Pro Val
545                 550                 555                 560

Asn Arg Val Ala Tyr Asn Thr Gly Gly Gln Met Ala Thr Asn Ala Gln
                565                 570                 575

Asn Ala Thr Thr Ala Pro Thr Val Gly Thr Tyr Asn Leu Gln Glu Val
            580                 585                 590

Leu Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro
        595                 600                 605

Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro
    610                 615                 620

Ala Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile
625                 630                 635                 640

Lys Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro
                645                 650                 655

Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu
            660                 665                 670
```

Met Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
        675   680   685

Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala
    690   695   700

Pro Asp Gly Ser Gly Glu Tyr Arg Thr Thr Arg Ala Ile Gly Thr Arg
705   710   715   720

Tyr Leu Thr Arg Pro Leu
                725

<210> 557
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 557
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

```
Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 558
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 558
acggctccga ccggagacaa gcggaaaggc gaagacgaac ctcgtttgcc cgacacttct 60

tcacagactc ccaagaaaaa caagaagcct cgcaaggaaa gaccttccgg cggggcagaa 120

gatccgggcg aaggcacctc ttccaacgct ggagcagcag cacccgcctc tagtgtggga 180

tcatctatca tggctgaagg aggtggcggc ccagtgggcg atgcaggcca gggtgccgat 240

ggagtgggca attcctccgg aaattggcat tgcgattccc aatggctgga aaacggagtc 300

gtcactcgaa ccacccgaac ctgggtcttg cccagctaca acaaccacct gtacaaacga 360

atccaaggac ccagcggagg cgacaacaac aacaaattct ttggattcag caccccctgg 420

ggatactttg actacaatcg attccactgc cacttttccc cgcgagactg gcaacgactc 480

atcaacaaca actggggcat ccgtcccaaa gcgatgcgct ttagactctt taacatccag 540

gttaaagagg tcacggtcca agacttcaac accaccatcg gcaacaacct caccagtacg 600

gtccaggtct ttgcggacaa ggactaccaa ctgccgtacg tcctcggatc ggctaccgaa 660

ggcaccttcc cgccgttccc agcggatatc tacacgatcc cgcagtacgg gtactgcacg 720

ctaaactaca acaacgaggc ggtggatcgt tcggccttct actgtctgga ctactttccc 780

tcagacatgc tgcggacagg aaataacttt gagtttactt acaccttcga ggacgttcct 840

ttccatagca tgtttgccca caaccagacg ctagaccggc tgatgaatcc cctcgtggat 900

cagtacctct gggctttcag ctccgtcagc caagcaggct catctggacg agctcttcat 960

tactcgcggg cgactaaaac caacatggcg gctcaatata ggaactggtt acctgggcct 1020

ttcttccgtg atcagcaaat ctttacgggc gctagcaaca tcactaaaaa taacgtcttt 1080

agcgtttggg aaaaaggcaa gcaatgggaa ctcgacaatc ggaccaacct aatgcagccc 1140

ggtcctgcgg cagcgaccac ctttagcgga gaacctgacc gtcaagccat gcaaaacacg 1200

ctggctttta gcaggaccgt ctacgatcaa acgaccgcca cgaccgatcg taaccagata 1260

ctcatcacca acgaagacga aatcagaccc accaactcgg tcggtatcga cgcgtgggga 1320

gcagttccca ccaacaacca gtcgatcgtg acccccggca ctcgcgcggc cgtcaacaat 1380

caaggggcgc ttcccgggat ggtgtggcaa aacagagaca tttaccctac agggacccat 1440

ttggccaaaa ttcccgacac tgacaatcac ttccatccgt ccccgcttat tgggcggttt 1500

ggctgcaagc atccccctcc ccagattttc attaaaaaca cacccgtccc tgccaaccct 1560 tcggaaacgt tccagacggc caaagtggcc tccttcatca accagtactc gaccggacag 1620

tgcaccgtcg aaatcttttg ggaactcaag aaggaaacct ccaagcgctg gaaccccgaa 1680

atccagttca cctccaactt tggcaacgcg gccgacatcc agtttgccgt ctccgacacg 1740

ggatcctatt ccgaacctcg tcccatcggt acccgttacc ttaccaaacc tctgtaa 1797

<210> 559
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 559
atgaggtcgt actacgaggt catcgttcag ctgcccaacg acgtcgagag tcaggtacct 60

ggaatctccg attcgttcgt caactggatt acgtcgcgag aatggacgtt gcctgaggac 120

gccgattggg atttggacca ggtcgatcaa gttcaactga cgctcggcga caaaatccaa 180

cgggagattc gaactcattg gggacgatg gccaaagaac cggactttca ctattttatc 240

caactggaac aaggtgaggt gttctttcat ttacacgtcc tgctggaaac gtgttccgta 300

aagccgatgg tactcggaag atatatccga catattcaac aaaaaattgt gagtaaagtc 360

tactgcgcca cgagcctacg atggaaggat ggatgcgtgg tgaccaagac caaaaatttc 420

gggggcgcga acaaggtccg ggccgagtcg tatattcccg cctacctgat cccgaaacag 480

caaccggaag tgcagtgggc gtggactaac gtgcccgagt atataaaagc gtgcttgcac 540

cgagaactgc gtgccagtct cgcgcgactt cacttcgagg aggcgggcgt ctcgcaatcc 600

aaggaaaatc tcgcgagaac tgcagacggc gctcccgtga tgccgacccg cgtcagcaaa 660

cgctacatgg agctcgtgga ttggctcgtg gagaagggga tcaccaccga gaaggaatgg 720

ctgctggaaa acagagaaag ctttcggagc tttcaggcct cgagcaactc ggcgcgtcag 780

atcaagacgg ccctgcaagg cgccattcag gagatgcttc tgaccaagac ggcggaggac 840

tacctcgtcg gaaaggatcc cgtctcggac gacgacatcc gtcagaaccg catctacaag 900

attctggaac tgaaccacta cgacccagcg tacgtgggga gtattttggt cgggtggtgc 960

cagaagaaat ggggcaagcg aaacacgctg tggctgttcg gacatgcgac caccggcaag 1020

accaacatcg cggaggctat tgcccatgct gtgccgttct atggatgcgt taactggacc 1080

aacgagaact ttccgttcaa cgactgcgtc gaaaaaatga ttatctggtg ggaggagggc 1140

aaaatgaccg ccaaagtggt ggaaacagcc aaggcgattc tgggaggatc tcgggtgaga 1200

gtggaccaaa aatgcaaagc ttcggttccg atcgaaccga cgccggtcat tattaccagt 1260

aacaccaaca tgtgttatgt catcgacggg aacacgacca cgttcgagca taagcagccg 1320

ttggaggaca ggatgtttaa gctcgaattg ctgactcggt tgcctgatga ctttggtaag 1380

gtgaccaaac aggaggtgcg tcaattcttc aggtggtctc aggatcacct gacccctgtg 1440

atcccagaat tcctagtgcg gaaggcggag tctcgcaaaa gacccgcccc ttccggggaa 1500 ggctatataa gcccgacaaa gcggcccgcg ctcgcagagc agcagcaggc gtcggagagc 1560

gcggacccgg ttcccaccag gtatcgtatc aaatgctcga aacattgcgg tatggataaa 1620

atgttgtttc cttgccaaat ttgtgaatcg atgaacagag atattaatat ttgtgctatt 1680

cataaaacga ccgactgtaa agagtgtttc cccgactacg gggataaaga tgatgtagaa 1740

ctacccccct gtacagaaca caacgtgtct cgttgttatc aatgtcattc gggcgaattg 1800

tatcgcgtga cttcggactc tgacgagaaa cctgcccccg agagtgatga aggcaccgag 1860

ccatcctatg ctccctgcac gattcaccac ctgatgggca agagtcacgg gttagtcact 1920

tgcgcggcgt gtcggttgaa aaatagtacg ttgcatgatg acttggatga cggtgatctc 1980

gaacaataa 1989

<210> 560
<211> 1626
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 560
atgaggtcgt actacgaggt catcgttcag ctgcccaacg acgtcgagag tcaggtacct 60

ggaatctccg attcgttcgt caactggatt acgtcgcgag aatggacgtt gcctgaggac 120

gccgattggg atttggacca ggtcgatcaa gttcaactga cgctcggcga caaaatccaa 180

cgggagattc gaactcattg ggggacgatg gccaaagaac cggactttca ctattttatc 240

caactggaac aaggtgaggt gttctttcat ttacacgtcc tgctggaaac gtgttccgta 300

aagccgatgg tactcggaag atatatccga catattcaac aaaaaattgt gagtaaagtc 360

tactgcgcca cgagcctacg atggaaggat ggatgcgtgg tgaccaagac caaaaatttc 420

gggggcgcga acaaggtccg ggccgagtcg tatattcccg cctacctgat cccgaaacag 480

caaccggaag tgcagtgggc gtggactaac gtgcccgagt atataaaagc gtgcttgcac 540

cgagaactgc gtgccagtct cgcgcgactt cacttcgagg aggcgggcgt ctcgcaatcc 600

aaggaaaatc tcgcgagaac tgcagacggc gctcccgtga tgccgacccg cgtcagcaaa 660

cgctacatgg agctcgtgga ttggctcgtg gagaagggga tcaccaccga gaaggaatgg 720

ctgctggaaa acagagaaag ctttcggagc tttcaggcct cgagcaactc ggcgcgtcag 780

atcaagacgg ccctgcaagg cgccattcag gagatgcttc tgaccaagac ggcggaggac 840

tacctcgtcg gaaaggatcc cgtctcggac gacgacatcc gtcagaaccg catctacaag 900

attctggaac tgaaccacta cgacccagcg tacgtgggga gtattttggt cgggtggtgc 960

cagaagaaat ggggcaagcg aaacacgctg tggctgttcg gacatgcgac caccggcaag 1020

accaacatcg cggaggctat tgcccatgct gtgccgttct atggatgcgt taactggacc 1080

aacgagaact ttccgttcaa cgactgcgtc gaaaaaatga ttatctggtg ggaggagggc 1140 aaaatgaccg ccaaagtggt ggaaacagcc aaggcgattc tgggaggatc tcgggtgaga 1200

gtggaccaaa aatgcaaagc ttcggttccg atcgaaccga cgccggtcat tattaccagt 1260

aacaccaaca tgtgttatgt catcgacggg aacacgacca cgttcgagca taagcagccg 1320

ttggaggaca ggatgtttaa gctcgaattg ctgactcggt tgcctgatga ctttggtaag 1380

gtgaccaaac aggaggtgcg tcaattcttc aggtggtctc aggatcacct gacccctgtg 1440

atcccagaat tcctagtgcg gaaggcggag tctcgcaaaa gacccgcccc ttccggggaa 1500

ggctatataa gcccgacaaa gcggcccgcg ctcgcagagc agcagcaggc gtcggagagc 1560

gcggacccgg ttcccaccag attggttgga gcggttggtc aaaaagggag tgaatgctgc 1620

agctga 1626

<210> 561
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 561
atggagctcg tggattggct cgtggagaag gggatcacca ccgagaagga atggctgctg 60

gaaaacagag aaagctttcg gagctttcag gcctcgagca actcggcgcg tcagatcaag 120

acggccctgc aaggcgccat tcaggagatg cttctgacca agacggcgga ggactacctc 180

gtcggaaagg atcccgtctc ggacgacgac atccgtcaga accgcatcta caagattctg 240

gaactgaacc actacgaccc agcgtacgtg gggagtattt tggtcgggtg gtgccagaag 300

aaatggggca agcgaaacac gctgtggctg ttcggacatg cgaccaccgg caagaccaac 360

atcgcggagg ctattgccca tgctgtgccg ttctatggat gcgttaactg gaccaacgag 420

aactttccgt tcaacgactg cgtcgaaaaa atgattatct ggtgggagga gggcaaaatg 480

accgccaaag tggtggaaac agccaaggcg attctgggag gatctcgggt gagagtggac 540

caaaaatgca aagcttcggt tccgatcgaa ccgacgccgg tcattattac cagtaacacc 600

aacatgtgtt atgtcatcga cgggaacacg accacgttcg agcataagca gccgttggag 660

gacaggatgt ttaagctcga attgctgact cggttgcctg atgactttgg taaggtgacc 720

aaacaggagg tgcgtcaatt cttcaggtgg tctcaggatc acctgacccc tgtgatccca 780

gaattcctag tgcggaaggc ggagtctcgc aaaagacccg ccccttccgg ggaaggctat 840

ataagcccga caaagcggcc cgcgctcgca gagcagcagc aggcgtcgga gagcgcggac 900

ccggttccca ccaggtatcg tatcaaatgc tcgaaacatt gcggtatgga taaaatgttg 960

tttccttgcc aaatttgtga atcgatgaac agagatatta atatttgtgc tattcataaa 1020

acgaccgact gtaaagagtg tttccccgac tacggggata aagatgatgt agaactaccc 1080

ccctgtacag aacacaacgt gtctcgttgt tatcaatgtc attcgggcga attgtatcgc 1140

gtgacttcgg actctgacga gaaacctgcc cccgagagtg atgaaggcac cgagccatcc 1200 tatgctccct gcacgattca ccacctgatg ggcaagagtc acgggttagt cacttgcgcg 1260

gcgtgtcggt tgaaaaatag tacgttgcat gatgacttgg atgacggtga tctcgaacaa 1320

taa 1323

<210> 562
<211> 960
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 562
atggagctcg tggattggct cgtggagaag gggatcacca ccgagaagga atggctgctg 60

gaaaacagag aaagctttcg gagctttcag gcctcgagca actcggcgcg tcagatcaag 120

acggccctgc aaggcgccat tcaggagatg cttctgacca agacggcgga ggactacctc 180

gtcggaaagg atcccgtctc ggacgacgac atccgtcaga accgcatcta caagattctg 240

gaactgaacc actacgaccc agcgtacgtg ggagtattt tggtcgggtg gtgccagaag 300

aaatggggca agcgaaacac gctgtggctg ttcggacatg cgaccaccgg caagaccaac 360

atcgcggagg ctattgccca tgctgtgccg ttctatggat gcgttaactg gaccaacgag 420

aactttccgt tcaacgactg cgtcgaaaaa atgattatct ggtgggagga gggcaaaatg 480

accgccaaag tggtggaaac agccaaggcg attctgggag gatctcgggt gagagtggac 540

caaaaatgca aagcttcggt tccgatcgaa ccgacgccgg tcattattac cagtaacacc 600

aacatgtgtt atgtcatcga cgggaacacg accacgttcg agcataagca gccgttggag 660

gacaggatgt ttaagctcga attgctgact cggttgcctg atgactttgg taaggtgacc 720

aaacaggagg tgcgtcaatt cttcaggtgg tctcaggatc acctgacccc tgtgatccca 780

gaattcctag tgcggaaggc ggagtctcgc aaaagacccg ccccttccgg ggaaggctat 840

ataagcccga caaagcggcc cgcgctcgca gagcagcagc aggcgtcgga gagcgcggac 900

ccggttccca ccagattggt tggagcggtt ggtcaaaaag ggagtgaatg ctgcagctga 960

<210> 563
<211> 1608
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 563
atggctgaag gaggtggcgg cccagtgggc gatgcaggcc agggtgccga tggagtgggc 60

aattcctccg gaaattggca ttgcgattcc caatggctgg aaaacggagt cgtcactcga 120

accacccgaa cctgggtctt gcccagctac aacaaccacc tgtacaaacg aatccaagga 180

cccagcggag gcgacaacaa caacaaattc tttggattca gcaccccctg ggggatacttt 240 gactacaatc gattccactg ccacttttcc ccgcgagact ggcaacgact catcaacaac 300

aactggggca tccgtcccaa agcgatgcgc tttagactct ttaacatcca ggttaaagag 360

gtcacggtcc aagacttcaa caccaccatc ggcaacaacc tcaccagtac ggtccaggtc 420

tttgcggaca aggactacca actgccgtac gtcctcggat cggctaccga aggcaccttc 480

ccgccgttcc cagcggatat ctacacgatc ccgcagtacg ggtactgcac gctaaactac 540

aacaacgagg cggtggatcg ttcggccttc tactgtctgg actactttcc ctcagacatg 600

ctgcggacag gaaataactt tgagtttact tacaccttcg aggacgttcc tttccatagc 660

atgtttgccc acaaccagac gctagaccgg ctgatgaatc ccctcgtgga tcagtacctc 720

tgggctttca gctccgtcag ccaagcaggc tcatctggac gagctcttca ttactcgcgg 780

gcgactaaaa ccaacatggc ggctcaatat aggaactggt tacctgggcc tttcttccgt 840

gatcagcaaa tctttacggg cgctagcaac atcactaaaa ataacgtctt tagcgtttgg 900

gaaaaaggca agcaatggga actcgacaat cggaccaacc taatgcagcc cggtcctgcg 960

gcagcgacca cctttagcgg agaacctgac cgtcaagcca tgcaaaacac gctggctttt 1020

agcaggaccg tctacgatca aacgaccgcc acgaccgatc gtaaccagat actcatcacc 1080

aacgaagacg aaatcagacc caccaactcg gtcggtatcg acgcgtgggg agcagttccc 1140

accaacaacc agtcgatcgt gacccccggc actcgcgcgg ccgtcaacaa tcaaggggcg 1200

cttcccggga tggtgtggca aaacagagac atttacccta cagggaccca tttggccaaa 1260

attcccgaca ctgacaatca cttccatccg tccccgctta ttgggcggtt tggctgcaag 1320

catccccctc cccagatttt cattaaaaac acacccgtcc ctgccaaccc ttcggaaacg 1380

ttccagacgg ccaaagtggc ctccttcatc aaccagtact cgaccggaca gtgcaccgtc 1440

gaaatctttt gggaactcaa gaaggaaacc tccaagcgct ggaaccccga aatccagttc 1500

acctccaact ttggcaacgc ggccgacatc cagtttgccg tctccgacac gggatcctat 1560

tccgaacctc gtcccatcgg tacccgttac cttaccaaac ctctgtaa 1608

<210> 564
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 564
atgtctctca tttctgatgc gattccagat tggttggagc ggttggtcaa aaagggagtg 60

aatgctgcag ctgatttcta ccatttggaa agcggtcctc ctcgtcctaa ggcaaatcag 120

caaactcaag aatctcttga aaaggacgat tcgagaggtc tcgtgttccc aggctacaat 180

tatctaggcc ctttcaacgg tctagataaa ggagaacccg tcaacgaggc agacgctgcc 240

gccttagaac acgacaaggc ttacgacctc gaaatcaagg acgggcacaa cccgtacttt 300 gagtacaacg aggccgacag acgtttccag gaacgtctca aagacgatac ctcctttgga 360

ggcaatttag gtaaagccat cttccaggcc aaaaagaggg ttctcgaacc ctttggtctg 420

gtggaagact caaagacggc tccgaccgga gacaagcgga aaggcgaaga cgaacctcgt 480

ttgcccgaca cttcttcaca gactcccaag aaaaacaaga agcctcgcaa ggaaagacct 540

tccggcgggg cagaagatcc gggcgaaggc acctcttcca acgctggagc agcagcaccc 600

gcctctagtg tgggatcatc tatcatggct gaaggaggtg gcggcccagt gggcgatgca 660

ggccagggtg ccgatggagt gggcaattcc tccggaaatt ggcattgcga ttcccaatgg 720

ctggaaaacg gagtcgtcac tcgaaccacc cgaacctggg tcttgcccag ctacaacaac 780

cacctgtaca aacgaatcca aggacccagc ggaggcgaca acaacaacaa attctttgga 840

ttcagcaccc cctggggata ctttgactac aatcgattcc actgccactt ttccccgcga 900

gactggcaac gactcatcaa caacaactgg ggcatccgtc ccaaagcgat gcgctttaga 960

ctctttaaca tccaggttaa agaggtcacg gtccaagact tcaacaccac catcggcaac 1020

aacctcacca gtacggtcca ggtctttgcg gacaaggact accaactgcc gtacgtcctc 1080

ggatcggcta ccgaaggcac cttcccgccg ttcccagcgg atatctacac gatcccgcag 1140

tacgggtact gcacgctaaa ctacaacaac gaggcggtgg atcgttcggc cttctactgt 1200

ctggactact ttccctcaga catgctgcgg acaggaaata actttgagtt tacttacacc 1260

ttcgaggacg ttcctttcca tagcatgttt gcccacaacc agacgctaga ccggctgatg 1320

aatcccctcg tggatcagta cctctgggct ttcagctccg tcagccaagc aggctcatct 1380

ggacgagctc ttcattactc gcgggcgact aaaaccaaca tggcggctca atataggaac 1440

tggttacctg ggcctttctt ccgtgatcag caaatcttta cgggcgctag caacatcact 1500

aaaaataacg tctttagcgt ttgggaaaaa ggcaagcaat gggaactcga caatcggacc 1560

aacctaatgc agcccggtcc tgcggcagcg accaccttta gcggagaacc tgaccgtcaa 1620

gccatgcaaa acacgctggc ttttagcagg accgtctacg atcaaacgac cgccacgacc 1680

gatcgtaacc agatactcat caccaacgaa gacgaaatca gacccaccaa ctcggtcggt 1740

atcgacgcgt ggggagcagt tcccaccaac aaccagtcga tcgtgacccc cggcactcgc 1800

gcggccgtca acaatcaagg ggcgcttccc gggatggtgt ggcaaaacag agacatttac 1860

cctacaggga cccatttggc caaaattccc gacactgaca atcacttcca tccgtccccg 1920

cttattgggc ggtttggctg caagcatccc cctccccaga ttttcattaa aaacacaccc 1980

gtccctgcca acccttcgga aacgttccag acggccaaag tggcctcctt catcaaccag 2040

tactcgaccg gacagtgcac cgtcgaaatc ttttgggaac tcaagaagga aacctccaag 2100

cgctggaacc ccgaaatcca gttcacctcc aactttggca acgcggccga catccagttt 2160

gccgtctccg acacgggatc ctattccgaa cctcgtccca tcggtacccg ttaccttacc 2220

aaacctctgt aa 2232

<210> 565

```
<211> 535
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 565
Met Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala
1               5                   10                  15

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp
            20                  25                  30

Leu Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro
        35                  40                  45

Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly
    50                  55                  60

Asp Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe
65                  70                  75                  80

Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
                85                  90                  95

Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg
            100                 105                 110

Leu Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Phe Asn Thr
        115                 120                 125

Thr Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys
    130                 135                 140

Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Phe
145                 150                 155                 160

Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys
                165                 170                 175

Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys
            180                 185                 190

Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu
        195                 200                 205

Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His
    210                 215                 220

Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu
225                 230                 235                 240
```

```
Trp Ala Phe Ser Ser Val Ser Gln Ala Gly Ser Ser Gly Arg Ala Leu
                245                 250                 255

His Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn
            260                 265                 270

Trp Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala
        275                 280                 285

Ser Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys
    290                 295                 300

Gln Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala
305                 310                 315                 320

Ala Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn
                325                 330                 335

Thr Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr
            340                 345                 350

Asp Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr
        355                 360                 365

Asn Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln
    370                 375                 380

Ser Ile Val Thr Pro Gly Thr Arg Ala Ala Val Asn Asn Gln Gly Ala
385                 390                 395                 400

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr
                405                 410                 415

His Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro
            420                 425                 430

Leu Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile
        435                 440                 445

Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala
    450                 455                 460

Lys Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val
465                 470                 475                 480

Glu Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro
                485                 490                 495

Glu Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe
            500                 505                 510
```

```
Ala Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr
        515                 520                 525


Arg Tyr Leu Thr Lys Pro Leu
    530                 535


<210> 566
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 566
Met Glu Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys
1               5                   10                  15


Glu Trp Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser
            20                  25                  30


Ser Asn Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln
        35                  40                  45


Glu Met Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp
    50                  55                  60


Pro Val Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu
65                  70                  75                  80


Glu Leu Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly
                85                  90                  95


Trp Cys Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly
            100                 105                 110


His Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala
        115                 120                 125


Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe
    130                 135                 140


Asn Asp Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met
145                 150                 155                 160


Thr Ala Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg
                165                 170                 175


Val Arg Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr
            180                 185                 190


Pro Val Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly
```

```
        195                 200                 205


Asn Thr Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe
    210                 215                 220


Lys Leu Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr
225                 230                 235                 240


Lys Gln Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr
                245                 250                 255


Pro Val Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg
            260                 265                 270


Pro Ala Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala
        275                 280                 285


Leu Ala Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr
    290                 295                 300


Arg Tyr Arg Ile Lys Cys Ser Lys His Cys Gly Met Asp Lys Met Leu
305                 310                 315                 320


Phe Pro Cys Gln Ile Cys Glu Ser Met Asn Arg Asp Ile Asn Ile Cys
                325                 330                 335


Ala Ile His Lys Thr Thr Asp Cys Lys Glu Cys Phe Pro Asp Tyr Gly
            340                 345                 350


Asp Lys Asp Asp Val Glu Leu Pro Pro Cys Thr Glu His Asn Val Ser
        355                 360                 365


Arg Cys Tyr Gln Cys His Ser Gly Glu Leu Tyr Arg Val Thr Ser Asp
    370                 375                 380


Ser Asp Glu Lys Pro Ala Pro Glu Ser Asp Glu Gly Thr Glu Pro Ser
385                 390                 395                 400


Tyr Ala Pro Cys Thr Ile His His Leu Met Gly Lys Ser His Gly Leu
                405                 410                 415


Val Thr Cys Ala Ala Cys Arg Leu Lys Asn Ser Thr Leu His Asp Asp
            420                 425                 430


Leu Asp Asp Gly Asp Leu Glu Gln
        435                 440


<210> 567
<211> 319
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 567
Met Glu Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys
1               5                   10                  15


Glu Trp Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser
            20                  25                  30


Ser Asn Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln
        35                  40                  45


Glu Met Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp
    50                  55                  60


Pro Val Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu
65                  70                  75                  80


Glu Leu Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly
                85                  90                  95


Trp Cys Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly
            100                 105                 110


His Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala
        115                 120                 125


Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe
    130                 135                 140


Asn Asp Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met
145                 150                 155                 160


Thr Ala Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg
                165                 170                 175


Val Arg Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr
            180                 185                 190


Pro Val Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly
        195                 200                 205


Asn Thr Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe
    210                 215                 220


Lys Leu Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr
225                 230                 235                 240


Lys Gln Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr
                245                 250                 255
```

```
Pro Val Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg
            260                 265                 270


Pro Ala Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala
        275                 280                 285


Leu Ala Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr
    290                 295                 300


Arg Leu Val Gly Ala Val Gly Gln Lys Gly Ser Glu Cys Cys Ser
305                 310                 315


<210> 568
<211> 662
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 568
Met Arg Ser Tyr Tyr Glu Val Ile Val Gln Leu Pro Asn Asp Val Glu
1               5                   10                  15


Ser Gln Val Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ile Thr Ser
            20                  25                  30


Arg Glu Trp Thr Leu Pro Glu Asp Ala Asp Trp Asp Leu Asp Gln Val
        35                  40                  45


Asp Gln Val Gln Leu Thr Leu Gly Asp Lys Ile Gln Arg Glu Ile Arg
    50                  55                  60


Thr His Trp Gly Thr Met Ala Lys Glu Pro Asp Phe His Tyr Phe Ile
65                  70                  75                  80


Gln Leu Glu Gln Gly Glu Val Phe Phe His Leu His Val Leu Leu Glu
                85                  90                  95


Thr Cys Ser Val Lys Pro Met Val Leu Gly Arg Tyr Ile Arg His Ile
            100                 105                 110


Gln Gln Lys Ile Val Ser Lys Val Tyr Cys Ala Thr Ser Leu Arg Trp
        115                 120                 125


Lys Asp Gly Cys Val Val Thr Lys Thr Lys Asn Phe Gly Gly Ala Asn
    130                 135                 140


Lys Val Arg Ala Glu Ser Tyr Ile Pro Ala Tyr Leu Ile Pro Lys Gln
145                 150                 155                 160


Gln Pro Glu Val Gln Trp Ala Trp Thr Asn Val Pro Glu Tyr Ile Lys
```

165 170 175

Ala Cys Leu His Arg Glu Leu Arg Ala Ser Leu Ala Arg Leu His Phe
180 185 190

Glu Glu Ala Gly Val Ser Gln Ser Lys Glu Asn Leu Ala Arg Thr Ala
195 200 205

Asp Gly Ala Pro Val Met Pro Thr Arg Val Ser Lys Arg Tyr Met Glu
210 215 220

Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys Glu Trp
225 230 235 240

Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser Ser Asn
245 250 255

Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln Glu Met
260 265 270

Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp Pro Val
275 280 285

Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300

Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly Trp Cys
305 310 315 320

Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly His Ala
325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365

Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380

Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
385 390 395 400

Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr Pro Val
405 410 415

Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly Asn Thr
420 425 430

Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe Lys Leu

```
        435                 440                 445


Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460


Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr Pro Val
465                 470                 475                 480


Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg Pro Ala
                485                 490                 495


Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala Leu Ala
            500                 505                 510


Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr Arg Tyr
        515                 520                 525


Arg Ile Lys Cys Ser Lys His Cys Gly Met Asp Lys Met Leu Phe Pro
    530                 535                 540


Cys Gln Ile Cys Glu Ser Met Asn Arg Asp Ile Asn Ile Cys Ala Ile
545                 550                 555                 560


His Lys Thr Thr Asp Cys Lys Glu Cys Phe Pro Asp Tyr Gly Asp Lys
                565                 570                 575


Asp Asp Val Glu Leu Pro Pro Cys Thr Glu His Asn Val Ser Arg Cys
            580                 585                 590


Tyr Gln Cys His Ser Gly Glu Leu Tyr Arg Val Thr Ser Asp Ser Asp
        595                 600                 605


Glu Lys Pro Ala Pro Glu Ser Asp Glu Gly Thr Glu Pro Ser Tyr Ala
    610                 615                 620


Pro Cys Thr Ile His His Leu Met Gly Lys Ser His Gly Leu Val Thr
625                 630                 635                 640


Cys Ala Ala Cys Arg Leu Lys Asn Ser Thr Leu His Asp Asp Leu Asp
                645                 650                 655


Asp Gly Asp Leu Glu Gln
            660


<210> 569
<211> 541
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide
```

```
<400> 569
Met Arg Ser Tyr Tyr Glu Val Ile Val Gln Leu Pro Asn Asp Val Glu
1               5                   10                  15


Ser Gln Val Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ile Thr Ser
            20                  25                  30


Arg Glu Trp Thr Leu Pro Glu Asp Ala Asp Trp Asp Leu Asp Gln Val
        35                  40                  45


Asp Gln Val Gln Leu Thr Leu Gly Asp Lys Ile Gln Arg Glu Ile Arg
    50                  55                  60


Thr His Trp Gly Thr Met Ala Lys Glu Pro Asp Phe His Tyr Phe Ile
65                  70                  75                  80


Gln Leu Glu Gln Gly Glu Val Phe Phe His Leu His Val Leu Leu Glu
                85                  90                  95


Thr Cys Ser Val Lys Pro Met Val Leu Gly Arg Tyr Ile Arg His Ile
            100                 105                 110


Gln Gln Lys Ile Val Ser Lys Val Tyr Cys Ala Thr Ser Leu Arg Trp
        115                 120                 125


Lys Asp Gly Cys Val Val Thr Lys Thr Lys Asn Phe Gly Gly Ala Asn
    130                 135                 140


Lys Val Arg Ala Glu Ser Tyr Ile Pro Ala Tyr Leu Ile Pro Lys Gln
145                 150                 155                 160


Gln Pro Glu Val Gln Trp Ala Trp Thr Asn Val Pro Glu Tyr Ile Lys
                165                 170                 175


Ala Cys Leu His Arg Glu Leu Arg Ala Ser Leu Ala Arg Leu His Phe
            180                 185                 190


Glu Glu Ala Gly Val Ser Gln Ser Lys Glu Asn Leu Ala Arg Thr Ala
        195                 200                 205


Asp Gly Ala Pro Val Met Pro Thr Arg Val Ser Lys Arg Tyr Met Glu
    210                 215                 220


Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys Glu Trp
225                 230                 235                 240


Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser Ser Asn
                245                 250                 255


Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln Glu Met
            260                 265                 270
```

```
Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp Pro Val
        275                 280                 285

Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly Trp Cys
305                 310                 315                 320

Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly His Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr Pro Val
                405                 410                 415

Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly Asn Thr
            420                 425                 430

Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe Lys Leu
        435                 440                 445

Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr Pro Val
465                 470                 475                 480

Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg Pro Ala
                485                 490                 495

Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala Leu Ala
            500                 505                 510

Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr Arg Leu
        515                 520                 525

Val Gly Ala Val Gly Gln Lys Gly Ser Glu Cys Cys Ser
    530                 535                 540
```

```
<210> 570
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 570
Met Ser Leu Ile Ser Asp Ala Ile Pro Asp Trp Leu Glu Arg Leu Val
1               5                   10                  15


Lys Lys Gly Val Asn Ala Ala Ala Asp Phe Tyr His Leu Glu Ser Gly
            20                  25                  30


Pro Pro Arg Pro Lys Ala Asn Gln Gln Thr Gln Glu Ser Leu Glu Lys
        35                  40                  45


Asp Asp Ser Arg Gly Leu Val Phe Pro Gly Tyr Asn Tyr Leu Gly Pro
    50                  55                  60


Phe Asn Gly Leu Asp Lys Gly Glu Pro Val Asn Glu Ala Asp Ala Ala
65                  70                  75                  80


Ala Leu Glu His Asp Lys Ala Tyr Asp Leu Glu Ile Lys Asp Gly His
                85                  90                  95


Asn Pro Tyr Phe Glu Tyr Asn Glu Ala Asp Arg Arg Phe Gln Glu Arg
            100                 105                 110


Leu Lys Asp Asp Thr Ser Phe Gly Gly Asn Leu Gly Lys Ala Ile Phe
        115                 120                 125


Gln Ala Lys Lys Arg Val Leu Glu Pro Phe Gly Leu Val Glu Asp Ser
    130                 135                 140


Lys Thr Ala Pro Thr Gly Asp Lys Arg Lys Gly Glu Asp Glu Pro Arg
145                 150                 155                 160


Leu Pro Asp Thr Ser Ser Gln Thr Pro Lys Lys Asn Lys Lys Pro Arg
                165                 170                 175


Lys Glu Arg Pro Ser Gly Gly Ala Glu Asp Pro Gly Glu Gly Thr Ser
            180                 185                 190


Ser Asn Ala Gly Ala Ala Ala Pro Ala Ser Ser Val Gly Ser Ser Ile
        195                 200                 205


Met Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala
    210                 215                 220


Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp
```

225   230   235   240

Leu Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro
                245   250   255

Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly
            260   265   270

Asp Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe
        275   280   285

Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
    290   295   300

Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg
305   310   315   320

Leu Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Phe Asn Thr
                325   330   335

Thr Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys
            340   345   350

Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Phe
        355   360   365

Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys
    370   375   380

Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys
385   390   395   400

Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu
                405   410   415

Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His
            420   425   430

Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu
        435   440   445

Trp Ala Phe Ser Ser Val Ser Gln Ala Gly Ser Ser Gly Arg Ala Leu
    450   455   460

His Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn
465   470   475   480

Trp Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala
                485   490   495

Ser Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys

```
            500                 505                 510


Gln Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala
        515                 520                 525


Ala Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn
    530                 535                 540


Thr Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr
545                 550                 555                 560


Asp Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr
                565                 570                 575


Asn Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln
            580                 585                 590


Ser Ile Val Thr Pro Gly Thr Arg Ala Ala Val Asn Asn Gln Gly Ala
        595                 600                 605


Leu Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr
    610                 615                 620


His Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro
625                 630                 635                 640


Leu Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile
                645                 650                 655


Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala
            660                 665                 670


Lys Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val
        675                 680                 685


Glu Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro
    690                 695                 700


Glu Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe
705                 710                 715                 720


Ala Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735


Arg Tyr Leu Thr Lys Pro Leu
            740


<210> 571
<211> 598
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 571
Thr Ala Pro Thr Gly Asp Lys Arg Lys Gly Glu Asp Glu Pro Arg Leu
1               5                   10                  15


Pro Asp Thr Ser Ser Gln Thr Pro Lys Lys Asn Lys Lys Pro Arg Lys
            20                  25                  30


Glu Arg Pro Ser Gly Gly Ala Glu Asp Pro Gly Glu Gly Thr Ser Ser
        35                  40                  45


Asn Ala Gly Ala Ala Ala Pro Ala Ser Ser Val Gly Ser Ser Ile Met
    50                  55                  60


Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala Asp
65                  70                  75                  80


Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu
                85                  90                  95


Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro Ser
            100                 105                 110


Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly Asp
        115                 120                 125


Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp
    130                 135                 140


Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu
145                 150                 155                 160


Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg Leu
                165                 170                 175


Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Phe Asn Thr Thr
            180                 185                 190


Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys Asp
        195                 200                 205


Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Phe Pro
    210                 215                 220


Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys Thr
225                 230                 235                 240


Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys Leu
                245                 250                 255
```

Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu Phe
            260   265   270

Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His Asn
        275   280   285

Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Trp
    290   295   300

Ala Phe Ser Ser Val Ser Gln Ala Gly Ser Ser Gly Arg Ala Leu His
305   310   315   320

Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn Trp
                325   330   335

Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala Ser
            340   345   350

Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys Gln
        355   360   365

Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala Ala
    370   375   380

Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn Thr
385   390   395   400

Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr Asp
                405   410   415

Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr Asn
            420   425   430

Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln Ser
        435   440   445

Ile Val Thr Pro Gly Thr Arg Ala Ala Val Asn Asn Gln Gly Ala Leu
    450   455   460

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr His
465   470   475   480

Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro Leu
                485   490   495

Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile Lys
            500   505   510

Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala Lys
        515   520   525

Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val Glu
530 535 540

Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro Glu
545 550 555 560

Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe Ala
565 570 575

Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg
580 585 590

Tyr Leu Thr Lys Pro Leu
595

<210> 572
<211> 4694
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 572
tggccagttt ccaagacagg ctcgctcgct cactcgggcc ggggccccaa aggggcccct 60

agcgaccgct tcgcggtcgc ggcccgagtg agcgagcgag cctgtcttgg aaactggcca 120

gcactccggt gaggtaatgc cgtcacgtgg tcgggaatgg gaacgggaaa tctcgcgaga 180

acgtaaacaa atataagacg gcgccacacg gcgctgcgtc atacgcgcgc gcgcaccggc 240

gagatgaggt cgtactacga ggtcatcgtt cagctgccca acgacgtcga gagtcaggta 300

cctggaatct ccgattcgtt cgtcaactgg attacgtcgc gagaatggac gttgcctgag 360

gacgccgatt gggatttgga ccaggtcgat caagttcaac tgacgctcgg cgacaaaatc 420

caacgggaga ttcgaactca ttgggggacg atggccaaag aaccggactt tcactatttt 480

atccaactgg aacaaggtga ggtgttcttt catttacacg tcctgctgga aacgtgttcc 540

gtaaagccga tggtactcgg aagatatatc cgacatattc aacaaaaaat tgtgagtaaa 600

gtctactgcg ccacgagcct acgatggaag gatggatgcg tggtgaccaa gaccaaaaat 660

ttcgggggcg cgaacaaggt ccgggccgag tcgtatattc ccgcctacct gatcccgaaa 720

cagcaaccgg aagtgcagtg ggcgtggact aacgtgcccg agtatataaa agcgtgcttg 780

caccgagaac tgcgtgccag tctcgcgcga cttcacttcg aggaggcggg cgtctcgcaa 840

tccaaggaaa atctcgcgag aactgcagac ggcgctcccg tgatgccgac ccgcgtcagc 900

aaacgctaca tggagctcgt ggattggctc gtggagaagg ggatcaccac cgagaaggaa 960

tggctgctgg aaaacagaga aagctttcgg agctttcagg cctcgagcaa ctcggcgcgt 1020

cagatcaaga cggccctgca aggcgccatt caggagatgc ttctgaccaa gacggcggag 1080

gactacctcg tcggaaagga tcccgtctcg gacgacgaca tccgtcagaa ccgcatctac 1140

```
aagattctgg aactgaacca ctacgaccca gcgtacgtgg ggagtatttt ggtcgggtgg     1200
tgccagaaga aatggggcaa gcgaaacacg ctgtggctgt tcggacatgc gaccaccggc     1260
aagaccaaca tcgcggaggc tattgcccat gctgtgccgt tctatggatg cgttaactgg     1320
accaacgaga actttccgtt caacgactgc gtcgaaaaaa tgattatctg gtgggaggag     1380
ggcaaaatga ccgccaaagt ggtggaaaca gccaaggcga ttctgggagg atctcgggtg     1440
agagtggacc aaaaatgcaa agcttcggtt ccgatcgaac cgacgccggt cattattacc     1500
agtaacacca acatgtgtta tgtcatcgac gggaacacga ccacgttcga gcataagcag     1560
ccgttggagg acaggatgtt taagctcgaa ttgctgactc ggttgcctga tgactttggt     1620
aaggtgacca aacaggaggt gcgtcaattc ttcaggtggt ctcaggatca cctgacccct     1680
gtgatcccag aattcctagt gcggaaggcg gagtctcgca aaagacccgc cccttccggg     1740
gaaggctata taagcccgac aaagcggccc gcgctcgcag agcagcagca ggcgtcggag     1800
agcgcggacc cggttcccac caggtatcgt atcaaatgct cgaaacattg cggtatggat     1860
aaaatgttgt ttccttgcca aatttgtgaa tcgatgaaca gagatattaa tatttgtgct     1920
attcataaaa cgaccgactg taaagagtgt ttccccgact acggggataa agatgatgta     1980
gaactacccc cctgtacaga acacaacgtg tctcgttgtt atcaatgtca ttcgggcgaa     2040
ttgtatcgcg tgacttcgga ctctgacgag aaacctgccc ccgagagtga tgaaggcacc     2100
gagccatcct atgctccctg cacgattcac cacctgatgg gcaagagtca cgggttagtc     2160
acttgcgcgg cgtgtcggtt gaaaaatagt acgttgcatg atgacttgga tgacggtgat     2220
ctcgaacaat aaatgattga aatgtagcca tgtctctcat ttctgatgcg attccagatt     2280
ggttggagcg gttggtcaaa aagggagtga atgctgcagc tgatttctac catttggaaa     2340
gcggtcctcc tcgtcctaag gcaaatcagc aaactcaaga atctcttgaa aaggacgatt     2400
cgagaggtct cgtgttccca ggctacaatt atctaggccc tttcaacggt ctagataaag     2460
gagaacccgt caacgaggca gacgctgccg ccttagaaca cgacaaggct tacgacctcg     2520
aaatcaagga cgggcacaac ccgtactttg agtacaacga ggccgacaga cgtttccagg     2580
aacgtctcaa agacgatacc tcctttggag gcaatttagg taaagccatc ttccaggcca     2640
aaaagagggt tctcgaaccc tttggtctgg tggaagactc aaagacggct ccgaccggag     2700
acaagcggaa aggcgaagac gaacctcgtt tgcccgacac ttcttcacag actcccaaga     2760
aaaacaagaa gcctcgcaag gaaagacctt ccggcggggc agaagatccg ggcgaaggca     2820
cctcttccaa cgctggagca gcagcacccg cctctagtgt gggatcatct atcatggctg     2880
aaggaggtgg cggcccagtg ggcgatgcag gccagggtgc cgatggagtg ggcaattcct     2940
ccggaaattg gcattgcgat tcccaatggc tggaaaacgg agtcgtcact cgaaccaccc     3000
gaacctgggt cttgcccagc tacaacaacc acctgtacaa acgaatccaa ggacccagcg     3060
gaggcgacaa caacaacaaa ttctttggat tcagcacccc ctggggatac tttgactaca     3120
atcgattcca ctgccacttt tccccgcgag actggcaacg actcatcaac aacaactggg     3180
```

gcatccgtcc caaagcgatg cgctttagac tctttaacat ccaggttaaa gaggtcacgg 3240

tccaagactt caacaccacc atcggcaaca acctcaccag tacggtccag gtctttgcgg 3300

acaaggacta ccaactgccg tacgtcctcg gatcggctac cgaaggcacc ttcccgccgt 3360

tcccagcgga tatctacacg atcccgcagt acgggtactg cacgctaaac tacaacaacg 3420

aggcggtgga tcgttcggcc ttctactgtc tggactactt tccctcagac atgctgcgga 3480

caggaaataa ctttgagttt acttacacct tcgaggacgt tcctttccat agcatgtttg 3540

cccacaacca gacgctagac cggctgatga atcccctcgt ggatcagtac ctctgggctt 3600

tcagctccgt cagccaagca ggctcatctg gacgagctct tcattactcg cgggcgacta 3660

aaaccaacat ggcggctcaa tataggaact ggttacctgg gcctttcttc cgtgatcagc 3720

aaatctttac gggcgctagc aacatcacta aaaataacgt ctttagcgtt tgggaaaaag 3780

gcaagcaatg ggaactcgac aatcggacca acctaatgca gcccggtcct gcggcagcga 3840

ccacctttag cggagaacct gaccgtcaag ccatgcaaaa cacgctggct tttagcagga 3900

ccgtctacga tcaaacgacc gccacgaccg atcgtaacca gatactcatc accaacgaag 3960

acgaaatcag acccaccaac tcggtcggta tcgacgcgtg gggagcagtt cccaccaaca 4020

accagtcgat cgtgaccccc ggcactcgcg cggccgtcaa caatcaaggg gcgcttcccg 4080

ggatggtgtg gcaaaacaga gacatttacc ctacagggac ccatttggcc aaaattcccg 4140

acactgacaa tcacttccat ccgtccccgc ttattgggcg gtttggctgc aagcatcccc 4200

ctccccagat tttcattaaa aacacacccg tccctgccaa cccttcggaa acgttccaga 4260

cggccaaagt ggcctccttc atcaaccagt actcgaccgg acagtgcacc gtcgaaatct 4320

tttgggaact caagaaggaa acctccaagc gctggaaccc cgaaatccag ttcacctcca 4380

actttggcaa cgcggccgac atccagtttg ccgtctccga cacgggatcc tattccgaac 4440

ctcgtcccat cggtacccgt taccttacca aacctctgta aattaaaccc ttcaataaac 4500

cgtttatgcg taactgtatt tccgtctcct gtcgttattc agtcacatga tgcggcatta 4560

cctcaccgga gtgctggcca gtttccaaga caggctcgct cgctcactcg ggccggggcc 4620

ccaaaggggc ccctagcgac cgcttcgcgg tcgcggcccg agtgagcgag cgagcctgtc 4680

ttggaaactg gcca 4694

<210> 573
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 573
atggctgctg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgcggagttc 300

cagcagcggc ttcagggcga cacatcgttt gggggcaacc tcggcagagc agtcttccag 360

gccaaaaaga gggttcttga acctcttggt ctggttgagc aagcgggtga gacggctcct 420

ggaaagaaga gaccgttgat tgaatccccc cagcagcccg actcctccac gggtatcggc 480

aaaaaaggca agcagccggc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcagacgtc ttcatggtgc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc agtaggacgc tcttcatttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtaccgg aaacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

```
tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a             2211


<210> 574
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 574
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 575
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
```

polynucleotide

<400> 575
atggcttccg atggttatct tccagattgg ctcgaggaca acctctctga gggcatccgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca gagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

```
gagttttcgg ctacaaagtt tgcttcattc atcacccagt attctactgg ccaagtcagc     2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag     2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgtcccat tggcacccgt tacctcaccc gtcccctgta a              2211


<210> 576
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 576
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Arg Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
```

```
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 577
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 577
atggctgctg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgcggagttc 300

cagcagcggc ttcagggcga cacatcgttt gggggcaacc tcggcagagc agtcttccag 360

gccaaaaaga gggttcttga acctcttggt ctggttgagc aagcgggtga gacggctcct 420

ggaaagaaga gaccgttgat tgaatccccc cagcagcccg actcctccac gggtatcggc 480

aaaaaaggca agcagccggc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcagacgtc ttcatggtgc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc agtaggacgc tcttcatttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtaccgg aaacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ctgaaagatt tgggactgtg 1740

```
gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgccatggga     1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc     1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc     2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag     2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a              2211
```

<210> 578
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 578

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
```

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
```

```
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Thr Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
```

705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 579
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 579
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcaatcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt cgacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgat 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

```
ggcactgcta tggcctcaca taaagacgac gaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt     1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga     1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc     1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagc     2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag     2100

tatacatcta actatgcaaa atctgccaac attgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtccccagta a              2211


<210> 580
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 580
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Ile Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Gln
                725                 730                 735


<210> 581
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 581
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc        60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac       120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac       180

aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt       300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaaaaaga gggttctcga acctctcggt ctggttgagg aagcggctaa gacggctcct       420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc       480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag       540

tcagtccccg acccacaacc tctcggagaa cctcccgcag ccccctcagg tgtgggatct       600

cttacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga       660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc       720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc       780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg       840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc       900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa       960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg      1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag      1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg      1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca      1200

tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct      1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac      1320
```

```
cagtacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac     1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct     1440

ggaccctgtt accggcagca gtgcgtttct aaaacaaaaa cagacaacaa caacagcaac     1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct     1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc     1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg     1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga     1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc     1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagc     2040

gtggagattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a              2211


<210> 582
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 582
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Cys Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 583
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 583
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gaatggtggg acttgaaacc tggagccccg aaacccaaag tcaaccagca aaagcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggacgagc agtcttccag 360

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

```
ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca     1200

tcgcagatgc tgagaacggg caataacttt accttcagct acacttttga ggacgttcct     1260

ttccacagca gctacgctca cagccagagc ctggaccggc tgatgaatcc tctcatcgac     1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac     1380

ttgctgttta gccgtgggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct     1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac     1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct     1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc     1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ctgaaagatt tgggactgtg     1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgccatggga     1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc     1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt     1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca     1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc     2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag     2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a              2211

<210> 584
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 584
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Val Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Thr Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 585
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<220>
<221> modified_base
<222> (955)..(955)
<223> a, c, t or g

<220>
<221> modified_base
<222> (971)..(972)
<223> a, c, t or g

<220>
<221> modified_base
<222> (981)..(981)
<223> a, c, t or g

<220>
<221> modified_base
<222> (986)..(986)
<223> a, c, t or g

<220>
<221> modified_base
<222> (1235)..(1235)
<223> a, c, t or g

<220>
<221> modified_base
<222> (1694)..(1696)
<223> a, c, t or g

<220>
<221> modified_base
<222> (1698)..(1698)
<223> a, c, t or g

<220>
<221> modified_base
<222> (1763)..(1765)
<223> a, c, t or g

<220>
<221> modified_base
<222> (1778)..(1778)
<223> a, c, t or g

<220>
<221> modified_base
<222> (2204)..(2204)
<223> a, c, t or g

<400> 585
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gaatggtggg acttgaaacc tggagccccg aaacccaaag tcaaccagca aaagcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggacgagc agtcttccag 360

gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaataaca attggggatt ccggcccaag agactcaact tcaaactctt caacntccaa 960

gtcaaggagg nnacgacgaa ngatgncgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt acctncagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct 1440 ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag agannncnaa gccactaacc ccgtggccac tgaaagattt gggactgtgg 1740

cagtcaatct ccaagcagca cannnaccct gcgaccgnag atgtgcatgc catgggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

attcctcaca cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag 1920

cacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag 1980

ttttcggcta caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga agtgcagtat 2100

acatctaact atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat 2160

actgagcctc gccccattgg cacccgttac ctcacccgtc cccngtaa 2208

<210> 586
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 586
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Val Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Gln Val
305                 310                 315                 320

Lys Glu Thr Thr Asp Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400
```

```
Arg Thr Gly Asn Asn Phe Thr Ser Tyr Thr Phe Glu Asp Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser
        435                 440                 445

Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Thr
    450                 455                 460

Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile
            500                 505                 510

Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys
        515                 520                 525

Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly
    530                 535                 540

Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr Asp Glu Glu Ala
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Leu
                565                 570                 575

Gln Ser Ser Pro Ala Thr Asp Val His Ala Met Gly Ala Leu Pro Gly
            580                 585                 590

Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595                 600                 605

Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly
    610                 615                 620

Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr
625                 630                 635                 640

Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu
            660                 665                 670
```

Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln
675 680 685

Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp
690 695 700

Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro

<210> 587
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 587
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggtc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200 cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacgct ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 588
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 588
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445


Asp Ala Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 589
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 589
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga   60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac   120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac   180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac   240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt   300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag   360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg   420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga   480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcaaac   540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact   600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga   660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc   720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt   780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg   840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc   900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc   960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt   1020 caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcgggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac gaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

acagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 590
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 590

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asn Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Arg Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 591
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 591

```
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc      480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag      540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct      600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga      660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc      720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc      780
```

```
tccagtgctt cgacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg      840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc      900

atcaacaata actggggatt ccggcccaag agactcagct tcaagctctt caacatccag      960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg     1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag     1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg     1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct     1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct     1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgat     1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac     1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct     1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat     1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct     1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt     1680

acggacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga     1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc     1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcactcaat actccacagg acaagtgagc     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag     2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a                2211


<210> 592
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 592
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
```

35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln

```
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
```

580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 593
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 593
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asn Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Gln
                725   730   735

<210> 594
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 594
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggaacgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

```
aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc      960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct     1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc     1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag     1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt     1380

cagttttctc aggccggagc gagtgacatt cggaaccagt ctaggaactg gcttcctgga     1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc     1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc     1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca     1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa     1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atcagtaa                  2208
```

```
<210> 595
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 595
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
```

```
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac      540

tcagtacctg atccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt      780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg      840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc      900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc      960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020

caggtgttta ctgactcgga gtaccagctc ccgtatgtcc tcggctcggc gcatcaagga     1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct     1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc     1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag     1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt     1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga     1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc     1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc     1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca     1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa     1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa                  2208
```

```
<210> 596
<211> 735
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 596
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445


Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495


Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 597
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 597
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt        60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat       120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg       180
```

```
tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat      240
cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg      300
gatgactgtg tttctgaaca ataaatgact taaaccaggt atgactgccg atggttatct      360
tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc      420
tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct      480
tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc      540
agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga      600
caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga      660
tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga      720
acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga      780
gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc      840
taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc      900
aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg      960
tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa     1020
ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg     1080
ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg     1140
atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa     1200
cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg     1260
attccggcct aagcaactca acttcaagct cttcaacatt caggtcaaag aggttacgga     1320
caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga     1380
ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt     1440
cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca     1500
ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac     1560
gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc     1620
tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct     1680
ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg     1740
acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca     1800
acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc     1860
ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca     1920
caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg     1980
aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa     2040
aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc     2100
ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg     2160
gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg     2220
```

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 598
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 598
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260 attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggggcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacgggcgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tggaggtgta tatagtgaac ccgcccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 599
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 599
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggactcg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360 tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattgac aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcggactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

```
gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa     2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat     2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt     2580

cgtttcagtt gaactgcggc c                                               2601


<210> 600
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 600
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt       60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat      120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg      180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat      240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg      300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct      360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc      420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct      480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc      540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga      600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga      660

tacgtctttt gggggcaacc tcgggcgagc agtcctccag gccaaaaaga ggcttcttga      720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga      780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc      840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc      900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg      960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa     1020

ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg     1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg     1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa     1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg     1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga     1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga     1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt     1440
```

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

atccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaattttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccag gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 601
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 601
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacag ggcctacgac cagcagctca aggccggaga 600
caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660
tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720
acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780
gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840
taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900
aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960
tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020
ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080
ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140
atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200
cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260
attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320
caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380
ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440
cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500
ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560
gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620
tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680
ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740
acctagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800
acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860
ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920
caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980
aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040
aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100
ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160
gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220
caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280
cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340
gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400
gcagaagaaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460
gtctaataat gttgaatttg ctgttaacac tgaaggtgta tatagtgaac cccgccccat 2520
tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 602
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 602
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620 tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacgg gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 603
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 603
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agtagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720 acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

atttcggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 604
<211> 2580

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 604
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct cgggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800 acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggaact 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

<210> 605
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 605
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtctttcag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcatgtgg 960 tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 606
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 606

ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cgatcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctggagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040 aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacgtacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 607
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 607
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgccacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgctg ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggggа cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140 atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacatga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca atgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcctggc ctagagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc atggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 608
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 608
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240
cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300
gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360
tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420
tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480
tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540
agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600
caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660
tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720
acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780
gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840
taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900
aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960
tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020
ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080
ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140
atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200
cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260
attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320
caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380
ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440
cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500
ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560
gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620
tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680
ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740
acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800
acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctagagcttc 1860
ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920
caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980
aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040
aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100
ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160
gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 609
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 609
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320 caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctagagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagcg 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac ccgcccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 610
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 610
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360 tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcgcgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctagagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400 gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 611
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 611
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aagggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500 ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa attgcttggc ctagagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccagtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattgcaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac ccgcccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 612
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 612
ccatcgacgt cagacgcgga agcttcgatc aactacgcgg acaggtacca aaacaaatgt 60

tctcgtcacg tgggcatgaa tctgatgctg tttccctgca gacaatgcga gagactgaat 120

cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgtctgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgat aagggggagc cggtcaacgc 540 agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctggggga cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

tcacagccaa agcctggacc gactaatgaa tccactcatc gaccaatact tgtactatct 1680

ctcaaagact attaacggtt ctggacagaa tcaacaaacg ctaaaattca gtgtggccgg 1740

acccagcaac atggctgtcc agggaagaaa ctacatacct ggacccagct accgacaaca 1800

acgtgtctca accactgtga ctcaaaacaa caacagcgaa tttgcttggc ctagagcttc 1860

ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580 cgtttcagtt gaactgcggc c   2601

<210> 613
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 613
Met Thr Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Gln Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 614
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 614
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn

```
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
```

```
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Gly Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Gly Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 615
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 615
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Asp
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 616
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 616
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
```

65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Leu Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu

```
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Ser Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

```
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 617
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 617
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Lys Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 618
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 618
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly

```
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
```

```
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Arg Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
```

    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 619
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 619
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Val Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

```
Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

```
<210> 620
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 620
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Arg Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn

```
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 621
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 621
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Cys Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260   265   270

```
Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 622
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 622
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Ile Asn Ala Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
```

            580   585   590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Tyr Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 623
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 623
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro His Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Asn
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Met Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 624
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 624
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
```

```
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

```
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
```

            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 625
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 625
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435   440   445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450   455   460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465   470   475   480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485   490   495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500   505   510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515   520   525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530   535   540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545   550   555   560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565   570   575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580   585   590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Arg Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

```
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 626
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 626
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
```

465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 627

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 627
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Ile Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Cys Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 628
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 628
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

        275   280   285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290   295   300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305   310   315   320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325   330   335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340   345   350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355   360   365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370   375   380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385   390   395   400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405   410   415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420   425   430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435   440   445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450   455   460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465   470   475   480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485   490   495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500   505   510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515   520   525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530   535   540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile

```
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 629
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 629
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc        60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac       120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac       180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc       300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360
```

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttcg gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctgggaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 630
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 630
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccgcttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacgcccctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 631
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 631
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcagcgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccgcgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380 ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 632
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 632
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840 tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac acggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 633
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 633
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcggctca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtagcaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggcagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

cacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac ccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 634
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 634
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaggct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aagccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctccccagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 635
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 635
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgcccgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tggaggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggcct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcggacgtt ttcatgattc ctcagtacgg gtatctgacg 1140

cttaatgatg gaagccaggc cgtgggtcgt tcgtcctttt actgcctgga atatttcccg 1200

tcgcaaatgc taagaacggg taacaacttc cagttcagct acgagtttga gaacgtacct 1260

ttccatagca gctacgctca cagccaaagc ctggaccgac taatgaatcc actcatcgac 1320

caatacttgt actatctctc aaagactatt aacggttctg gacagaatca acaaacgcta 1380 aaattcagtg tggccggacc cagcaacatg gctgtccagg gaagaaacta catacctgga 1440

cccagctacc gacaacaacg tgtctcaacc actgtgactc aaaacaacaa cagcgaattt 1500

gcttggcctg gagcttcttc ttgggctctc aatggacgta atagcttgat gaatcctgga 1560

cctgctatgg ccagccacaa agaaggagag gaccgtttct ttcctttgtc tggatcttta 1620

atttttggca aacaaggaac tggaagagac aacgtggatg cggacaaagt catgataacc 1680

aacgaagaag aaattaaaac tactaacccg gtagcaacgg agtcctatgg acaagtggcc 1740

acaaaccacc agagtgccca agcacaggcg cagaccggct gggttcaaaa ccaaggaata 1800

cttccgggta tggtttggca ggacagagat gtgtacctgc aaggacccat ttgggccaaa 1860

attcctcaca cggacggcaa ctttcaccct tctccgctga tgggagggtt tggaatgaag 1920

cacccgcctc ctcagatcct catcaaaaac acacctgtac ctgcggatcc tccaacggcc 1980

ttcaacaagg acgagctgaa ctctttcatc acccagtatt ctactggcca agtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaagcgct ggaacccgga gatccagtac 2100

acttccaact attacaagtc taataatgtt gaatttgctg ttaatactga aggtgtatat 2160

agtgaacccc gccccattgg caccagatac ctgactcgta atctg 2205

<210> 636
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 636
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gacaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

```
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900

ctcatcaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag      960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg     1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag     1080

ggctgcctcc cgccgttccc agcggacgtt ttcatgattc ctcagtacgg gtatctgacg     1140

cttaatgatg gaagccaggc cgtgggtcgt tcgtcctttt actgcctgga atatttcccg     1200

tcgcaaatgc taagaacggg taacaacttc caattcagct acgagtttga gaacgtacct     1260

ttccatagca gctacgctca cagccaaagc ctggaccgac taatgaatcc actcatcgac     1320

caatacttgt actatctctc aaagactatt aacggttctg gacagaatca acaaacgcta     1380

aaattcagtg tggccggacc cagcaacatg gctgtccagg gaagaaacta catacctgga     1440

cccagctacc gacaacaacg tgtctcaacc actgtgactc aaaacaacaa cagcgaattt     1500

gcttggcctg gagcttcttc ttgggctctc aatggacgta atagcttgat gaatcctgga     1560

cctgctatgg ccagccacaa agaaggagag gaccgtttct ttcctttgtc tggatcttta     1620

atttttggca aacaaggaac tggaagagac aacgtggatg cggacaaagt catgataacc     1680

aacgaagaag aaattaaaac tactaacccg gtagcaacgg agtcctatgg acaagtggcc     1740

acaaaccacc agagtgccca agcacaggcg cagaccggct gggttcaaaa ccaaggaata     1800

cttccgggta tggtttggca ggacagagat gtgtacctgc aaggacccat ttgggccaaa     1860

attcctcaca cggacggcaa ctttcaccct tctccgctga tgggagggtt tggaatgaag     1920

cacccgcctc ctcagatcct catcaaaaac acacctgtac ctgcggatcc tccaacggcc     1980

ttcaacaagg acaagctgaa ctctttcatc acccagtatt ctactggcca agtcagcgtg     2040

gagatcgagt gggagctgca gaaggaaaac agcaagcgct ggaacccgga gatccagtac     2100

acttccaact attacaagtc taataatgtt gaatttgctg ttaatactga aggtgtatat     2160

agtgaacccc gccccattgg caccagatac ctgactcgta atctg                     2205


<210> 637
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 637
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
```

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagccatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgaca 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 638
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 638
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaatgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

accaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg gctcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgcactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 639
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 639
atggctgccg atggttattt tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa tctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatctc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgcactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

```
ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct     1560

ggacctgctg tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata     1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208


<210> 640
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 640
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcttga acctcttggt ccggttgagg aagcggctaa gacggctcct      420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840
```

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagcg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 641
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 641
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcggg gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

```
gccaaaaaga ggcttcttga acctcttggt ccggttgagg aagcggctaa gacggctcct      420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480
aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540
tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600
cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780
tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcggcga      900
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960
caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020
acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080
gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta     1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc     1320
gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg     1380
ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440
ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct     1560
ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620
ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata     1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800
atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860
aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920
aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980
gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040
gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208
```

<210> 642
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 642
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc   60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac   120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac   180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac   240

cagcagctca aggccggaga caacctgtac ctcaagtaca accacgccga cgccgagttc   300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag   360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct   420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc   480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag   540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct   600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga   660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc   720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc   780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc   840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga   900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt   960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc   1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac   1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg   1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc   1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta   1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc   1320

gaccaatact tgcactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg   1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct   1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa   1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct   1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct   1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata   1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg   1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga   1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc   1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 643
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 643
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caagaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgcactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380 ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 644
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (1325)..(1325)
<223> a, c, t, g, unknown or other

<400> 644
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

```
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780

tccaccagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta     1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc     1320

gaccnatact tgcactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg     1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct     1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata     1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800

atacttccgg atatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208
```

<210> 645
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 645

```
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180
```

```
aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240
cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480
aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540
tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600
cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc      720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780
tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960
caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020
acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080
gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta     1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc     1320
gaccaatact tgcactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg     1380
ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440
ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct     1560
ggacctgcta tggccagcta caaagaagga gaggacagtt tctttccttt gtctggatct     1620
ttaattttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata     1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800
atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860
aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920
aagcacccgc ctcctcagac cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980
gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040
gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208
```

<210> 646
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 646
```
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc        60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac       120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac       180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac       240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc       300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag       360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct       420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc       480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag       540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct       600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga       660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc       720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc       780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc       840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga       900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt       960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc      1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac      1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg      1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc      1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttcg gctacgagtt tgagaacgta      1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc      1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg      1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct      1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa      1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct      1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct      1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata      1680
```

```
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctgggaccc ggagatccag     2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208
```

<210> 647
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 647

```
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaggg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agccgacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020

acggtccagg tcttcacgga ctcagactgt cagctcccgt acgtgctcgg gtcggctcac     1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200
```

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaacgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaattttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccca tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 648
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 648
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taagaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccacccatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatggtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 649
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 649
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ccggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaattttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 650
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 650
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc aattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccggcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

```
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920

aagcacccgc ctcctcagat cctcatcaag aacacacctg tacctgcgga tcctccaacg     1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208


<210> 651
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 651
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac agataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggtaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtatcggc      480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960

caggtcaaag aggttacgga caacaatgga gtcaagaccg tcgccaataa ccttaccagc     1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200
```

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtggac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 652
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 652
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 653
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 653
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acgtcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

```
aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240
cagcagctca aggccggagg caacccgtgc ctcaagtaca accacgccga cgccgagttc      300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480
agatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540
tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600
cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780
tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960
caggtcaaag aggttacgga caacaatgga gtcaaggcca tcgccaataa ccttaccagc     1020
acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080
gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta     1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc     1320
gaccaatact tgtactatct ctcaaagact attgacggtt ctggacagaa tcaacaaacg     1380
ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440
ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatggatcct     1560
ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620
ttaattttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata     1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800
atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860
aaaattcctc acacgggcgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920
aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980
gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040
gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                2208
```

<210> 654
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 654
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

```
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100

tacacttcca actattacaa gcctaataat gttgaatttg ctgttaatac tgaaggtgta     2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208


<210> 655
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 655
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacaacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcctcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgagatct      600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct ttttactgcct ggaatatttc     1200
```

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctacta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 656
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 656
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg tgcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcacga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tgggccccga tacctgactc gtaatttt 2208

<210> 657
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 657
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

```
aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacaacaa ggcctacgac      240
cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc      300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480
aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540
tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgagatct      600
cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780
tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc      840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960
caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020
acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080
gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta     1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc     1320
gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg     1380
ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440
ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct     1560
ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620
ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata     1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800
atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860
aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920
aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980
gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040
gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208
```

<210> 658
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 658
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc   60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac   120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac   180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac   240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc   300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag   360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct   420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc   480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag   540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct   600

cttacaatgg cttcaggcgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga   660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc   720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc   780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc   840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga   900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcgagct cttcaacatt   960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc   1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac   1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg   1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc   1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagtcca gctacgagtt tgagaacgta   1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc   1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg   1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct   1440

ggacccagct accgacaaca acgtgcctca accactgtga ctcaaaacaa caacagcgaa   1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct   1560

ggacctgcta tggccagcca caaagaaggg gaggaccgtt tctttccttt gtctggatct   1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata   1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 659
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 659
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccccccagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcggaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attagcggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa cagcagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atactttcgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 660
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 660
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 661
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 661
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

```
aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240
cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc      300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480
aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540
tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600
cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc       720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780
tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc      840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960
caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020
acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080
gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta     1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc     1320
gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg     1380
ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440
ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct     1560
ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620
ttaattttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata      1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800
atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860
aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920
aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980
gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040
gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208
```

<210> 662
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 662
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcgacta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcagggcaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac ccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 663
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 663
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 664
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 664
atggctgccg atggttatcc tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccgggga caacccgcac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcccgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taagaagaga ctcaatttcg gtcagactgg cgacactgag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaggct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 665
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 665
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

```
aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240
cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480
aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540
tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600
cttacaatgg cttcaggtgg tggcgcacca gtggcggaca ataacgaagg tgccgatgga      660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780
tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960
caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020
acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac     1080
gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg     1140
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc     1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta     1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc     1320
gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg     1380
ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct     1440
ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa     1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagttt gatgaatcct     1560
ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct     1620
ttaattttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata      1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800
atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860
aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg     1920
aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980
gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040
gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208
```

<210> 666
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 666
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acttacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcaccaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatatc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 667
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 667
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct ttttactgcct ggaatatttc 1200 ccgtcgcaaa tgctaagaac gggtaacaac ttccagttta gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttctg gcaaacaagg aactggaaga gacaacgtgg atgcgaacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttgaaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 668
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 668
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatag cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcgaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct tttcaacatt 960

cgggtcaaag aggttacgga caacaatgga gtcaagacca tcaccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgcttgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcgaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 669
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 669
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggcg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

ccagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcgggc gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgcga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaattttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 670
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 670
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgggttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag tccctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg agctggaaga gacaacgtgg atgcggacaa agtcatgata 1680

```
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg     1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga     1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc     1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg     1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg     1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc     2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag     2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta     2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg                  2208


<210> 671
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide


<220>
<221> modified_base
<222> (377)..(377)
<223> a, c, t, g, unknown or other

<400> 671
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagaggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcntga acctcttggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc      480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag      540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct      600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga      660

gtgggtagtt cctcggggaa ttggcattgc gattcccaat ggctggggga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc      780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc      840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga      900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt      960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc     1020
```

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcccggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 672
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 672
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480 aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac ccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 673
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 673
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccag agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct ggactctttc atcacccagt attctactgg ccaagtcagc 2040 gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggtgatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 674
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 674
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtggggcct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgtcgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtt acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgattttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ccacaaagct tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 675
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 675
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagagac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcgttc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 676
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 676
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ccgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgggg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tcccatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 677
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 677
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacgacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgcgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggcc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acggacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 678
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 678
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cggctcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tcccatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg ggagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

```
tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct     1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc     1620

atgattttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt     1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga     1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc     1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc     1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg     1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgacttta ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg                  2208


<210> 679
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 679
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caagagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc      480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag      540

tcagtccccg atccgcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct      600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga      660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc      720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc      780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg      840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc      900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa      960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg     1020
```

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgctg tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 680
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 680
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcaactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcac cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccgac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 681
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 681
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccgcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cctccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ccacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgacgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgattttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 682
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 682
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca agagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgattttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctacggga 1800

acattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa accacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacga caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 683
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 683
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcta caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacga caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 684
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 684
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagctccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagcgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcgaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccgt tggcacccgt taccttaccc gtcccctg 2208

<210> 685
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 685
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccatac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaaa tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cactttccac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgtcgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggtccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 686
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 686
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc acgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgggc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 687
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 687
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg ccccaggaaa ttggcattgc gactccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcacagcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgattttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acaggcgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 688
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 688
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cagactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaggaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480 aagacaggcc agcagcccgc taaaaagaga ctcaatttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcgcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcggccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatatagc ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gggcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgccatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 689
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 689
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcgg cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaactct accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

acattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 690
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 690
atggctgccg atggttatct cccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaagagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ccaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgattttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 691
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 691
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag gggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 692
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 692
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

```
aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag      540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct      600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga      660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc      720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc      780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg      840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc      900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa      960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg     1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag     1080

ggctgcctcc ctccgttccc ggcggacgtg tttatgattc cgcagtacgg ctacctaacg     1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcccgga atatttccct     1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct     1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac     1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac     1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct     1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat     1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct     1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc     1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag caacacagac cccgcgaccg gagatgtgca tgttatggga     1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc     1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt     1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca     1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg                  2208
```

<210> 693
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 693
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgattttgg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cgacacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 694
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 694
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcagggc 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccaaca ctcgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gttacgggca cagccagagc ctggaccggc tgatgaatct tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtttgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 695
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 695
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccaaca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

```
gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag     1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaatg     1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct     1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct     1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac     1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac     1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct     1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat     1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct     1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc     1680

acagatgaag aggaaattaa agccactaac cctgcggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga     1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc     1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt     1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca     1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg                  2208


<210> 696
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 696
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc      480
```

aagacgggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtccgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 697
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (305)..(305)
<223> a, c, t, g, unknown or other

<400> 697
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggngcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcgg cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggccacag cacccoctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgtcccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaaca 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag caacacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 698
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 698
atggctgccg atggttattt tccagattgg ctcgaggaca acctttctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttgggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aggacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcga cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320 caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcccagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatagtgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 699
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 699
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaacc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccccctgg 840 gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagactacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 700
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 700
atggctgccg atggttatcc tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagtcccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccсctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 701
<211> 2196
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 701
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagcct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

ccatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

```
aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt     1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca     1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt tacctt                               2196


<210> 702
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 702
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctttiggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc      480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag      540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct      600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga      660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc      720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc      780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg      840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc      900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa      960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg     1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag     1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg     1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct     1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct     1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac     1320
```

```
caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac     1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct     1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat     1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct     1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc     1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc     1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg     1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga     1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc     1860

aaaattcctc acacggatgg acactctcac ccgtctcctc tcatgggcgg ctttggactt     1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca     1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg                  2208


<210> 703
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 703
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc      480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag      540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct      600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga      660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc      720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc      780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg      840
```

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

ctatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggaact tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 704
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 704
atggctgccg atggttatct tccagattgg ctcgaggaca gcctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacgatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

cccaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caataccagt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 705
<211> 2208
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 705
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga accttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacgggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtccgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

```
aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt     1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca     1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt     2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag     2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt     2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg                  2208


<210> 706
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 706
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac      540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt      780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg      840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc      900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc      960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt     1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga     1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg     1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct     1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc     1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag     1320
```

```
tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt     1380

cagttttctc gggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga     1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac     1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc     1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc     1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca     1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct     1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt     1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag     1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa     1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc     1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg     2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac     2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat     2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctg                     2205


<210> 707
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 707
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Asp Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Val Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Gly Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Pro
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 708
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 708
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Arg Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
```

145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260   265   270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275   280   285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290   295   300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305   310   315   320

Gln Ile Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325   330   335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Leu Asp Tyr Gln Leu
            340   345   350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355   360   365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370   375   380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385   390   395   400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405   410   415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu

            420   425   430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435   440   445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450   455   460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465   470   475   480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485   490   495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500   505   510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515   520   525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530   535   540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545   550   555   560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565   570   575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580   585   590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn

```
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 709
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 709
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Ser Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Ser Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525


Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asp Val Asp Ala Asp Lys Val Ile Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

```
<210> 710
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 710
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Gly Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Val
```

225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gly Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Ser Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn

```
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525


Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 711
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide
```

```
<400> 711
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Val
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270
```

```
Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser His Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly His Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525


Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Gly Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 712
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 712
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn Arg Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Pro Phe Asn Ile
```

305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
515 520 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln

580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 713
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 713
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525


Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 714
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 714
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
515 520 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 715
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 715
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Leu Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Lys Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 716
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 716

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
```

465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485   490   495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 717

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 717
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Gly Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515   520   525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530   535   540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545   550   555   560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565   570   575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580   585   590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 718
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 718
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

        275   280   285

Phe His Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290   295   300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305   310   315   320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325   330   335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340   345   350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355   360   365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370   375   380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385   390   395   400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405   410   415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420   425   430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435   440   445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450   455   460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465   470   475   480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485   490   495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500   505   510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515   520   525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530   535   540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile

545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Ala Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 719
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 719
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 720
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 720
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
```

```
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Thr Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 721
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 721
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Ser Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Ala Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln His Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 722
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 722
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Arg Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
```

```
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
```

```
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 723
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 723
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Arg Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Ala Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe
                405                 410                 415

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
        435                 440                 445

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
    450                 455                 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
465                 470                 475                 480
```

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
                485   490   495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
            500   505   510

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
        515   520   525

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
    530   535   540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr
545   550   555   560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
                565   570   575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
            580   585   590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595   600   605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
625   630   635   640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645   650   655

Pro Pro Thr Ala Phe Asn Lys Asp Glu Leu Asn Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 724
<211> 735
<212> PRT

```
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 724
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Asp Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe
405 410 415

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
435 440 445

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
450 455 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
485 490 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
500 505 510

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu

```
        515                 520                 525


Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr
545                 550                 555                 560


Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
                565                 570                 575


Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
            580                 585                 590


Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655


Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 725
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 725
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Ala Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Thr
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 726
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 726
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
```

```
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Thr Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Gly Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
```

```
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 727
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 727
Met Ala Ala Asp Gly Tyr Phe Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Ser Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Leu
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Val Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 728
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 728
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
```

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
```

```
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Ala Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

```
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 729
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 729
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Arg Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

```
Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 730
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 730
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Leu Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
```

210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn

```
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 731
<211> 736
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 731
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 732
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<221> MOD_RES
<222> (442)..(442)
<223> Any amino acid

```
<400> 732
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Thr Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270
```

```
Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Xaa Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Asp Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 733
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 733
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
```

```
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 734
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 734
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Gly Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 735
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 735
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Arg Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Cys Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

```
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


His Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 736
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 736
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Gly Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 737
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 737
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
```

465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 738

```
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 738
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asn Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Gly Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 739
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 739
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Arg Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

```
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Val Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
```

545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Gly Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 740
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 740
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 741
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 741
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln Arg Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Gly Asn Pro Cys Leu Lys Tyr Asn His Ala
```

```
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Arg Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Ala Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
```

```
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asp Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asp Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Gly Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 742
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 742
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Pro Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 743
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 743
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asn Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Pro Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
```

```
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Arg Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
```

```
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Thr Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
```

705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 744
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 744
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Val His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Thr Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480
```

```
Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Pro Arg Tyr Leu Thr Arg Asn Phe
                725                 730                 735


<210> 745
<211> 736
<212> PRT
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 745
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asn Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Arg Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 746
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 746
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Glu Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Ser Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Ala Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565   570   575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580   585   590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 747
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 747
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Pro Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Ser Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Ser Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Ser Gly Met Val Trp Gln
```

        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 748
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 748
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85   90   95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 749
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 749
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
```

```
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 750
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 750
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Asp Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 751
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 751
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser

```
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
```

485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 752
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 752
Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro His Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Arg Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 753
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 753
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
```

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
```

290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser

565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 754
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 754
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Thr Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Ile
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 755
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 755
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
```

```
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Ser Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asn Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Glu Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

```
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 756
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 756
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Ile Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Arg Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Arg Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Thr Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Arg Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 757
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 757
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro

            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260   265   270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275   280   285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290   295   300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305   310   315   320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325   330   335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340   345   350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355   360   365

Ala Gly Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370   375   380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385   390   395   400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405   410   415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420   425   430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435   440   445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser

```
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Ala Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 758
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 758
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Gly Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Val Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 759
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
```

polypeptide

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Any amino acid

<400> 759
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Arg Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Xaa Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Pro
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 760
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 760
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

```
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
```

545   550   555   560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565   570   575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580   585   590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 761
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 761
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asp Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Val Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 762
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 762
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Val Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
```

```
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
```

625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Leu Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 763
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 763
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Arg Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 764
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 764
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Gly Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
```

```
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
```

```
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 765
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 765
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Arg Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Pro Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 766
<211> 736
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 766
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Gly Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
```

```
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 767
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 767
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560
```

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 768
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 768
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Gln Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
```

```
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Thr Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
```

        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asp Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 769
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 769
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Pro Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly His Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 770
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 770
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Glu Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
```

    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260   265   270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275   280   285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290   295   300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305   310   315   320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325   330   335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340   345   350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355   360   365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370   375   380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385   390   395   400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe

```
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Thr Gly Thr Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Thr Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asp Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 771
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 771
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Leu Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asp Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

```
Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 772
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 772
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Ala Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
```

485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Val Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 773
<211> 736
<212> PRT
<213> Artificial Sequence

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 773
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asn Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260   265   270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275   280   285

His Cys His Phe Pro Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290   295   300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305   310   315   320

Val Lys Glu Val Thr Ser Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325   330   335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340   345   350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355   360   365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370   375   380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385   390   395   400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405   410   415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420   425   430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435   440   445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450   455   460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485   490   495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 774
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 774
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
```

    290   295   300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305   310   315   320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325   330   335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340   345   350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355   360   365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370   375   380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385   390   395   400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405   410   415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420   425   430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435   440   445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450   455   460

Arg Gly Ser Pro Ala Gly Thr Ser Val Gln Pro Lys Asn Trp Leu Pro
465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485   490   495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg

                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Gly Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 775
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 775
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Pro Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Gly Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 776
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 776
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Arg Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
```

```
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Arg Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
```

```
    370                 375                 380

Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Ser Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Gly Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Ala Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

```
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 777
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 777
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Gly Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Thr Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 778
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 778
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Glu Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
```

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
```

    450   455   460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485   490   495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu

                725   730   735

<210> 779
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 779
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500   505   510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Gly Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 780
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

```
      polypeptide

<400> 780
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
```

```
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
```

    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asn Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 781
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 781
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260   265   270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275   280   285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290   295   300

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asp Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 782
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 782
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Gly Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Asn Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260   265   270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275   280   285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290   295   300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305   310   315   320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325   330   335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro

```
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Gly His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Leu Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Phe Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

```
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 783
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 783
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Asn Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Met Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Ala Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 784
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 784
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
```

```
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
```

```
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
```

```
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 785
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide


<220>
<221> MOD_RES
<222> (102)..(102)
<223> Any amino acid

<400> 785
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Xaa Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
```

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Gly Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly His Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Ser Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
```

```
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asn Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
```

705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 786
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 786
Met Ala Ala Asp Gly Tyr Phe Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Arg Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195   200   205

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Pro Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 787
<211> 736
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 787
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu

245 250 255

Tyr Lys Gln Thr Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Tyr
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys

        515   520   525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530   535   540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565   570   575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580   585   590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 788
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 788
Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Val Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560
```

```
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735

<210> 789
<211> 732
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 789
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
```

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
```

```
                325                 330                 335

Leu Thr Ser Thr Val Gln Ala Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Pro Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
```

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu
725 730

<210> 790
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 790
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Ser His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 791
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 791
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
```

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
```

```
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Leu Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Thr Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690   695   700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705   710   715   720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725   730   735

<210> 792
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 792
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Ser Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350


Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365


Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn Asn Gly
    370                 375                 380


Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Gln Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720
```

```
Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 793
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 793
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 794
<211> 735
<212> PRT
<213> Artificial Sequence

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 794
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Arg
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 795
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 795
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt      60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac     120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac     180
```

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240
cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300
caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360
gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420
ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480
aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540
tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600
aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720
accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780
tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900
aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960
aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020
caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080
tgcctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140
aacaacggaa gtcaagcggt gggacgctca tccttttact gcccggagta cttcccttcg 1200
cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260
cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320
tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380
ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440
gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500
tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560
ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620
ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680
acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740
gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800
gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860
aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920
aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980
actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040
gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100
tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160
tatagtgaac ctcaccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 796
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 796
atggctgctg atggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actgttgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcaactc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680 acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 797
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 797
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccggccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tcctttact gcctggagta cttcccttcg 1200 cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acggcaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagtg tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 798
<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (1283)..(1283)
<223> a, c, t, g, unknown or other

<400> 798
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gaccgggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480 aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtc 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgccttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacggcagct acgctcacag ccngagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagacttttc aaagactgct aacgacaaca acaacagtaa 1500

ctttccttgg acagcggcca gcaaatatca tctcaatggc cgcgactcgc tggtgaatcc 1560

aggaccagct atggccagtc acaaggacga tgaagaaaaa tttttcccta tgcacggcaa 1620

tctaatattt ggcaaagaag ggacaacggc aagtaacgca gaattagata atgtaatgat 1680

tacggatgaa gaagagattc gtaccaccaa tcctgtggca acagagcagt atggaactgt 1740

ggcaaataac ttgcagagct caaatacagc tcccacgact agaactgtca atgatcaggg 1800

ggccttacct ggcatggtgt ggcaagatcg tgacgtgtac cttcaaggac ctatctgggc 1860

aaagattcct cacacggatg gacactttca tccttctcct ctgatgggag gctttggact 1920

gaaacatccg cctcctcaaa tcatgatcaa aaatactccg gtaccggcaa atcctccgac 1980

gactttcagc ccggccaagt ttgcttcatt tatcactcag tactccactg gacaggtcag 2040

cgtggaaatt gagtgggagc tacagaaaga aaacagcaaa cgttggaatc cagagattca 2100

gtacacttcc aactacaaca agtctgttaa tgtggacttt actgtagaca ctaatggtgt 2160

ttatagtgaa cctcgcccta ttggaacccg gtatctcaca cgaaactcgt aa 2212

<210> 799
<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 799
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcttgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccatctcta caagcaaatc 780

tccggccaat caggagcttc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatccc 1560

aggaccagct atggccagtc acaaggacga tgaagaaaaa tttttcccta tgcacggcaa 1620

tctaatattt ggcaaagaag ggacaacggc aagtaacgca gaattagata atgtaatgat 1680

tacggatgaa gaagagattc gtaccaccaa tcctgtggca acagagcagt atggaactgt 1740

ggcaaataac ttgcagagct caaatacagc tcccacgact agaactgtca atgatcaggg 1800

ggccttacct ggcatggtgt ggcaagatcg tgacgtgtac cttcaaggac ctatctgggc 1860

aaagattcct cacacggatg gacactttca tccttctcct ctgatgggag gctttggact 1920

gaaacatccg cctcctcaaa tcatgatcaa aaatactccg gtaccggcaa atcctccgac 1980

gactttcagc ccggccaagt ttgcttcatt tatcactcag tactccactg gacaggtcag 2040 cgtggaaatt gagtgggagc tacagaaaga aaacagcaaa cgttggaatc cagagattca 2100

gtacacttcc aactacaaca agtctgttaa tgtggacttt actgtagaca ctaatggtgt 2160

ttatagtgaa cctcgcccta ttggaacccg gtatctcaca cgaaacttgt aa 2212

<210> 800
<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 800
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

gaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtgc ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tagcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tggatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500 tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaaggacga tgaagaaaaa tttttcccta tgcacggcaa 1620

tctaatattt ggcaaagaag ggacaacggc aagtaacgca gaattagata atgtaatgat 1680

tacggatgaa gaagagattc gtaccaccaa tcctgtggca acagagcagt atggaactgt 1740

ggcaaataac ttgcagagct caaatacagc tcccacgact agaactgtca atgatcaggg 1800

ggccttacct ggcatggtgt ggcaagatcg tgacgtgtac cttcaaggac ctatctgggc 1860

aaagattcct cacacggatg gacactttca tccttctcct ctgatgggag gctttggact 1920

gaaacatccg cctcctcaaa tcatgatcaa aaatactccg gtaccggcaa atcctccgac 1980

gactttcagc ccggccaagt ttgcttcatt tatcactcag tactccactg gacaggtcag 2040

cgtggaaatt gagtgggagc tacagaaaga aaacagcaaa cgttggaatc cagagattca 2100

gtacacttcc aactacaaca agtctgttaa tgtggacttt actgtagaca ctaatggtgt 2160

ttatagtgaa cctcgcccta ttggaacccg gtatctcaca cgaaacctgt aa 2212

<210> 801
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 801
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

gaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcaa cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020 caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 802
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 802
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

gaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480 aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagtgcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 803
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 803

```
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt        60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac       120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac       180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac       240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt       300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag       360

gccaaaaagg ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct       420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc       480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag       540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct       600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga       660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc       720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc       780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg       840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt       900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt       960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt      1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgt tcgggtcggc gcaccaaggc      1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg      1140

aacaacggaa gtcaagcggt gggacgctca tcctttact gcctggagta cttcccttcg       1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt      1260

cacagcagct acgctcacag ccagagttcg gatcgcttga tgaatcctct tattgatcag      1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg      1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct      1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac      1500

tttccttgaa cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca      1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat       1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt      1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg      1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg      1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca      1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg      1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg      1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc      2040
```

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 804
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 804
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

gaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccacctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500 tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 805
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 805
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggt 840

attttgactt taacagattc cactgccact tctcaccacg tgactggcag cgactcatta 900

acaacaactg ggattccgg cccaagaaac tcagcttcaa gctcttcaac atccaagtta 960

aagaggtcac gcagaacgat ggcacgacga ctattgccaa taaccttacc agcacggttc 1020 aagtgtttac ggactcggag tatcagctcc cgtacgtgct cgggtcggcg caccaaggct 1080

gtctcccgcc gtttccagcg gacgccttca tggtccctca gtatggatac ctcaccctga 1140

acaacggaag tcaagcggtg ggacgctcat ccttttactg cctggagtac ttcccttcgc 1200

agatgctaag gactggaaat aacttccaat tcagctatac cctcgaggat gtaccttttc 1260

acagcagcta cgctcacagc cagagtttgg atcgcttgat gaatcctctt attgatcagt 1320

atctgtacta cctgaacaga acgcaaggaa caacctctgg aacaaccaac caatcacggc 1380

tgctttttag ccaggctggg cctcagtcta tgtctttgca ggccagaaat tggctacctg 1440

ggccctgcta ccggcaacag agactttcaa agactgctaa cgacaacaac aacagtaact 1500

ttccttggac agcggccagc aaatatcatc tcaatggccg cgactcgctg gtgaatccag 1560

gaccagctat ggccagtcac aaaggacgat gaagaaaaat tttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagatag tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 806
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 806
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaggg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

actggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acctttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgctacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 807
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 807
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atcccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccctgg ggatactttg acttcaaccg cttccactgc 840

cacttcttac cacgtgactg gcagcgactc atcaacaaca actggggcgt gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcgacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 808
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 808
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacgag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500 ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgctacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 809
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 809
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acggaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattccc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggcgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020 ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg ggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 810
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 810
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

```
aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac      540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca      600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt      660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc      720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc      780

aacacctaca acggattctc caccccctgg ggatactttg acttcaaccg cttccactgc      840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa      900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag      960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa     1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc     1080

tttatggtgc cccagtacgg ctaccgtgga ctggtgaccg gcaacacttc gcagcaacag     1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc     1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac     1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa     1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg     1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag     1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt     1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga     1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt     1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct     1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc     1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg     1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt     1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac     1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc     1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag     2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc     2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact     2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa                     2205
```

<210> 811
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 811
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttca gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc ccttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ccggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaata actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg ggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgcccg gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 812
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 812
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaggctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cggaggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 813
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 813
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atcctccggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgcta gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 814
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 814
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgaca ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caaccccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagagc 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 815
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 815
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ctgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg tccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgccgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtgca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

```
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac     2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctattggaac ccgatacctt     2160

acccgacccc tttaa                                                      2175


<210> 816
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 816
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag       60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa      120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga      180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag      240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag      300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc      360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc      420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc      480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc      540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca      600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc      660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc      720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc      780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc      840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg      900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc      960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag     1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc     1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacaccga aaatcccacc     1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac     1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt     1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc     1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc     1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg     1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg     1500
```

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggcg cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 817
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 817
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacggggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagcgt ttacggacga cgactaccag 1020

```
ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc     1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc     1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac     1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt     1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc     1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc     1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg     1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg     1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc     1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc     1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc     1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc     1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac     1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc     1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac     1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc     1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc     2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac   2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt     2160

acccgacccc tttaa                                                      2175


<210> 818
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 818
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag       60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa      120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga      180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag      240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag      300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc      360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc      420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc      480
```

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caaccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttactagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagggggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaag cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 819
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 819
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg tccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

gagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctattggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 820
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 820
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacagcgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accgccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 821
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 821
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ctgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagacccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatgacc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtaccccc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacagg accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 822
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 822
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcctctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat gaagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 823
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 823
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaggcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca ccccgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 824
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 824
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

cacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gtcgaacggc atgaccaaca acctccgggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 825
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 825
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca gcgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

acgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cagactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 826
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 826
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caaccccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc gcgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggcg gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatac caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 827
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 827
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggtagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcggca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggggcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccctcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 828
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 828
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgagccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatgcaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 829
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 829
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatcct caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtgggccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac gagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggc caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 830
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 830
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg cctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accatcatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgcccccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 831
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 831

atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcctc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 832
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 832
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg ccaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcgggcgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

ggctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataata ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 833
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 833
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagcctccca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccgcc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 834
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 834
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gccgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgcgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 835
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 835

atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagcctccca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggа cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

```
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac     2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt     2160

acccgacccc tttaa                                                      2175


<210> 836
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 836
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag       60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa      120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga      180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag      240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag      300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc      360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc      420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc      480

aagcctccca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc      540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca      600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc      660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgccgccc      720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc      780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc      840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg      900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc      960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag     1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc     1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc     1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac     1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt     1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc     1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc     1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg     1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg     1500
```

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt cgccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 837
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 837
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgcgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 838
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 838
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gctgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag ccaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aaccttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggtgcaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccggagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 839
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 839
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aggcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgggactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgcgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa gggaaactcc 2040

```
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac     2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt     2160

acccgacccc tttaa                                                      2175


<210> 840
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 840
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag       60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa      120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga      180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag      240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag      300

gagaagctcg ccgacgacac gtccttcggg ggaaacctcg gaaaggcagt ctttcaggcc      360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc      420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc      480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc      540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca      600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc      660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc      720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc      780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc      840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg      900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc      960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag     1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc     1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc     1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac     1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt     1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc     1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc     1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg     1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg     1500
```

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggtgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 841
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (1652)..(1652)
<223> a, c, t, g, unknown or other

<400> 841
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga ggaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggа cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840 cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcagcat gctcatcacc ancgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 842
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 842
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

```
caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag      360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct      420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc      480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag      540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct      600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga      660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc      720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc      780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg      840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt      900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt      960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt     1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc     1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg     1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg     1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt     1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag     1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg     1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct     1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac     1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca     1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat tttccctat gcacggcaat      1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt     1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg     1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg     1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca     1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg     1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg     1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc     2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag     2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt     2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a              2211
```

<210> 843
<211> 2205
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 843
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccсctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg ggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860 cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 844
<211> 2234
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 844
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

```
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc     1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg     1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg     1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc     1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc     1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc     1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc     1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac     1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc     1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac     1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc     1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc     2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac     2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt     2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaaccgtgta ttcgtgtcag     2220

taaaatactg cctc                                                       2234
```

```
<210> 845
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 845
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
```

            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145   150   155   160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260   265   270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275   280   285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290   295   300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305   310   315   320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325   330   335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340   345   350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355   360   365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser

```
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445


Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460


Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
```

645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 846
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 846
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Val Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445


Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460


Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 847
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 847
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
```

```
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Gly Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
```

    450   455   460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465   470   475   480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Gly Asn
                485   490   495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500   505   510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515   520   525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530   535   540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545   550   555   560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565   570   575

Cys Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580   585   590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595   600   605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu

725 730 735

<210> 848
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 848
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Ala Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Gly Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Ser
                725                 730                 735
```

<210> 849
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

```
      polypeptide

<400> 849
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Leu Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Gly Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
```

```
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445


Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460


Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
```

```
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 850
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 850
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Cys Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Ser
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asp Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575
```

```
Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 851
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 851
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
```

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asn Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
```

```
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 852
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 852
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445


Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460


Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Val Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 853
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 853
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Gly Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
```

145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Phe Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Ser Asp Arg

```
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Thr Ala Ala Ser Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr Thr
            580                 585                 590

Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
```

```
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 854
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 854
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Glu Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460
```

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
485 490 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
530 535 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
580 585 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

```
<210> 855
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 855
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

```
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Ile Leu Thr Leu Thr Asp Ser Thr
        275                 280                 285


Ala Thr Ser His His Val Thr Gly Ser Asp Ser Leu Thr Thr Thr Gly
    290                 295                 300


Asp Ser Gly Pro Arg Asn Ser Ala Ser Ser Ser Ser Thr Ser Lys Leu
305                 310                 315                 320


Lys Arg Ser Arg Arg Thr Met Ala Arg Arg Leu Leu Pro Ile Thr Leu
                325                 330                 335


Pro Ala Arg Phe Lys Cys Leu Arg Thr Arg Ser Ile Ser Ser Arg Thr
            340                 345                 350


Cys Ser Gly Arg Arg Thr Lys Ala Val Ser Arg Arg Phe Gln Arg Thr
        355                 360                 365


Pro Ser Trp Ser Leu Ser Met Asp Thr Ser Pro Thr Thr Glu Val Lys
    370                 375                 380


Arg Trp Asp Ala His Pro Phe Thr Ala Trp Ser Thr Ser Leu Arg Arg
385                 390                 395                 400


Cys Gly Leu Glu Ile Thr Ser Asn Ser Ala Ile Pro Ser Arg Met Tyr
                405                 410                 415


Leu Phe Thr Ala Ala Thr Leu Thr Ala Arg Val Trp Ile Ala Ile Leu
            420                 425                 430


Leu Leu Ile Ser Ile Cys Thr Thr Thr Glu Arg Lys Glu Gln Pro Leu
        435                 440                 445


Glu Gln Pro Thr Asn His Gly Cys Phe Leu Ala Arg Leu Gly Leu Ser
    450                 455                 460


Leu Cys Leu Cys Arg Pro Glu Ile Gly Tyr Leu Gly Pro Ala Thr Gly
465                 470                 475                 480


Asn Arg Asp Phe Gln Arg Leu Leu Thr Thr Thr Thr Thr Val Thr Phe
                485                 490                 495


Leu Gly Gln Arg Pro Ala Asn Ile Ile Ser Met Ala Ala Thr Arg Trp
```

            500   505   510

Ile Gln Asp Gln Leu Trp Pro Val Thr Arg Thr Met Lys Lys Asn Phe
        515   520   525

Ser Leu Cys Thr Ala Ile Arg Gly Pro Tyr Leu Ala Trp Cys Gly Lys
    530   535   540

Ile Val Thr Cys Thr Phe Lys Asp Leu Ser Gly Gln Arg Phe Leu Thr
545   550   555   560

Arg Met Asp Thr Phe Ile Leu Leu Leu Trp Glu Ala Leu Asp Asn Ile
                565   570   575

Arg Leu Leu Lys Ser Ser Lys Ile Leu Arg Tyr Arg Gln Ile Leu Arg
            580   585   590

Arg Leu Ser Ala Arg Pro Ser Leu Leu His Leu Ser Leu Ser Thr Pro
        595   600   605

Leu Asp Arg Ser Ala Trp Lys Leu Ser Gly Ser Tyr Arg Lys Lys Thr
    610   615   620

Ala Asn Val Gly Ile Gln Arg Phe Ser Thr Leu Pro Thr Thr Thr Ser
625   630   635   640

Leu Leu Met Trp Thr Leu Leu Thr Leu Met Val Phe Ile Val Asn Leu
                645   650   655

Ala Leu Leu Glu Pro Gly Ile Ser His Glu Thr Cys
            660   665

<210> 856
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 856
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1   5   10   15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20   25   30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50   55   60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65   70   75   80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115   120   125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130   135   140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145   150   155   160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165   170   175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180   185   190

Asp Asp Ser Glu Met Arg Ala Ala Thr Gly Gly Ala Ala Val Glu Gly
        195   200   205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210   215   220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225   230   235   240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245   250   255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260   265   270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275   280   285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290   295   300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305   310   315   320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325   330   335

```
Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Leu Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605
```

```
Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620


Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640


Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655


Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670


Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685


Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700


Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720


Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 857
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 857
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                   10                  15


Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30


Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60


Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80


Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
```

            100   105   110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115   120   125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130   135   140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145   150   155   160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165   170   175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180   185   190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195   200   205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210   215   220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225   230   235   240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245   250   255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260   265   270

Phe Asp Phe Asn Arg Phe His Cys His Phe Leu Pro Arg Asp Trp Gln
        275   280   285

Arg Leu Ile Asn Asn Asn Trp Gly Val Arg Pro Lys Ala Met Arg Val
    290   295   300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305   310   315   320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325   330   335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340   345   350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355   360   365

Cys Gly Leu Val Thr Gly Asp Thr Ser Gln Gln Gln Thr Asp Arg Asn

370 375 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
405 410 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
420 425 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
435 440 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
450 455 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465 470 475 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
485 490 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
500 505 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
515 520 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
530 535 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545 550 555 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
565 570 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
580 585 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
595 600 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro

```
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 858
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 858
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                   10                  15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Glu Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140
```

```
Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415
```

```
Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685
```

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690   695   700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705   710   715   720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725   730

<210> 859
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 859
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1   5   10   15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20   25   30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50   55   60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65   70   75   80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115   120   125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130   135   140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145   150   155   160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Gly Thr
                165   170   175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser

```
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Pro Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Ala Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
```

```
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
```

725 730

<210> 860
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 860
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
130 135 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145 150 155 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
165 170 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
180 185 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
195 200 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
210 215 220

```
Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240


Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255


Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320


Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335


Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350


Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365


Arg Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380


Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400


Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415


Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430


Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445


Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460


Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480


Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495
```

```
Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510


Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525


Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540


Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560


Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575


Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590


Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605


Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620


Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640


Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655


Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670


Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685


Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700


Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720


Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 861
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
```

polypeptide

<400> 861
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1   5   10   15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20   25   30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Gln Gly
        35   40   45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50   55   60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65   70   75   80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115   120   125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130   135   140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145   150   155   160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165   170   175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180   185   190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195   200   205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210   215   220

Asp Ser Thr Arg Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225   230   235   240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245   250   255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr

```
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320


Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335


Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350


Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365


Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380


Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400


Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415


Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430


Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445


Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460


Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480


Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495


Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510


Arg Trp Ser Ala Arg Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525


Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
```

    530   535   540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545   550   555   560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565   570   575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580   585   590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595   600   605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610   615   620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625   630   635   640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645   650   655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660   665   670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675   680   685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690   695   700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705   710   715   720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725   730

<210> 862
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 862
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

```
Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Arg Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300
```

```
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575
```

```
Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Glu Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 863
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 863
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
```

```
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Ser Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335


Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
```

```
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
```

```
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 864
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 864
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110
```

```
Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335


Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350


Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365


Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400


Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415


Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430


Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445


Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460


Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480


Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560


Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Ser
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655
```

```
Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 865
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 865
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Pro Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Val Arg Thr Glu Glu Asp Ser
```

```
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Pro Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
```

```
            420                     425                     430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                     440                     445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                     455                     460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                     470                     475                     480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                     490                     495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                     505                     510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                     520                     525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                     535                     540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                     550                     555                     560

Val Ala Cys Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                     570                     575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                     585                     590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                     600                     605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                     615                     620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                     630                     635                     640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                     650                     655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                     665                     670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                     680                     685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
```

```
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 866
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 866
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190
```

```
Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335


Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350


Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365


Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380


Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400


Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415


Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430


Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445


Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460
```

```
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480


Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560


Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Ala Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu
```

```
<210> 867
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 867
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Gly Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

225   230   235   240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245   250   255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260   265   270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275   280   285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290   295   300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305   310   315   320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Ala Phe Thr Asp
                325   330   335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340   345   350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355   360   365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370   375   380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385   390   395   400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405   410   415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420   425   430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435   440   445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450   455   460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465   470   475   480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485   490   495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr

            500   505   510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515   520   525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530   535   540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545   550   555   560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565   570   575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580   585   590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595   600   605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610   615   620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625   630   635   640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645   650   655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660   665   670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675   680   685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690   695   700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705   710   715   720

Thr Arg Pro Leu

<210> 868
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

```
<400> 868
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270
```

```
Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Val Pro Pro Gln Pro Asn Gly Met Thr Asn
            500                 505                 510

Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe
        515                 520                 525

Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly
    530                 535                 540
```

```
Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg Val
545                 550                 555                 560


Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser Thr
                565                 570                 575


Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly
            580                 585                 590


Ser Val Trp Met Glu Gly Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595                 600                 605


Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
    610                 615                 620


Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625                 630                 635                 640


Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
                645                 650                 655


Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
            660                 665                 670


Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
        675                 680                 685


Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
    690                 695                 700


Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705                 710                 715                 720


Arg Pro Leu



<210> 869
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 869
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
```

```
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Val Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
```

305   310   315   320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325   330   335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340   345   350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355   360   365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370   375   380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385   390   395   400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405   410   415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420   425   430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435   440   445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450   455   460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465   470   475   480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485   490   495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500   505   510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515   520   525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530   535   540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545   550   555   560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565   570   575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro

            580   585   590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595   600   605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610   615   620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625   630   635   640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645   650   655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660   665   670

Trp Glu Leu Lys Lys Glu Asn Ser Glu Arg Trp Asn Pro Glu Ile Gln
        675   680   685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690   695   700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705   710   715   720

Thr Arg Pro Leu

<210> 870
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 870
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Ser Glu
65   70   75   80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115   120   125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130   135   140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145   150   155   160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165   170   175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180   185   190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195   200   205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210   215   220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225   230   235   240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245   250   255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260   265   270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275   280   285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290   295   300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305   310   315   320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325   330   335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340   345   350

```
Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620
```

```
Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Ala Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 871
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 871
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Pro Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
```

115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn

385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
435 440 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
450 455 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465 470 475 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Thr Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Pro Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu

            660   665   670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675   680   685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690   695   700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705   710   715   720

Thr Arg Pro Leu

<210> 872
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 872
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65   70   75   80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115   120   125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130   135   140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145   150   155   160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Leu Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

```
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Lys Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

```
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 873
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 873
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Pro Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
```

```
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
```

```
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu


<210> 874
```

```
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 874
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240
```

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
435 440 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr His Lys Asn Trp
450 455 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465 470 475 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Ser Asn Gly Met Thr
500 505 510

Asn Asn Leu Arg Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 875
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 875
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu

```
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
```

```
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335


Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350


Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365


Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380


Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400


Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415


Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430


Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445


Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460


Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480


Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
```

```
545                 550                 555                 560


Val Ala Tyr Ser Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Thr Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Arg Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 876
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 876
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45
```

```
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320
```

```
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Ala Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

Gly Gly Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595   600   605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610   615   620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625   630   635   640

Thr Pro Val Pro Gly Asn Thr Thr Ser Phe Ser Asp Val Pro Val Ser
                645   650   655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660   665   670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675   680   685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690   695   700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705   710   715   720

Thr Arg Pro Leu

<210> 877
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 877
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65   70   75   80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp

```
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Val Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Gly Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Gly Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335


Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350


Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
```

```
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Leu Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
```

```
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 878
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 878
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125
```

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335


Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350


Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365


Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380


Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400
```

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
435 440 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
450 455 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465 470 475 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Ala
595 600 605

Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
610 615 620

Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625 630 635 640

Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
645 650 655

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
660 665 670

```
Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
        675                 680                 685


Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
    690                 695                 700


Thr Gly Glu Cys Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705                 710                 715                 720


Arg Pro Leu



<210> 879
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 879
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
```

```
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Leu Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Gly
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
```

```
        435                 440                 445

Phe Asn Glu Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Ala Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
```

705 710 715 720

Thr Arg Pro Leu

<210> 880
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 880
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
195 200 205

```
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Ile Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480
```

```
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560


Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu


<210> 881
<211> 724
<212> PRT
```

```
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 881
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
```

```
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
```

```
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Leu Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu



<210> 882
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 882
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15
```

```
Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Ala
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Gly
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Gly Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335


Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350


Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365


Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380


Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400


Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415


Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430


Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445


Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460


Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480


Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560
```

```
Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 883
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 883
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
```

```
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255


Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270


Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285


Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300


Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Ala
305                 310                 315                 320


Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
```

```
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
```

        595   600   605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610   615   620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625   630   635   640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645   650   655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660   665   670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675   680   685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690   695   700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705   710   715   720

Thr Arg Pro Leu

<210> 884
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 884
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65   70   75   80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

```
Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Pro Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365
```

```
Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380


Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400


Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415


Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430


Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445


Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460


Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480


Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560


Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640
```

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 885
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 885
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile

```
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
```

```
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
```

```
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu



<210> 886
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 886
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175
```

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Pro Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445
```

```
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ala Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720
```

Thr Arg Pro Leu

<210> 887
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 887
```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
```

```
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
```

485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 888
<211> 724
<212> PRT
<213> Artificial Sequence

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 888
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Ala Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205


Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220


Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240


Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255
```

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Ala
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Leu Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
435 440 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
450 455 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465 470 475 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

```
Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560


Val Val His Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 889
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 889
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
```

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Gly Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
```

```
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
```

```
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Gly Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu


<210> 890
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 890
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60
```

```
Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605
```

```
Ala Lys Ile Pro Glu Thr Gly Val His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 891
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide


<220>
<221> MOD_RES
<222> (551)..(551)
<223> Any amino acid

<400> 891
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80
```

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115   120   125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130   135   140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145   150   155   160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165   170   175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180   185   190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195   200   205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210   215   220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225   230   235   240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245   250   255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260   265   270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275   280   285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290   295   300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305   310   315   320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325   330   335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340   345   350

```
Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365


Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380


Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400


Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415


Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430


Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445


Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460


Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480


Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Ser Met Leu Ile Thr Xaa Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560


Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620
```

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625   630   635   640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645   650   655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660   665   670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675   680   685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690   695   700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705   710   715   720

Thr Arg Pro Leu

<210> 892
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 892
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
```

```
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
```

```
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 893
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 893
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                   10                  15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160
```

```
Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430
```

```
Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700
```

```
Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720


Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 894
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 894
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140


Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160


Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175


Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190


Met Ser Ala Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala Asp
```

```
        195                 200                 205

Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Met
    210                 215                 220

Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro Ser
225                 230                 235                 240

Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp Gly
                245                 250                 255

Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
            260                 265                 270

Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln Arg
        275                 280                 285

Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val Lys
    290                 295                 300

Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr Thr
305                 310                 315                 320

Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Asp
                325                 330                 335

Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys Leu
            340                 345                 350

Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr Ala
        355                 360                 365

Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser Phe
    370                 375                 380

Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn Asn
385                 390                 395                 400

Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser Phe
                405                 410                 415

Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp Gln
            420                 425                 430

Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln Phe
        435                 440                 445

Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe
    450                 455                 460

Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly Val
```

```
465                 470                 475                 480


Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu Leu
                485                 490                 495


Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr Asn
            500                 505                 510


Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe
        515                 520                 525


Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly
    530                 535                 540


Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg Val
545                 550                 555                 560


Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser Thr
                565                 570                 575


Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly
            580                 585                 590


Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595                 600                 605


Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
    610                 615                 620


Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625                 630                 635                 640


Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
                645                 650                 655


Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
            660                 665                 670


Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
        675                 680                 685


Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
    690                 695                 700


Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705                 710                 715                 720


Arg Pro Leu


<210> 895
```

<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 895
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Thr Leu Ala Val
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
            740
```

<210> 896
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 896
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctctagaact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg taccggcaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaaactttg gcggtgcctt ttaaggcaca ggcgcagacc 1800

ggttgggttc aaaaccaagg aatacttccg ggtatggttt ggcaggacag agatgtgtac 1860

ctgcaaggac ccatttgggc caaaattcct cacacggacg gcaactttca cccttctccg 1920

ctgatgggag ggtttggaat gaagcacccg cctcctcaga tcctcatcaa aaacacacct 1980

```
gtacctgcgg atcctccaac ggccttcaac aaggacaagc tgaactcttt catcacccag     2040

tattctactg gccaagtcag cgtggagatc gagtgggagc tgcagaagga aaacagcaag     2100

cgctggaacc cggagatcca gtacacttcc aactattaca agtctaataa tgttgaattt     2160

gctgttaata ctgaaggtgt atatagtgaa ccccgcccca ttggcaccag atacctgact     2220

cgtaatctgt aa                                                         2232


<210> 897
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 897
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
                20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
            35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
        50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
                100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
            115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
        130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
                180                 185                 190
```

```
Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Gln Ser Ser Gln Thr Pro Arg Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 898
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 898
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Ile Leu Gly Thr Gly Thr Ser Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Thr Arg Thr Asn
            580                 585                 590


Pro Glu Ala Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605


Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620


Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640


Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655


Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670


Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685


Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700


Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720


Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735


Arg Tyr Leu Thr Arg Asn Leu
            740


<210> 899
<211> 743
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 899
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Ile Leu Gly Thr Gly Thr Ser Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Asn Gly Gly Thr
            580                 585                 590

Ser Ser Ser Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
            740

<210> 900
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 900
```

```
Thr Leu Ala Val Pro Phe Lys
1               5


<210> 901
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 901
Lys Phe Pro Val Ala Leu Thr
1               5


<210> 902
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 902
Leu Ala Val Pro Phe Lys
1               5


<210> 903
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 903
Ala Val Pro Phe Lys
1               5


<210> 904
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 904
Val Pro Phe Lys
1


<210> 905
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide
```

```
<400> 905
Thr Leu Ala Val Pro Phe
1               5


<210> 906
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 906
Thr Leu Ala Val Pro
1               5


<210> 907
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 907
Thr Leu Ala Val
1


<210> 908
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 908
Ser Val Ser Lys Pro Phe Leu
1               5


<210> 909
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 909
Phe Thr Leu Thr Thr Pro Lys
1               5


<210> 910
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
```

```
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 910
Met Asn Ala Thr Lys Asn Val
1               5


<210> 911
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 911
Gln Ser Ser Gln Thr Pro Arg
1               5


<210> 912
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 912
Ile Leu Gly Thr Gly Thr Ser
1               5


<210> 913
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 913
Thr Arg Thr Asn Pro Glu Ala
1               5


<210> 914
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 914
Asn Gly Gly Thr Ser Ser Ser
1               5


<210> 915
<211> 7
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 915
Tyr Thr Leu Ser Gln Gly Trp
1               5


<210> 916
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 916
aagtttcctg tggcgttgac t                                                21


<210> 917
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 917
actttggcgg tgccttttaa g                                                21


<210> 918
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 918
agtgtgagta agcctttttt g                                                21


<210> 919
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 919
tttacgttga cgacgcctaa g                                                21


<210> 920
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
```

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 920
atgaatgcta cgaagaatgt g 21

<210> 921
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 921
cagtcgtcgc agacgcctag g 21

<210> 922
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 922
attctgggga ctggtacttc g 21

<210> 923
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 923
acgcggacta atcctgaggc t 21

<210> 924
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 924
aatgggggga ctagtagttc t 21

<210> 925
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 925
tatactttgt cgcagggttg g   21

<210> 926
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 926
Ser Ala Asp Asn Asn Asn Ser Glu Tyr
1   5

<210> 927
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 927
Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
1   5

<210> 928
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 928
Val Pro Gln Tyr Gly Tyr Leu Thr Leu
1   5

<210> 929
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 929
Thr Thr Ser Thr Arg Thr Trp Ala Leu
1   5

<210> 930
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 930
Tyr His Leu Asn Gly Arg Asp Ser Leu
1   5

<210> 931
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 931
Ser Gln Ala Val Gly Arg Ser Ser Phe
1   5

<210> 932
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 932
Val Pro Ala Asn Pro Ser Thr Thr Phe
1   5

<210> 933
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 933
Phe Pro Gln Ser Gly Val Leu Ile Phe
1   5

<210> 934
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 934
Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
1   5   10   15

<210> 935
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

```
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 935
Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met
1               5                   10                  15


<210> 936
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 936
Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg
1               5                   10                  15


<210> 937
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 937
Gly Ala Ser Asp Ile Arg Gln Ser Arg Asn Trp Leu Pro
1               5                   10


<210> 938
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 938
Gly Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val
1               5                   10                  15


<210> 939
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 939
Leu Asp Arg Leu Met Asn Pro Leu Ile
1               5


<210> 940
<211> 9
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 940
Gln Pro Ala Lys Lys Arg Leu Asn Phe
1   5

<210> 941
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 941
Gln Ala Val Arg Thr Ser Leu
1   5

<210> 942
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 942
Leu Ala Lys Glu Arg Leu Ser
1   5

<210> 943
<211> 106
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<220>
<221> modified_base
<222> (1)..(13)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (16)..(48)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (53)..(60)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (62)..(97)
<223> a, c, u, g, unknown or other

```
<220>
<221> modified_base
<222> (99)..(100)
<223> a, c, u, g, unknown or other

<220>
<221> modified_base
<222> (102)..(106)
<223> a, c, u, g, unknown or other

<400> 943
nnnnnnnnnn nnnugnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnug ugnnnnnnnn       60

unnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnncnn cnnnnn                     106
```